

501

```

201 TATCCGTCAG GGTTCGAGG AAGGCGGCAA AACGTCCGAA CAGGGCGGTT
251 TGGTTCACGT CGGCATACCA CGCGCTGACC CCCTGCCACA TCGGATTGCC
301 GCCTTCGGGC AGCATCCAGC CCAATATCAT GCGTTCTACC GCCTGCTTCC
351 AGGTGAACAG CTGATCCGTG CCGCCGCGCA TTTCTCCGTC CAAACCCAG
401 CGGACGTTCA AATCGGCAAC CATGTCGTGC AAAAGCGGCA AATCGTCTC
451 AGTCAGTCCG AAATGGCGCA ACACGGGCGC GGTTCCTAAA AGCACAAGCA
501 CTTTATCGAC TTCAAATCGG CTTTCCAACA AGTCGAACAG GCATGACAAA
551 GCATGAAACA GCGGTTGTCG GCGGCTGATT TTCACATCCG AAACGGAATA
601 CGGCAATGCC TCGCGCCCGG GCTGCGCCTG TCCGAACACG GCTTCGATAA
651 AAGGCGTATA GGATTGCATA TTCGGGGTTA A

```

This corresponds to the amino acid sequence <SEQ ID 768; ORF 217.a>:

```

a217.pep
  1 VADDGVQRQL SGKLRQFGFR LPFDPFVFEA LDCLLVIAFD LEQCFKQIPA
 51 TRHFPVNRRL LPPYPYNIQ GFEEGGKTSE QGGLVHVIGIP RADPLPHRIA
101 AFGQHPAQYH AFYRLLPGEQ LIRAAAHFSV QTPADVQIGN HVVQKRQIVL
151 SQSEMAQHGR GF*KHKHFID FKSAFQQVEQ A*QSMKQRLS AADFHIRNGI
201 RQCLRAGLRL SEHGFDKRR I GFDIRG*

```

m217/a217 90.3% identity in 226 aa overlap

m217.pep	10	20	30	40	50	60
	MADDGVRRLSGKLRQFGFRLPFDPFVFKVLDXLLVIGFSLEQCFKQIPATRHFPADRCG					
a217	VADDGVQRQLSGKLRQFGFRLPFDPFVFEALDCLLVIAFDLEQCFKQIPATRHFPVNRRL					
m217.pep	70	80	90	100	110	120
	LPPYPYNIQGFEEGGKTSEHGGLIHVGIPRADILPHRIA AFGQHPAQYHAFYRLLPGEQ					
a217	LPPYPYNIQGFEEGGKTSEQGGLVHVIGIPRADPLPHRIA AFGQHPAQYHAFYRLLPGEQ					
m217.pep	130	140	150	160	170	180
	LIRAAAHFSVQTPVDVQIGNHVQKRQIVLSQSETAQHGRGFXKHKHFIDFKSAFQQVEQ					
a217	LIRAAAHFSVQTPADVQIGNHVQKRQIVLSQSEMAQHGRGFXKHKHFIDFKSAFQQVEQ					
m217.pep	190	200	210	220		
	AXQSMKQRLAAADFHVXHGIRQCLRTGLRLSEHGFDKRRIGFDIRGX					
a217	AXQSMKQRLSAAADFHIRNGIRQCLRAGLRLSEHGFDKRRIGFDIRGX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 769>:

```

g218.seq
  1 atggttgccg tggatcctta tacggcaaaa gtggtcaaca ccatgccgcg
 51 caatcagggt tggatcacca ctatggatga aatccacggc gatatgatgc
101 tcggtgcggc aggcgattat cttttggaaa cggcagcttc actgaccatt
151 attatggttg tcagcggctt gtacctttgg tgggcgaaac agcgcggcat
201 taaagcgatg ctgctgccgc caaaaagcag ggcgcgttct tgggtggcgga
251 atctgcacgg cgcgtttgga acttgggtgt cgttgatttt actgttggtc
301 tgcctgtcgg gtattgcttg ggcaggtatt tggggcgga aattcgtgca
351 ggcttggaat cagttcccgg ccggcaaatg ggggtgcgaa cgaaccccg
401 tttcaatcgt gccgaccac gccgaggtat tgaatgacgg caagggttaag
451 gaagtgccgt ggattttgga gcttatgcct atgcctgtct cagggaacgac
501 tgtgggtgaa aacggcatta accccaccga gcccataaac attggaaacc
551 gtcgaccgtt tcgcgcggga aatcggtttc aaagggcggt atcagttgaa
601 tttgcccataa ggcgaggacg ggggtatggac tttgtcgag gattctatga
651 gttatga

```

This corresponds to the amino acid sequence <SEQ ID 770; ORF 218.ng>:

```

g218.pep
  1 MVAVDPYTAK VVNTMPRNQG WYHTMDEIHG DMMLGAAGDY LLETAASLTI

```

m218.seq

m218.pep

m218/g218

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 773>:

a218.seq

```

1 ATGGTCGCGG TCGATCCTTA TACGGCAAAA GTGGTCAGTA CCATGCCGCG
51 CAATCAGGGT TGGTATTACG CGATGGATGA AATCCACAGC GATATGATGC
101 TCGGTTTCGAC AGGTGATTAT CTTTGGAAA CGGCTGCATC GCTGACGATT
151 ATCATGATAA TCAGCGGTTT GTACCTTTGG TGGGTGAAAC GGCGCGGCAT
201 CAAGGCGATG CTGCTGCCGC CAAAAGGCAG GGCGCGTTCT TGGTGGCGGA
251 ATCTGCACGG CGCGTTTGGA ACTTGGGTGT CGTTGATTTT ACTGTTGTTC
301 TGCCTGTCGG GTATTGCTTG GGCAGGTATT TGGGGCGGCA AGTTCGTGCA
351 GGCTTGGAGT CAGTTCCTCG CAGGCAAATG GGGTGTGCGA CCGAACCCTG
401 TTTCACTCGT GCCGACCCAC GGCGAGGTAT TGAATGACGG CAAGGTTAAG
451 GAAGTGCCGT GGGTTTTGGA GCTTACGCCT ATGCCTGTTT CAGGGACGAC
501 TGTGGGCAAA GACGGTATTA ACCCTGACGA GCCGATGACA TTGGAACCG
551 TCGACCGTTT TCGCGG.GA AATCGGTTTC AAAGGGCGTT ATCAGCTGAA
601 TTTGCCCAAA GGCGAGGACG GCGTATGGAC TTTGTGCGAG GATTCTATGA
651 GTTA

```

This corresponds to the amino acid sequence <SEQ ID 774; ORF 218.a>:

a218.pep

```

1 MVAVDPYTAK VVSTMPRNQG WYYAMDEIHS DMMLGSTGDY LLETAASLTI
51 IMIISGLYLW WVKRRGIKAM LLPPKGRARS WWRNLHGAFG TWVSLILLLF
101 CLSGIAWAGI WGGKFVQAWS QFPAGKWGVE PNPVSVVPTH GEVLNDGKVK
151 EVPWVLELTP MPVSGTTVGK DGINPDEPMT LETVDRFARX NRFQALSAE
201 FAQRRGRMD FVAGFYEL

```

m218/a218 95.9% identity in 218 aa overlap

m218.pep	10	20	30	40	50	60
	MVAVDPYTAKVVSTMPRNQGWYYTMD	DEIHS	DMMLGAAGDYL	LLETAASLTI	IMVVSGLYLW	
a218	MVAVDPYTAKVVSTMPRNQGWYYAMDEIHS	DMMLGSTGDYL	LLETAASLTI	IMIISGLYLW		
m218.pep	70	80	90	100	110	120
	WVKRRGIKAMLLPSKXARS	WWRNLHGT	FGTWVSLILLLF	CLSGIAWAGI	WGGKFVQAWS	
a218	WVKRRGIKAMLLPPKGRARS	WWRNLHGAFG	TWVSLILLLF	CLSGIAWAGI	WGGKFVQAWS	
m218.pep	130	140	150	160	170	180
	QFPAGKWGVEPNPVSVVPTH	GEVLNDGKVKEVPWVLELTP	MPVSGTTVGK	DGINPDEPMT		
a218	QFPAGKWGVEPNPVSVVPTH	GEVLNDGKVKEVPWVLELTP	MPVSGTTVGK	DGINPDEPMT		
m218.pep	190	200	210			
	LETVDRFARXNRFQALS	VEFAQRRGRMD	FVAGFYEL			
a218	LETVDRFARXNRFQALS	AEFAQRRGRMD	FVAGFYEL			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 775>:

```
g219.seq
1  atgacggcaa ggttaaggaa gtgccgtgga ttttggagct tatgcctatg
51  cctgtctcag ggacgactgt gggtgaaaac ggcattaacc ccaccgagcc
101 caataacatt ggaaccgctc gaccgtttcg cgcgggaaat cggtttcaaa
151 gggcgttatc agttgaattt gcccaaaggc gaggacgggg tatggacttt
201 gtccgaggat tctatgagtt atgacatgat cagcccgttt gccgaccgca
251 cggtagatat cgaccagtac agcggcgaga ttcttgccga catccgtttt
301 gacgattaca acccgttcgg caaatattat gcggaagca ttgcgtgca
351 tatggggact ttgggctggt ggagcgtgtt gggaacgct gtgttctgcc
401 ttgccgtgat ttttatcggc atcagcggct gcgtgatgtg gtggaaacgc
451 cgtccgtccg gcgtggcggg cattgttcct ccggcgcaaa aaatcaaact
501 gcccgtctgg tgggcgatgg cattgccgct gctgttgatt gcaactgctt
551 tcccgaccgc gctgcttgcc attgccgtga tttggctgtt ggataccttg
601 ctgctgtcgc ggattcctgt gttgaggaaa tggtttaaat ga
```

This corresponds to the amino acid sequence <SEQ ID 776; ORF 219.ng>:

```
g219.pep
1  MTARLRKCRG FWSLCLCLSQ GRLWVKALT PPSITLETV DRFAREIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGEILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV VFCLAVIFIG ISGCVMWKR
151 RPSGVAGIVP PAQIKLPVW WAMALPLLLI ALLFPTALLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 777>:

```
m219.seq
1  ATGACGGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGaCyGt gGGCAAAGAC GGCATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGCTTTGC GCGGnGAAAT CGGTTTCAAA
151 GGGCGTTATC AGTTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCCTTT GCCGACCGCA
251 CCGTACATAT CGACCAGTAC AGCGGCAAAA TCCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGTGCA
351 TATGGGGACT CTGGGCTGGT GGAGCGTGTT GGCGAACGTC TTGTTCTGCC
401 TTGCCGTCAT TTTTATCGGT ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGACCG GAGCGGTGGG CATCGTTCCG CCGGCGCAGA AAGTCAAGCT
501 GCCGGTTTGG TGGATGATGG CATTGCCGCT ATTGGCAATC GCACTGCTCT
551 TCCCGACCTC ACTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCTCTG TTTGAGGAGA TGGTTTAAAT GA
```

This corresponds to the amino acid sequence <SEQ ID 778; ORF 219>:

```
m219.pep
1  MTARLRKCRG FWSLRLCLFQ GRXWAKTALT LTSRXHWKPS TALRGEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG T LGWWSVLANV LFCLAVIFIG ISGCVMWKR
151 RPTGAVGIVP PAQVKLPVW WMMALPLLAI ALLFPTSLLA IAVIWLLDTL
201 LLSRIPVLRK WFK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 219 shows 86.9% identity over a 213 aa overlap with a predicted ORF (ORF 219.ng) from *N. gonorrhoeae*:

```
m219/g219
10      20      30      40      50      60
m219.pep MTARLRKCRGFWSLRLCLFQGRXWAKTALTLSRXHWKPSALRGEIGFKGRYQLNLPKG
||| ||| ||| ||| : ||| | : : ||| ||| ||| |||
g219      MTARLRKCRGFWSLCLCLSQGRLWVKALTTPSPITLETVDRFAREIGFKGRYQLNLPKG
10      20      30      40      50      60

70      80      90      100     110     120
m219.pep EDGVWTLSDSMSYDMISPFADRTVHIDQYSGKILADIRFDDYNPFGKFMAASIALHMG
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g219      EDGVWTLSDSMSYDMISPFADRTVHIDQYSGEILADIRFDDYNPFGKFMAASIALHMG
```

505

	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVL	ANVLFCL	AVIFIGIS	GCVMWVK	RRTGAVG	IVPPAQK
g219	LGWWSVL	ANVVFCL	AVIFIGIS	GCVMWVK	RPSGAVG	IVPPAQK
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTS	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
g219	ALLFPTA	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 779>:

```

a219.seq
1  ATGACGCAA GGTAAAGGAA GTGCCGTGGG TTTTGGAGCT TACGCCTATG
51  CCTGTTTCAG GGACGACTGT GGGCAAAGAC GGTATTAACC CTGACGAGCC
101 GATGACATTG GAAACCGTCG ACCGTTTTCG GCGG.GAAAT CGGTTTCAAA
151 GGGCGTTATC AGCTGAATTT GCCCAAAGGC GAGGACGGCG TATGGACTTT
201 GTCGCAGGAT TCTATGAGTT ACGACATGAT CAGCCCGTTT GCTGACCGCA
251 CGGTGCATAT CGACCAGTAC AGCGGCAAGA TTCTTGCCGA CATCCGTTTT
301 GACGATTACA ACCCGTTCGG CAAATTTATG GCGGCAAGCA TTGCGCTGCA
351 TATGGGGACT TTGGGCTGGT GGAGCGTGTG GCGGAACGTT TTGTTCTGCC
401 TTGCCGTGAT TTTTATCGGC ATCAGCGGCT GCGTGATGTG GTGGAAACGC
451 CGTCCGTCCG GCGCGGTGGG CATGGTTCCG CCGGCGCAAA AAATCAAGCT
501 GCCCGTCTGG TGGGCAATGG CGGTGCCGCT GCTGCTGATT GCATTGCTTT
551 TCCCGACCGC GTTGCTTGCC ATTGCCGTGA TTTGGCTGTT GGATACGCTG
601 CTGTTGTCGC GGATTCTCTG TTTGAGGAGA TGGTTTAAAT GA
  
```

This corresponds to the amino acid sequence <SEQ ID 780; ORF 219.a>:

```

a219.pep
1  MTARLRKCRG FWSLRCLFQ GRLWAKTVLT LTSR*HWKPS TVLRXEIGFK
51  GRYQLNLPKG EDGVWTLSD SMSYDMISPF ADRTVHIDQY SGKILADIRF
101 DDYNPFGKFM AASIALHMG LGWWSVLANV LFCLAVIFIG ISGCVMWWR
151 RPSGAVGMVP PAQKIKLPVW WAMAVPLLLI ALLFPTALLA IAVIWLDDTL
201 LLSRIPVLRW WFK*
  
```

m219/a219 94.8% identity in 213 aa overlap

	10	20	30	40	50	60
m219.pep	MTARLRKCRG	FWSLRCLFQ	GRLWAKTVLT	LTSR*HWKPS	TVLRXEIGFK	GRYQLNLPKG
a219	MTARLRKCRG	FWSLRCLFQ	GRLWAKTVLT	LTSR*HWKPS	TVLRXEIGFK	GRYQLNLPKG
	10	20	30	40	50	60
	70	80	90	100	110	120
m219.pep	EDGVWTLSD	SMSYDMISPF	ADRTVHIDQY	SGKILADIRE	DDYNPFGKFM	AASIALHMG
a219	EDGVWTLSD	SMSYDMISPF	ADRTVHIDQY	SGKILADIRE	DDYNPFGKFM	AASIALHMG
	70	80	90	100	110	120
	130	140	150	160	170	180
m219.pep	LGWWSVL	ANVLFCL	AVIFIGIS	GCVMWVK	RRTGAVG	IVPPAQK
a219	LGWWSVL	ANVLFCL	AVIFIGIS	GCVMWVK	RPSGAVG	IVPPAQK
	130	140	150	160	170	180
	190	200	210			
m219.pep	ALLFPTS	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
a219	ALLFPTA	LLAIAVI	WLLDTLL	LSRIPVL	RRLRWFK	X
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 781>:

```
g221.seq
1  atgcacgacc acggcgccat ggatcgccgc ctccccgctt tcggaagtct
51  gatcgggcga gccgtaaata adatcgacgc tgacggattt gaaccttgcc
101 tcacgggcgg catcgatgac ttctttgggt tcttcgtagc ttgggatgcy
151 gttgactgcc gcctgcactt tggggtcgaa atcctgaatg ccgacgtca
201 tgcggttgaa gccgagtcct cggagcatga ggacggtgtc gcggtgact
251 ttgcgcgggt cgatttcgat ggaatattcg ccggacggta tcagttcgaa
301 atgtttgcgg atcatgcgga agacacgttc gatctgttcg tcgctcaaaa
351 aggtcggcgt gccgccgcgc aagtgcagtt gggcaagctg gtgccgtccg
401 ttcagatgtg gagcgagcag ttccatttct ttttcaagat attcgatgta
451 ggtatcggcg cggcttttgt ctttgggtgat gattttgttg cagccgcagt
501 agtagcagat ggtgttgcaa aacggaatgt gaatgtaaag ggaaagcgg
551 ttgtttaa
```

This corresponds to the amino acid sequence <SEQ ID 782; ORF 221.ng>:

```
g221.pep
1  MHDHGAMDRR LPAFGSLMRR AVNXIDADGF EPCLTGGIDD FFGFFVALDA
51  VDCRLHFGVE ILNADAHAVE AESAEHEDGV AADFARVDFD GIFAGRYQFE
101 MFADHAEDTF DLFVAQKGRR AAAEVQLGKL VPSVQMWSEQ FHHFFKIFDV
151 GIGAAAFVFGD DFVAAAVVAD GVAKRNVNVK GKRFV*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 783>:

```
m221.seq
1  ATGGyGGTTT TGATGcwcmg AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGAAGAC
301 ACGTTCGATC TGTTCTGTCG TCAAAAAGGt GCGTGCCCG CCGAAGTGCA
351 GTTGGGCAAG CTGGTGCCGT CCGTTCAGAT GTGGAGCGAG CAGTTCATT
401 TCTTTTCAA GATATTCGAT GTAGGCATCG GCGGGCTTT TGTCTTTGGT
451 GATGATTTG TTGCAGCCGC AGTAGTAGCA GATGGTGTG CAGAACGGAA
501 TGTGAATGTA AAGGGAAAGC GGTGTGTTA A
```

This corresponds to the amino acid sequence <SEQ ID 784; ORF 221>:

```
m221.pep
1  MXVLMXRSLV RQAVNQIDAD GFEPFRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAH VEAESAHEH GVAADFARVD FDGVFAGGDX LEMFAYHAED
101 TFDLFVAQKG ACPAEVQLGK LVPSVQMWSE QFHHFFKIFD VGIGAAAFVFG
151 DDFVAAAVVA DGVAERNVNV KGKRFV*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 221 shows 87.6% identity over a 170 aa overlap with a predicted ORF (ORF 221.ng) from *N. gonorrhoeae*:

m221/g221

	10	20	30	40	50
m221.pep	MXVLMXRSLVRQAVNQIDADGFEPFRFARRIDDFGFFVTLDAVDRRLHFGVE				
	: :				
g221	MHDHGAMDRRLPAFGSLMRRAVNXIDADGFEPCLTGGIDDFFGFFVALDAVDCRLHFGVE				
	10	20	30	40	50
	60	70	80	90	100
m221.pep	ILNADAHAVEAESAEHEDGVAADFARVDFDGVFAGGDXLEMFAYHAEDTFDLFVAQKGA-				
g221	ILNADAHAVEAESAEHEDGVAADFARVDFDGFIFAGRYQFEMFADHAEDTFDLFVAQKGRR				
	70	80	90	100	110
	120	130	140	150	160
	170				

507

```

m221.pep    CPAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
             |||||||
g221        AAAEVQLGKLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVK
             130      140      150      160      170      180

m221.pep    GKRFVX
             |||||
g221        GKRFVX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 785>:

```

a221.seq
1   ATGGTGGTTT TGATGCTCCG AAGTCTGGTG CGGCAGGCCG TAAATCAAAT
51  CGACGCTGAC GGATTTGAAC CCCGCTTCGC GCGCCGCATC GATGACTTCT
101 TTGGTTTCTT CGTAACTTTG GATGCGGTTG ACCGCCGCCT GCACTTTGGG
151 GTCGAAATCC TGAATGCCGA TGCTCATGCG GTTGAAGCCG AGTCTGCCGA
201 GCATGAGGAC GGTGTCGCGG CTGACTTTGC GCGGGTCGAT TTCGATGGAG
251 TATTCGCCGG TGGGGATTAA CTCGAAATGT TTGCGTATCA TCGGGAAGAC
301 ACGTTTCGAT TGGTCGTCGC TCAAAAAGGT CGCGGTGCCG CCGCCGAAGT
351 GCAGTTGGGC AAGCTGGTGC CGTCCGTTCA GATGTGGAGC GAGCAGTTCC
401 ATTTCTTTTT CAAGAAATTC GATGTAGGCA TCGGCGCGGC TTTTGTCTTT
451 GGTGATGATT TTGTTGCAGC CGCAGTAGTA GCAGATGGTG TTGCAGAACG
501 GAATGTGAAT GTAAAGGGAA AGCGTTTGT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 786; ORF 221.a>:

```

a221.pep
1   MVVLMRLSLV RQAVNQIDAD GFEPRFARRI DDFGFFVTL DAVDRRLHFG
51  VEILNADAHA VEAESAEHED GVAADFARVD FDGVFAGGD* LEMFAYHAED
101 TFDLVVAQKG RRAAAEVQLG KLVPSVQMWS EQFHFFFKF DVGIGAAAFV
151 GDDFVAAAVV ADGVAERNVN VKGKRFV*

```

m221/a221 95.5% identity in 177 aa overlap

```

m221.pep    10      20      30      40      50      60
             MXVLMXRSLVRQAVNQIDADGFEPRFARRIDDFGFFVTLDAVDRRLHFGVEILNADAHA
             | | | | |
a221        10      20      30      40      50      60
             MVVLMRLSLVRQAVNQIDADGFEPRFARRIDDFGFFVTLDAVDRRLHFGVEILNADAHA

m221.pep    70      80      90      100     110     119
             VEAESAEHEDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLFVAQKGA-CPAEVQLG
             | | | | |
a221        70      80      90      100     110     120
             VEAESAEHEDGVAADFARVDFDGVFAGGD*LEMFAYHAEDTFDLVVAQKGRRAAAEVQLG

m221.pep    120     130     140     150     160     170
             KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFVX
             | | | | |
a221        130     140     150     160     170
             KLVPSVQMWSEQFHFFFKIFDVGIGAAAFVFGDDFVAAAVVADGVAERNVNVKGRFVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 787>:

```

g223.seq
1   atggaattca ggcaccaggt agtggtagtt ggtgtcgaac catttggtca
51  ttctgatggc gaattggtct ttgttgccgc gcgccagttg gaagaattgt
101 tccaaaggca ggttttggct atcgaagccg aaacgggagg gaatcgcgcc
151 cgtggatact tgcaggtcga ggatgtgatg gtagaaagtg aaatcacgta
201 cagcaacgta atcagcggtt ggagcagctt ggtgtttcca gtttttctcg
251 cgcaggtctt tggcaacgtc gagcagctct tgttactga tctctttgcg
301 ccagtatttt tcttgggcga atttcaattc acggaaggcg ccgacacgcg
351 ggaagcctga

```

This corresponds to the amino acid sequence <SEQ ID 788; ORF 223.ng>:

g223.pep..

508

```

1  MEFRHQVVVV GVEPFGHFDG ELVFVAARQL EELFQRQVLA IEAETGGNRA
51  RGYLQVEDVM VESEITYSNV ISVRSSLVFP VFLAQVFGNV EQLLFTDLFA
101 PVFFLGEFQF TEGADTREAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 789>:

```

m223.seq
1  GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTGCAAC CATTGTTGTC
51  TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
101 TCCAAAGACA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCCTAC
201 GGCAACGAAA TCGGCGTTGG CAGCGACCTG GTGTTTCCAG TTTTCTCGC
251 GCAAGTCTTT AGCAACAGCC AGCAATTCTT GCTCGCTGAT TTCTTTGCGC
301 CAGTATTTTT CTTGTGCGAA TTTCAATTCT CGGAAGCGCG CGACACGCGG
351 GAAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 790; ORF 223>:

```

m223.pep
1  VEFRHQVVVV GVEPFGHFDS ELVFVTARQL EELFQRQVLA VEAEGGNRA
51  GDLQVEDVV VESEIXYGNV IGVGSDLVFP VFLAQVFSNS QQFLADFFA
101 PVFFLGEFQF AEGADTREAA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 223 shows 80.7% identity over a 119 aa overlap with a predicted ORF (ORF 223.ng) from *N. gonorrhoeae*:

```

m223/g223
10      20      30      40      50      60
m223.pep VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g223      MEFRHQVVVVGVEPFGHFDGELVFVAARQLEELFQRQVLAIEAETGGNRARGYLQVEDVM
10      20      30      40      50      60

70      80      90      100     110     120
m223.pep VESEIXYGNVIGVGSDLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX
|||||:|:| |:| :|||||:|||||:| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g223      VESEITYSNVISVRSSLVFPVFLAQVFGNVEQLLFTDLFAPVFFLGEFQFTEGADTREAX
70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 791>:

```

a223.seq
1  GTGGAATTCA GGCACCAAGT AGTGGTAGTT GGTGTGCAAC CATTGTTGTC
51  TTTCGATAGC GAATTGGTCT TTGTTACCGC GCGCCAGTTG GAAGAATTGT
101 TCCAAAGATA GGTTTTGGCT GTCGAAGCCG AAGCGGGCGG GAATCGCGCC
151 GGTGGCGACT TGCAGGTCGA GGATGTGGTC GTAGAAAGTG AAATCGCCTA
201 CGGCAACGTA ATCGGCGTTG GCAGCGGCCT GGTGTTTCCA GTTTTCTCG
251 CGCAAGTCTT TAGCAACAGC CAGCAATTCT TGCTCGCTGA TTTCTTTGCG
301 CCAGTATTTT TCTTGTGCGA ATTTCAATTC GCGGAAGGCA CCGACACGCG
351 GGAAGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 792; ORF 223.a>:

```

a223.pep
1  VEFRHQVVVV GVEPFGHFDS ELVFVTARQL EELFQR*VLA VEAEGGNRA
51  GDLQVEDVV VESEIAYGNV IGVGSLVFP VFLAQVFSNS QQFLADFFA
101 PVFFLGEFQF AEGDTTREAA*

```

m223/a223 95.8% identity in 119 aa overlap

```

10      20      30      40      50      60
m223.pep VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRQVLAVEAEAGGNRAGGDLQVEDVV
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a223      VEFRHQVVVVGVEPFGHFDSELVFVTARQLEELFQRXVLAVEAEAGGNRAGGDLQVEDVV
10      20      30      40      50      60

70      80      90      100     110     120
m223.pep VESEIXYGNVIGVGSDLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGADTREAX
|||||:|:| |:| :|||||:|||||:| |:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a223      VESEIAYGNVIGVGSLVFPVFLAQVFSNSQQFLADFFAPVFFLGEFQFAEGDTTREAX

```

70 80 90 100 110 120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 793>:

```
g225.seq
1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgccgtccgc cccgcccttg cgcacgagtt gaccaacctg ctcagcagcc
101 gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttacc
151 gtcaaccgag cccccgccc gcgggcgggc aatgccgacg aactcatcgg
201 cggcgcgatg gggcttaacg aacagcccgt tgtacgcgtc aaccgagccn
251 ccgcccgcg ggcgggcaat gccgacaaac tcatcggcag cgcgatcgcg
301 cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggtt
351 tgactgcagc ggattcatgc agcacatctt caaacgcgcc atgggcatca
401 acctgccgcg cactcgcgcg gaacaggcgc ggatgggagc acccgttgcc
451 cgaagcgaat tgcagcccgg ggatatggtg tttttccgca cgctcggcgg
501 cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcaccc
551 acgcgcgcg caggggaaa aatatcgaaa tcaccagcct gagccacaaa
601 tattggagcg gcaaatatgc gttcgcccg cgggtcaaga aaaacgaccc
651 gtcacgcttt ctgaactga
```

This corresponds to the amino acid sequence <SEQ ID 794; ORF 225.ng>:

```
g225.pep
1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101 LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151 RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201 YWSGKYAFAR RVKKNPSRF LN*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 795>:

```
m225.seq (partial)
1  ..TTTCAAACC CGGCAGTTTG GCGGTTTTG TGGCTGAwGT TTGCCGTCCG
51  CCCC GCCCTT GCCGACGAGT TGACCAACCT GCTCAGCAGC CGCGAGCAGA
101 TTCTCAGACA GTTTGCCGAA GACGAACAGC CCGTTTACC CATCAACCGA
151 GCCCCGCCC GCGGGCGGG CAATGCCGAC GAACTCATCG GCAGCGCGAT
201 GGGGCTTAAC GAACAGCCCG TTTTACCCGT CAACCGAGTC CCCGCCCGGC
251 GGGCGGGCAA TGCCGACGAA CTCATCGGCA ACGCGATGGG GCTTAACGAA
301 CAGCCCGTTT TACCCGTCAA CCGAGCCCC GCGGCGGGG CGGGCAATGC
351 CGACGAACTC ATCGGCAACG CGATGGGACT TTTGGGTATT GCCTACCGCT
401 ACGGCGGCAC ATCGGTTTCT ACCGTTTTG ACTGCAGCGG CTTTCATGAG
451 CACATCTTCA AACGCGCCAT GGGCATCAAC CTGCCGCGCA CGTCGGCAGA
501 ACAGGCACGG ATGGGTACGC CGTTGCCCC AAGCGAATTG CAGCCCGGAG
551 ATATGGTGTT TTTCCGACG CTCGGCGGCA GCCGCATTTC CCATGTCGGA
601 CTTTATATCG GCAACAACCG CTTTCATCCAC GCGCCGCGCA CGGGGAAAAA
651 TATCGAAATC ACCAGCCTGA GCCACAAATA TTGGAGCGGC AAATACGCGT
701 TCGCCCGCCG GGTC AAGAAA AACGACCGT CCCGCTTCT GAACTGA
```

This corresponds to the amino acid sequence <SEQ ID 796; ORF 225>:

```
m225.pep (partial)
1  ..FSNPAVWAVL WLXFAVRPAL ADELTNLLSS REQILRQFAE DEQVLPINR
51  APARRAGNAD ELIGSAMGLN EQVLPVNRV PARRAGNADE LIGNAMGLNE
101 QVLPVNRAP ARRAGNADEL IGNAMGLLGI AYRYGGTSVS TGFDSCGFEMQ
151 HIFKRAMGIN LPRTSAEQAR MGTPVARSEL QPGDMVFFRT LGGSRISHVG
201 LYIGNNRFIH APRTGKNIEI TSLSHKYWSG KYAFARRVKK NDPSRFLN*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 225 shows 83.5% identity over a 248 aa overlap with a predicted ORF (ORF 225.ng) from *N. gonorrhoeae*:

m225/g225

	10	20	30	40	50
m225.pep	FSNPAVWAVLWLXFAVRPALADELTNLSSREQILRQFAEDEQVLPINRAPARRAG				
	: :				
g225	MDSFFKPAVWAVLWLMFAVRPALADELTNLSSREQILRQFAEDEQVLPVNRAPARRAG				

		10	20	30	40	50	60
m225.pep	60	70	80	90	100	110	
	NADELIGSAMGLNEQPVLPVNRVPARRAGNADELIGNAMGLNEQPVLPVNRAPARRAGNA						
	: :						
g225	NADELIG-----GAMGLNEQPVVRVNRAXARRAGNA						
		70	80	90			
m225.pep	120	130	140	150	160	170	
	DELIGNAMGLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR						
	: : : : : : :						
g225	DKLIGSAMRLLGIAYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR						
	100	110	120	130	140	150	
m225.pep	180	190	200	210	220	230	
	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR						
	: : : :						
g225	SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIHAPRTGKNIEITSLSHKYWSGKYAFARR						
	160	170	180	190	200	210	
m225.pep	240	249					
	VKKNDP SRFLNX						
g225	VKKNDP SRFLN						
	220						

```

a225.seq
1    ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51   TGCCGTCCCG CCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAN CCCCCGCCCC GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251  CCGCCCGGGC GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCGTTTTT ACCGCTCAAC CGAGTCCCCG CCGCGCGGGC
351  GGGCAATGCC GACGAACCTA TCGGCAACGC GATGGGGCTT AACGAACAGC
401  CCGTTTTACC CGTCAACCGA GCCCCCGCCC GCGGGGCGGG CAATGCCGAC
451  GAACTCATCG GCAACCGCAT GGGAGTTTTG GGTATTGCCT ACCGCTACGG
501  CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551  TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601  GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651  GGTGTNTTTC CGCACGTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701  ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751  GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAAT ACGGTTTCGC
801  CGCCCGGGTC AAGAAAACG ACCCGTCCCG CTTTCTGAAC TGA

```

```
a225.pep
1  MDSFFKPAVW  AVLWLMFAVR  PALADELTNL  LSSREQILRQ  FAEDEQPVLP
51  INRXPARRAG  NADELIGSAM  GLNEQPVLPV  NRXPARRAGN  ADXLIGNAMG
101 LNEQPVLPVN  RVPARRAGNA  DELIGNAMGL  NEQPVLPVNR  APARRAGNAD
151 ELIGNAMGLL  GIAYRYGGS  ISTGFDCSGF  MQHIFKRAMG  INLPRTSAEQ
201 ARMGTPVARS  ELQPGDMVXF  RTLGGSRIS  VGLYIGNNRF  IHPRTGKNI
251 EITSLSHKYW  SKGYAFARRV  KKNDPSRFLN  *
```

```

m225.pép      FSNPAVWAVLWLXFAVRPALADELTNLLSSREQILRQFAEDEQPVLPIINRAPARRAG
| : ||||| | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a225          MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPIINRXPAR
              10         20         30         40         50         60

              60        70        79                80
m225.pép      NADELIGSAMGLNEQPVLPIINR-----VPARRAGNA

```


511

```

      |||||
a225  NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA
      70      80      90      100      110      120

      90      100      110      120      130      140
m225.pep DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSVSTGFDCSGF
      |||||
a225  DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLLGIAYRYGGTSISTGFDCSGF
      130      140      150      160      170      180

      150      160      170      180      190      200
m225.pep MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF
      |||||
a225  MQHIFKRAMGINLPRTSAEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF
      190      200      210      220      230      240

      210      220      230      240      249
m225.pep IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX
      |||||
a225  IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX
      250      260      270      280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 799>:

g225-1.seq

```

1  atggattctt ttttcaaacc ggcagtttgg gcggttttgt ggctgatgtt
51  tgcggtccgc cccgcccttg ccgacgagtt gaccaacctg ctcagcagcc
101  gcgagcagat tctcagacag tttgccgaag acgaacagcc cgttttaccc
151  gtcaaccgag ccccgcccg gcgggcgggc aatgccgacg aactcatcgg
201  cggcgcgatg gggcttaacg aacagcccg tgtacgcgtc aaccgagccn
251  ccgcccgcg ggcgggcaat gccgacaaac tcacgagcag cgcgatgcgg
301  cttttgggta ttgcctaccg ctacggcggc acatcggtgt ctaccggttt
351  tgactgcagc ggattcatgc agcacatctt caaacgcgcc atggggcatca
401  acctgccgcg cactcggcg gaacaggcgc ggatgggcgc acccggtgcc
451  cgaagcgaat tgcagcccg ggatatggtg tttttccgca cgctcggcgg
501  cagccgcatt tcccatgtcg gactttatat cggcaacaac cgcttcatcc
551  acgcgccgcg cacggggaaa aatatcgaaa tcaccagcct gagccacaaa
601  tattggagcg gcaaatatgc gttcgccgcg cgggtcaaga aaaacgaccc
651  gtcacgcttt ctgaactga

```

This corresponds to the amino acid sequence <SEQ ID 800; ORF 225-1.ng>:

g225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  VNRAPARRAG NADELIGGAM GLNEQPVVRV NRAXARRAGN ADKLIGSAMR
101  LLGIAYRYGG TSVSTGFDCS GFMQHIFKRA MGINLPRTSA EQARMGAPVA
151  RSELQPGDMV FFRTLGGSR I SHVGLYIGNN RFIHAPRTGK NIEITSLSHK
201  YWSGKYAFAR RVKKNDFSRF LN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 801>:

m225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACyTG CTCAGCAGCC
101  GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151  ATCAACCGAG CCCCCGCCCC GCGGGCGGGC AATGCCGACG AACTCATCGG
201  CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGAGTCC
251  CCGCCCCGCG GCGGGGCAAT GCCGACGAAC TCATCGGCAA CGCGATGGGG
301  CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGCCCCCG CCGGCGGGC
351  GGGCAATGCC GACGAAGTCA TCGGCAACGC GATGGGACTT TTGGGTATTG
401  CCTACCGCTA CGGCGGCACA TCGGTTTCTA CCGGTTTTGA CTGCAGCGGC
451  TTCATGCAGC ACATCTTCAA ACGCGCCATG GGCATCAACC TGCCGCGCAC
501  GTCGGCAGAA CAGGCACGGA TGGGTACGCC GGTGCCCCGA AGCGAATTGC
551  AGCCCGGAGA TATGGTGTTT TTCCGCACGC TCGGCGGCAG CCGCATTTCC
601  CATGTCGGAC TTTATATCGG CAACAACCGC TTCATCCACG CGCCGCGCAC
651  GGGGAAAAAT ATCGAAATCA CCAGCCTGAG CCACAAATAT TGGAGCGGCA
701  AATACGCGTT CGCCCGCCGG GTCAAGAAAA ACGACCCGTC CCGCTTCTG
751  AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 802; ORF 217>:

m225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRAPARRAG NADELIGSAM GLNEQVLPV NRVPARRAGN ADELIGNAMG
101 LNEQVLPVN RAPARRAGNA DELIGNAMGL LGIAYRYGGT SVSTGFDCSG
151 FMQHIFKRAM GINLPRTSAE QARMGTPVAR SELQPGDMVF FRTLGGSRIS
201 HVGLYIGNNR FIHAPRTGKN IEITSLSHKY WSGKYAFARR VKKNDPSRFL
251 N*

```

m225-1/g225-1 84.9% identity in 251 aa overlap

```

              10      20      30      40      50      60
m225-1.pep    MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPINRAPARRAG
              |||||
g225-1        MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQVLPVNRAPARRAG
              10      20      30      40      50      60

              70      80      90      100     110     120
m225-1.pep    NADELIGSAMGLNEQVLPVNRVPARRAGNADELIGNAMGLNEQVLPVNRAPARRAGNA
              ||||
g225-1        NADE-----LIGGAMGLNEQPVVRVNRAXARRAGNA
                      70      80      90

              130     140     150     160     170     180
m225-1.pep    DELIGNAMGLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGTPVAR
              |:|:|:|
g225-1        DKLIGSAMRLLGIAIYRYGGTSVSTGFDCSGFMQHIFKRAMGINLPRTSAEQARMGAPVAR
              100     110     120     130     140     150

              190     200     210     220     230     240
m225-1.pep    SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
              |||||
g225-1        SELQPGDMVFFRTLGGSRISHVGLYIGNNRFIAPRTGKNIEITSLSHKYWSGKYAFARR
              160     170     180     190     200     210

              250
m225-1.pep    VKKNDPSRFLNX
              |||||
g225-1        VKKNDPSRFLNX
              220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 803>:

a225-1.seq

```

1  ATGGATTCTT TTTTCAAACC GGCAGTTTGG GCGGTTTTGT GGCTGATGTT
51  TGCCGTCCGC CCCGCCCTTG CCGACGAGTT GACCAACCTG CTCAGCAGCC
101 GCGAGCAGAT TCTCAGACAG TTTGCCGAAG ACGAACAGCC CGTTTTACCC
151 ATCAACCGAN CCCCGCCCCG GCGGGCGGGC AATGCCGACG AACTCATCGG
201 CAGCGCGATG GGGCTTAACG AACAGCCCGT TTTACCCGTC AACCGANTCC
251 CCGCCCGGCG GCGGGGCAAT GCCGACNAAC TCATCGGCAA CGCGATGGGG
301 CTTAACGAAC AGCCCGTTTT ACCCGTCAAC CGAGTCCCCG CCCGGCGGGC
351 GGGCAATGCC GACGAATCA TCGGCAACGC GATGGGGCTT AACGAACAGC
401 CCGTTTTACC CGTCAACCGA GCCCCGCCCC GCGGGCGGG CAATGCCGAC
451 GAACTCATCG GCAACGCGAT GGGACTTTTG GGTATTGCCT ACCGCTACGG
501 CGGCACATCG ATTTCTACCG GTTTTGACTG CAGCGGCTTC ATGCAGCACA
551 TCTTCAAACG CGCCATGGGC ATCAACCTGC CGCGCACGTC GGCAGAACAG
601 GCGCGGATGG GTACGCCGGT TGCCCGAAGC GAATTGCAGC CCGGGGATAT
651 GGTGTNTTTC CGCACGCTCG GCGGCAGCCG CATTTCCCAT GTCGGACTTT
701 ATATCGGCAA CAACCGCTTC ATCCACGCGC CGCGCACGGG GAAAAATATC
751 GAAATCACCA GCCTGAGCCA CAAATATTGG AGCGGCAAT ACGGTTTCG
801 CCGCCGGGTC AAGAAAAACG ACCCGTCCCC CTTTCTGAAC TGA

```

This corresponds to the amino acid sequence <SEQ ID 804; ORF 225-1.a>:

a225-1.pep

```

1  MDSFFKPAVW AVLWLMFAVR PALADELTNL LSSREQILRQ FAEDEQPVLP
51  INRXPARRAG NADELIGSAM GLNEQVLPV NRXPARRAGN ADXLIGNAMG
101 LNEQVLPVN RVPARRAGNA DELIGNAMGL NEQVLPVNR APARRAGNAD
151 ELIGNAMGLL GIAYRYGGTS ISTGFDCSGF MQHIFKRAMG INLPRTSAEQ
201 ARMGTPVAR ELQPGDMVXF RTLGGSRISH VGLYIGNNRF IHAPRTGKNI
251 EITSLSHKYW SGKYAFARRV KKNDDPSRFLN *

```

a225-1/m225-1 88.6% identity in 280 aa overlap

	10	20	30	40	50	60
a225-1.pep	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRXPARRAG					
m225-1	MDSFFKPAVWAVLWLMFAVRPALADELTNLLSSREQILRQFAEDEQPVLPINRAPARRAG					
	10	20	30	40	50	60
	70	80	90	100	110	120
a225-1.pep	NADELIGSAMGLNEQPVLPVNRXPARRAGNADXLIGNAMGLNEQPVLPVNRVPARRAGNA					
m225-1	NADELIGSAMGLNEQ-----VLPVNRVPARRAGNA					
	70	80	90			
	130	140	150	160	170	180
a225-1.pep	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLGIAYRYGGTSISTGFDCSGF					
m225-1	DELIGNAMGLNEQPVLPVNRAPARRAGNADELIGNAMGLGIAYRYGGTSVSTGFDCSGF					
	100	110	120	130	140	150
	190	200	210	220	230	240
a225-1.pep	MQHIFKRAMGINLPRTSABEQARMGTPVARSELQPGDMVXFRTLGGSRISHVGLYIGNNRF					
m225-1	MQHIFKRAMGINLPRTSABEQARMGTPVARSELQPGDMVFFRTLGGSRISHVGLYIGNNRF					
	160	170	180	190	200	210
	250	260	270	280		
a225-1.pep	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX					
m225-1	IHAPRTGKNIEITSLSHKYWSGKYAFARRVKKNDFSRFLNX					
	220	230	240	250		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 805>:

g226.seq

```

1  ATGAGCGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TCGGCTGAAA cccGccgtCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
301 GGCAGCGTTA cggGCATTGT tacggggATG TATTTTgccg cttggctcgg
351 gccggatacc caattctcct tcccgcctcg tcttcaatat ctgttattta
401 caccctctgg aatcccaatt cacaccctgt atgcgcgggt tctcccacca
451 tttctgttgc ctccgcctct cctgccgcgc ctggccccgc atacattgcg
501 ccggttcaca atacttccaa aaaaactacg gccgtttaag cccctcctcc
551 cagttgtggt cctttctcct Ccgggcctcg cccctcccct cttataa

```

This corresponds to the amino acid sequence <SEQ ID 806; ORF 226.ng>:

g226.pep

```

1  MSEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
51  LGIDYAVYHN AAQFIDFLRK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
101 GSVTGIVTGM YFAAWLGPDT QFSFPRLQY LLFTPSGIPI HTLYARVLPP
151 FLLPPPLLPR LGPHTLRRFT ILPKKL RPFK PLLPVVVLSP PGLAPPLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 807>:

m226.seq

```

1  ATGAACGAAA TCCTCAGGCA GCCCAGCGTT CTGCTTTTCC TCACGCTTGC
51  CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGC AATATCTTCT
101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAAT TCATTGATTT
201 TTGGCTGAAA CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
251 GCCGTAAAAT CTTCAACCAG TGGCTGCCCG TCATCGTTTC ACAGCTTGCG
301 GGCAGCGTTA CGGGCATTGT TACAGGGATG TATTTTGCCA AATGGCTGGG
351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAACC
401 CCATCGCTAT TGAAATCACC CGCTCCATCG GCGGCATTCC CGCCATTACC
451 GCCGCCACCG TCATCATTGC CGGTCTGGTC GGACAGATTG CCGGTTACAA

```

514

501 AATGCTGAAG AACACGGTCG TCATGCCCTC GTCCGTGGGT ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGGATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGTATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TCATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 808; ORF 226>:

m226.pep

1 MNEILRQPSV LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 226 shows 94.2% identity over a 121 aa overlap with a predicted ORF (ORF 226.ng) from *N. gonorrhoeae*:

m226/g226

	10	20	30	40	50	60
m226.pep	MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	:					
g226	MSEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m226.pep	AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAKWLGAER					
g226	AAQFIDFRLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGM YFAAWLGPDT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m226.pep	EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG					
	:					
g226	QFSFPRLQYLLFTPSGIPHTLYARVLPFPPLPPLPRLGPHTLRRFTILPKKLRFK					
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 809>:

a226.seq

1 ATGAACGAAA TCCTCAGGCA GCCGAGCATC CTGCTTTTCC TCACGCTTGC
 51 CGTGACGCG CTTGCGATTA TCGTGCGCAC GCGCACGGGT AATATCTTCT
 101 GCAACCCCGT ACTCGTCAGC ACTATCGTGC TGATTGCCTA CCTGAAAATC
 151 CTCGGTATCG ATTATGCGGT GTACCACAAC GCCGCGCAGT TTATCGATTT
 201 CTGGCTCAAG CCCGCCGTCG TCGTGCTTGC CGTGCCGCTC TACCAAAACC
 251 GCCGTAAAAT CTTCAACCAA TGGCTGCCCG TCATCGTTTC GCAGCTTGCG
 301 GGCAGCGTTA CGGGCATTGT TACGGGGATG TATTTTGCCA AATGGCTGGG
 351 CGCGGAACGC GAAGTCGTCC TCTCGCTCGC GTCCAAATCT GTTACCAATC
 401 CTATCGCCAT CGAAATCACC CGTCCATCG GCGGCATTCC CGCCATTACC
 451 GCCGCCACCG TCATCATTGC CGGCCTGGTC GGACAGATTG CCGGTTACAA
 501 AATGTTGAAA AACACGGTCG TTATGCCCTC ATCTGTCGGA ATGTCGCTCG
 551 GCACGGCTTC GCACGCGATG GGCATTGCCG CCTCGCTCGA ACGCAGCCGC
 601 CGCATGGCGG CATACGCGGG GCTGGGGCTG ACGTTCAACG GCGTACTGAC
 651 CGCGCTGATT GCGCCGCTGC TTATCCCCGT TTTGGGATTT TGA

This corresponds to the amino acid sequence <SEQ ID 810; ORF 226.a>:

a226.pep

1 MNEILRQPSI LLFLTLAVYA LAIIVRTRTG NIFCNPVLVS TIVLIAYLKI
 51 LGIDYAVYHN AAQFIDFWLK PAVVVLAVPL YQNRKIFNQ WLPVIVSQLA
 101 GSVTGIVTGM YFAKWLGAER EVVLSLASKS VTNPIAIEIT RSIGGIPAIT
 151 AATVIIAGLV GQIAGYKMLK NTVMPSSVG MSLGTASHAM GIAASLERSR
 201 RMAAYAGLGL TFNGVLTALI APLLIPVLGF *

m226/a226 99.6% identity in 230 aa overlap

10 20 30 40 50 60

515

```

m226.pep      MNEILRQPSVLLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
|||||:|||||
a226          MNEILRQPSILLFLTLAVYALAIIVRTRTGNIFCNPVLVSTIVLIAYLKILGIDYAVYHN
              10      20      30      40      50      60

              70      80      90      100     110     120
m226.pep      AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
|||||
a226          AAQFIDFWLKPAVVVLAVPLYQNRKIFNQWLPVIVSQLAGSVTGIVTGMYFAKWLGAER
              70      80      90      100     110     120

              130     140     150     160     170     180
m226.pep      EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
|||||
a226          EVVLSLASKSVTNPIAIEITRSIGGIPAITAATVIIAGLVGQIAGYKMLKNTVMPSSVG
              130     140     150     160     170     180

              190     200     210     220     230
m226.pep      MSLGTASHAMGIAASLERSRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
|||||
a226          MSLGTASHAMGIAASLERSRMAAYAGLGLTFNGVLTALIAPLLIPVLGFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 811>:

```

g227.seq
1   atgaacatca tccgcgcgct cctcatcatc ctcggctgcc tcgccgcggg
51  cgaaaccgcc gttttcctag caggcatcaa actgcccgcc agcatcgctc
101 gcatgggcgt gctgtttgcg cttttgcagg cgggttggtc caaaacgtct
151 tggctgcaac agcttaccga cgcgctgatg gcaaacctga cgctgttctt
201 cgtgccgccc tgcgtggcgg tcatcagcta tttggatttg attgccgacg
251 attggttttc gatactggtt tccgcctccg ccagcacttt gtgcgtactg
301 ctggttacgg gcaaggttca ccgctggata cggagcatta tctga

```

This corresponds to the amino acid sequence <SEQ ID 812; ORF 227.ng>:

```

g227.pep
1   MNIIRALLII LGCLAAGETA VFLAGIKLPG SIVGMGVLFA LLQAGWLKTS
51  WLQQLTDALM ANLTLEFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVRHWI RSII*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 813>:

```

m227.seq (partial)
1   ..ACGTCTTkgC TGCAACAGCT TACCGACGCG CTGATGTGCGA ACCTGACGCT
51  GTtCCTCGTG CCgCC.TGCG TGGCGGTCAT CAGCTATTtG GATTtGATTG
101 CCGACGATTG GTTTTCGATA CTGGTTTCCG CCTCCGCCAG cACTTTGTGC
151 GTACTGCTGG TTACGGGCAA AGTCCACCGG TGGATACGGG GTATTATCCG
201 ATGA

```

This corresponds to the amino acid sequence <SEQ ID 814; ORF 227>:

```

m227.pep (partial)
1   ..TSXLQQLTDA LMSNLTFLV PPCVAVISYL DLIADDWFSI LVSASASTLC
51  VLLVTGKVHR WIRGIIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 227 shows 95.5% identity over a 66 aa overlap with a predicted ORF (ORF 227.ng) from *N. gonorrhoeae*:

```

m227/g227
              10      20      30
m227.pep      TSXLQQLTDALMSNLTFLVPPCVAVISYL
              || |||||:|||||
g227          TAVFLAGIKLPGSIVGMGVLFALLQAGWLKTSWLQQLTDALMANLTFLVPPCVAVISYL
              20      30      40      50      60      70

              40      50      60

```

516

```

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||
g227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 815>:

```

a227.seq
1  ATGAACATCA TCCGCGCGCT CCTCATCATC CTCGGCTGCC TCGCCACCGG
51 CGAAACCGCC GTTTTCCTAG CAGGCATCAA ACTGCCCGGC AGCATCGTCG
101 GCATGGGCGT ACTGTTTGCG CTTTTCGAGG CGGGTTGGGT CAAAACGTCT
151 TGGCTGCAAC AGCTTACCGA CGCGCTGATG GCGAATCTGA CGTTGTTTCT
201 CGTGCCGCCC TGCCTGGCGG TCATCAGCTA TTTGGATTG ATTGCCGACG
251 ATTGGTTTTC GATACTGGTT TCCGCCTCCG CCAGCACTTT GTGCGTACTG
301 CTGGTTACAG GCAAGGTTCA CCGCTGGATA CGGAGCATT TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 816; ORF 227.a>:

```

a227.pep
1  MNIIRALLII LGCLATGETA VFLAGIKLPG SIVGMGVLEA LLQAGWVKTS
51 WLQQLTDALM ANLTLFLVPP CVAVISYLDL IADDWFSILV SASASTLCVL
101 LVTGKVHRWI RSII*

```

m227/a227 95.5% identity in 66 aa overlap

```

m227.pep      TSXLQQLTDALMSNLTLFLVPPCVAVISYL
               || |||||
a227          TAVFLAGIKLPGSIVGMGVLFALLQAGWVKTSWLQQLTDALMANLTLFLVPPCVAVISYL
               20      30      40      50      60      70

m227.pep      DLIADDWFSILVSASASTLCVLLVTGKVHRWIRGIIRX
               |||||
a227          DLIADDWFSILVSASASTLCVLLVTGKVHRWIRSIIX
               80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 817>:

```

m228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTAAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 818; ORF 228>:

```

m228.pep
1  MKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51 VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLTK AADATQEAAD
101 KMKDAAK*

```

Computer analysis of this amino acid sequence gave the following results:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 819>:

```

a228.seq
1  ATGAAAAAAT TATTGATTGC CGCAATGATG GCGGCTGCCT TGGCAGCTTG
51 TTCGCAAGAA GCCAAACAGG AGGTAAAGGA AGCGGTTCAA GCCGTTGAGT
101 CCGATGTAA AGACACTGCG GCTTCTGCCG CCGAGTCTGC CGCTTCTGCC
151 GTCGAAGAAG CGAAAGACCA AGTCAAAGAT GCTGCGGCTG ATGCAAAGGC
201 AAGTGCCGAG GAAGCTGTAA CTGAAGCCAA AGAAGCTGTA ACTGAAGCAG
251 CTAAAGATAC TTTGAACAAA GCTGCCGACG CGACTCAGGA AGCGGCAGAC
301 AAAATGAAAG ATGCCGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 820; ORF 228.a>:

517

```

a228.pep
1   MKKLLIAAMM AAALAACSQE AKQEVKEAVQ AVESDVKDTA ASAAESAASA
51  VEEAKDQVKD AAADAKASAE EAVTEAKEAV TEAAKDTLNK AADATQEAAD
101 KMKDAAK*

```

m228/a228 100.0% identity in 107 aa overlap

```

              10      20      30      40      50      60
m228.pep      MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a228           MKKLLIAAMMAAALAACSQEAKQEVKEAVQAVESDVKDTAASAAESAASAVEEAKDQVKD
              10      20      30      40      50      60

              70      80      90     100
m228.pep      AAADAKASAE EAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
              | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a228           AAADAKASAE EAVTEAKEAVTEAAKDTLNKAADATQEAADKMKDAAKX
              70      80      90     100

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 821>:

```

g229.seq
1   atggctgccg tatcgggcgg cggtgcggtc ttcctgataa tgcttcaca
51  tattgccgcg gttcagcgtc agccgccagc gttcgcccaa gcgtcgggag
101 aaatcgggcat tgaagccgcc ggcgaaattg tatcggtctc cgcccaagag
151 gttttgcccg acaaacggca cggtgccgaa cgagcgcggt accgaacggt
201 tttgatggcc gaacgacagg cgcaggttct gttcgctgaa atctttgtta
251 tcccaataat gcacgcgcgc gctgatgccg ccgtagagga aatgatgcc
301 gcccgcattg atttcgcgcg acacgcccga gccgtagcgc aaaccgtgtg
351 ccttttgccg caggctgtcg gcggttttcg tccagcttct gcccgcaaat
401 tcaatcgttt tttcggacga agcgttgttt atagcggatt aacaaaaatc
451 aggacaaggc ggcgggcccgc aggcagtacg gatggtacgg aaccggttcg
501 cccggtgctt ggacgcctta gggaaccggt ccctttgagc cggggcgggg
551 caacccgtag cggtttttgt tcatccgcca tattgtgttg a

```

This corresponds to the amino acid sequence <SEQ ID 822; ORF 229.ng>:

```

g229.pep
1   MAAVSGGGAV FLIMLPFIAR VQRQPPAFAQ ASGEIGIEAA GEIVSAAAEQ
51  VLPDKRHGAE RARYRTVLMA ERQAQVLFAE IFVIPIMHAA ADAAVEEMMP
101 ARIDFARHAQ AVAQTVCLLR QAVGGFRPAS ARKFNRFGR SVVYSGLTKI
151 RTRRRAAGST DGTEPVRPVL GRLREPFPLS RGGATRTGFC SSAILC*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 823>:

```

m229.seq (partial)
1   ..GCTCAAGCGT TGGGAGAAAT CGGCATTGAA GCCGCCGACG AAATTGTATC
51  GGCTGCCGCC TAAGAGGTTT TGCTCGACAA ACGGCACGAT GCCGAACGAG
101 CGCGTTACCG AACGGTTTTT ATAGCCGAAC GACAGGCGCA GGCTCTGTTC
151 GCTGAAATCT TTGTTATCCC AATAATGCAC GCCGCCGCCG CTGATGCCGC
201 CGTAGAGGAA ATGATGCCTG CCCGCATTGA TTTCGCGCGA CACGCCTAAG
251 CCCTAGCGCA AACCGTGTGC CTTTTCGCGC AGGCTGTCCG CGGTTTTTCG
301 CCAGCTTCTG CCCGCAAATT CAATCGTTTT TTCGACGAA GCGTTGTTTA
351 TAGCGGATTA ACAAAAATCA GGACAAGGCA ACGAAGCCGC AGACAGTACA
401 AATAGTACGG AACCGATTCA CTTGGTGCTT CAGCACCTTA GAGAATCGTT
451 CTCTTTTTTG TTCATCCGCT ATATTGTGTT GA

```

This corresponds to the amino acid sequence <SEQ ID 824; ORF 229>:

```

m229.pep (partial)
1   ..AQALGEIGIE AADEIVSAAA XEVLLDKRHD AERARYRTVF IAERQAQALF
51  AEIFVIPIMH AAAADA AVEE MPPARIDFAR HAXALAQTV LRLQAVGGFR
101 PASARKFNRF FGSRVVYSL TKIRTRQSA DSTNSTEPIH LVLQHLRESR
151 SLFCSSAILC *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 229 shows 80.5% identity over a 169 aa overlap with a predicted ORF (ORF 229.ng) from *N. gonorrhoeae*:

m229/g209

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      MAVSGGGAVFLIMLPFIARVQRPPAFAQASGEIGIEAAGEIVSAAAEVLPDKRHGAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFIPIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RARYRTVILMAERQAQVLF AEIVFIPIMHAAA-DA AVEEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110

                                100     110     120     130     140
m229.pep      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRQRSADSTNSTEPIHLVLQHLRE----
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
g229      RQAVGGFRPASARKFNRFGRSVVYSGLT KIRTRRRRAAGSTDGTGPVRPVLGRLEPFPL
                                120     130     140     150     160     170

                                150     160
m229.pep      -----SRSLFCSSAILCX
                :|: ||| ||| |||
g229      SRGGATRTGFCSSAILC
                                180     190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 825>:

```

a229.seq (partial)
1  ATGGCTGTCTG TATCGGGCGG CGGTGCGGTC TTCCTGATAA CGCTTCCACA
51 TATTGCCCAC GTTCAGCGTC AGCCGCCA.. GTTCGCTCAA GCGTCGGGAG
101 AAATCGGCAT TGAAGCCGCC GACGAAATTG TATCGGCTGC CGCCTAAGAG
151 GTTTTGCTCG ATAAACGGCA CGATGCCGAA TGAGCGCGTT ACTGAACGGT
201 TTTTATAGCC GAGCGACAGG CGCAGGCTCT GTTCGCTGAA ATCTTTGTTA
251 TCCTAATAGT GCACGCCGCC GCCGCTGATG TCTCCGTAGA GGAATGATG
301 CCCGCCCGCA TTGATTTCGC GCGACACGCC CAAGCCGTAG CGCAAACCGT
351 GTGCCTTTTG CGGCAGGCTG TCGGCGGTTT TCGTCCAGCT TCTGCCTGCA
401 AATTC AATCG TTTTTCGGA CGAAGCGTTG TTTATAGCGG ATTAACAAAA
451 ATCAGGACAA GGCGACGAAG CGCAGACAGT ACAGATAGTA CGGAACCGAT
501 TCACTTGGTG CTTCAGCACC TTAGAGAATC GTCTCTTTGA GCTAAGGCCA
551 GGCAACGCCG TACTGGTTTT TGTT CATCCA CTATA

```

This corresponds to the amino acid sequence <SEQ ID 826; ORF 229.a>:

```

a229.pep (partial)
1  MAVVSGGGAV FLITLPHIAH VQRQPPXFAQ ASGEIGIEAA DEIVSAAA*E
51 VL LDKRHDAE *ARY*TVFIA ERQAQALFAE IFVILIVHAA AADV SVEEMM
101 PARIDFARHA QAVAQTVCLL RQAVGGFRPA SACKFNRFEG RSVVYSGLTK
151 IRRRRSADS TDST EPIHLV LQHLRESSL* AKARQRTGF CSSTI

```

m229/a229 85.6% identity in 167 aa overlap

```

                                10      20      30
m229.pep                      AQALGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      MAVVSGGGAVFLITLPHIAHVQRQPPXFAQASGEIGIEAADEIVSAAAXEVLLDKRHDAE
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m229.pep      RARYRTVFIAERQAQALFAEIVFIPIMHAAAADA AVEEMMPARIDFARHAXALAQTVCLL
                ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
a229      XARYXTVFIAERQAQALFAEIVFVILIVHAAAADVSVEEMMPARIDFARHAQAVAQTVCLL
                                70      80      90      100     110     120

```


519

	100	110	120	130	140	149
m229.pep	RQAVGGFRPASARKFNRRFFGRSVVYSGLTKIRTRQRSADSTNSTEPIHLVLQHLRES---					
a229	RQAVGGFRPASACKFNRRFFGRSVVYSGLTKIRTRRRSADSTDSTEPIHLVLQHLRESSLX					
	130	140	150	160	170	180
	150	160				
m229.pep	-----RSLFCSSAILCX					
a229	AKARQRRRTGFCSSIT					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 827>:

```

g230.seq
1  atgttccatt ccatcgaaaa atacagaaca cccgcccagg tcttattagg
51  cctgattgca ttaacttttg tgggcttcgg cgtcagcacg gtttcccatc
101 cgggcgccga ctacatcgtc caagtgggcg acgaaaaaat cagcagcac
151 tcaatcaaca acgccatgca gaacgagcag gcggacggcg gcagcccttg
201 gcgcgacgcg gtgttccaat ccctgctgca acgcgcctac ctgaaacagg
251 qcgcgaagct gatgggcatt tcggtttctt ccgaacaaat caagcagatg
301 attgtggacg atcccaattt ccacgacgca aacggcaaat tcagtcacgc
351 gcttttgagt caatacctgt cgcaacgcca tatgtctgaa gaccagtttg
401 tcgaagaaat ccgcgatcag tttgccttgc agaatttggt aagcctcgtc
451 caaaacggcg tattggtcgg cgacgcgcag gcggaacagc tgatcaggct
501 gacgcaggct aaccgcacca tccgttcgca cactttcaac cccgacgagt
551 tcatcgccca agtcaaagcg tctgaagccg atttgcagaa attttataat
601 gcgaacaaaa aagactatct gctgccgcag gcggtcaaat tggaaatatg
651 cgccttgaat ctgaaggatt ttgcagacaa gcagaccgtc agtgaaacgg
701 aagtgaaaaa tgcgtttgaa gagcgcgtgg cgcgtttgcc ggcacatgaa
751 gccaaacctt ctttcgagca ggaaaaagcc gccgtcgaaa acgaattgaa
801 aatgaaaaag gcggttgccg acttcaacaa ggcaaaagaa aagctgggcg
851 acgatgcgtt caatcatccc tctcgccttg ccgaagccgc caaaaacagc
901 ggtttgaaag tggaaaccca agaaacttgg ctgagcaggc aggacgcaca
951 aatgtccggc atgcccgaaa acctaatcaa tgccgtattc agcgacgacg
1001 tattgaagaa aaaacacaat tccgaagtgc tgaccatcaa cagcgaaacc
1051 gcgtgggtcg tccgcgccaa agaagtcgcg gaagaaaaaa acctactgtt
1101 tgaagaagcc aaagatgcgg tcgctcaggc ctatatccgt accgaagccg
1151 ccaaactttt gaaaacaatg taa

```

This corresponds to the amino acid sequence <SEQ ID 828; ORF 230.ng>:

```

g230.pep
1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGA KLMI SVSSEIKQM
101 IVDDPNFHDA NGKFSHALLS QYLSQRHMSE DQFVEEIRDQ FALQNLVSLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLLKTM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 829>:

```

m230.seq (partial)
1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAaT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GcC.GACGCG GTGTTCCAAT CCCTGCTGCA ACGGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGTACCTTT CCCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC

```

520

```

451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTTCGCA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAAA AAGACTATCT GCTGCCGCAG gCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGg
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAGAA AAATTGGGCG
851 ACGATGC.GT cAACCATCCT TCyTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTCGAAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCGAAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAA TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 TCGTGGGTCT TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT...

```

This corresponds to the amino acid sequence <SEQ ID 830; ORF 230>:

```

m230.pep (partial)
  1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
 51 SINNAIQNEQ ADGGGSPDA VFQSLQRAY LKQGAQLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAVNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVL TINSET
351 AWWVRAKEVR EEKTLPFMEA KDAVRQAYIR TEAAKL....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 230 shows 95.9% identity over a 386 aa overlap with a predicted ORF (ORF 230.ng) from *N. gonorrhoeae*:

m230/g230

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
g230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ					
	10	20	30	40	50	60
m230.pep	70	80	90	100	110	120
	ADGGGSPSPDAVFQSLQRAYLKQGAQLMGISVSSEQIKQIIVDDPNFHDA NGKFDHALLN					
g230	ADGGSPWRDAVFQSLQRAYLKQGAQLMGISVSSEQIKQMIVDDPNFHDA NGKFSHALLS					
	70	80	90	100	110	120
m230.pep	130	140	150	160	170	180
	RYLSQRHMSEDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
g230	QYLSQRHMSEDQFVEEIRDQFALQNLVSLVQNGVLVGDAQAEQLIRLTQVNRRTIRSHTFN					
	130	140	150	160	170	180
m230.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
	190	200	210	220	230	240
m230.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAVNHPSSLAEAAKNS					
g230	ERVARLPAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
	250	260	270	280	290	300

521

	310	320	330	340	350	360
m230.pep	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
g230	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRKEVR					
	310	320	330	340	350	360
	370	380				
m230.pep	EEKTLPPFAEAKDAVRQAYIRTEAAKL					
	:					
g230	EEKNLLFEEAKDAVRQAYIRTEAAKLLKTM					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 831>:

a230.seq (partial)

```

1  ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTCAGCACG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGTACCTTT CCCAACGTCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAGGTC AACC GCACCA TCCGTTGCA CACTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCAAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCCGGT ATGCCCAGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTT

```

This corresponds to the amino acid sequence <SEQ ID 832; ORF 230.a>:

a230.pep (partial)

```

1  MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51  SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHTFN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHNS SEVLTINSET
351 AWWVVRKEVR EEKTLPPFAE KDAVRQAYIR TEAAKL

```

m230/a230 99.2% identity in 386 aa overlap

	10	20	30	40	50	60
m230.pep	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
a230	MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ					
	10	20	30	40	50	60
	70	80	90	100	110	120
m230.pep	ADGGGPSRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
a230	ADGGGPSRDAVFQSLQRAYLKQAKLMGISVSSEQIKQIIVDDPNFHDANGKFDHALLN					
	70	80	90	100	110	120
	130	140	150	160	170	180

522

m230.pep	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGD	QAQAEQL	IRLTQVN	RTIRSH	TEN
a230	RYLSQRHMS	EDQFVEE	IRDQFALQ	NLVNLVQ	NGVLVGD	QAQAEQL	IRLTQVN	RTIRSH	TEN
	130	140	150	160	170	180			
m230.pep		190	200	210	220	230	240		
a230		190	200	210	220	230	240		
m230.pep		250	260	270	280	290	300		
a230		250	260	270	280	290	300		
m230.pep		310	320	330	340	350	360		
a230		310	320	330	340	350	360		
m230.pep		370	380						
a230		370	380						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 833>:

g230-1.seq

```

1  ATGTTCCATT CCATCGAAAA ATACAGAAC A CCCGCCCAAG TCTTATTAGG
51  CCTGATTGCA TTAACCTTTG TCGGCTTCGG CGTCAGCACG GTTTCCCATC
101 CGGGCGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGAGCAC
151 TCAATCAACA ACGCCATGCA GAACGAGCAG GCGGACGGCG GCAGCCCTTG
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTCTT CCGAACAAAT CAAGCAGATG
301 ATTGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCAGTCACGC
351 GCTTTTGAGT CAATACCTGT CGCAACGCCA TATGTCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAGCCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGCAAGTC AACC GCACCA TCCGTCGCA CACTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGCG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAATA AAGACTATCT GCTGCCGCAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCGTTTGAA GAGCGCGTGG CGCGTTTGCC GGCACATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAGCTGGGCG
851 ACGATGCGTT CAATCATCCC TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TGGAAACCCA AGAACTTGG CTGAGCAGGC AGGACGCACA
951 AATGTCCGGC ATGCCCGAAA ACCTAATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCAA AGAAGTCCGC GAAGAAAAAA ACCTACTGTT
1101 TGAAGAAGCC AAAGATGCGG TGCGTCAGGC CTATATCCGT ACCGAAGCCG
1151 CCAAACCTTG CAAAAACAAG GAAAAAGAAG TGCTTACCCA ACTGAACGGC
1201 GGCAAGGCAG TTGACGTGAA ATGCTCGGAA GTGTCCGTTT TGGGCGCGCA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCCGCCATG TCACTATGAC CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAGGC GCAGGCAGTC ACGCCTCCGG AGGATATTGC
1401 CGCACAGCTT CCTCCTGCGA AACAGGCTTT GGCACAACAG CAGTCTGCCA
1451 ATACTTTTGA CCTGCTGATC CGCTATTTC ACGGAAAAAT CAAACAGACT
1501 AAAGGAGCAC AATCGGTTGA CAACGGCGAT GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 834; ORF 230-1.ng>:

g230-1.pep

```

1  MFHSIEKYRT PAQVLLGLIA LTFVFGVST VSHPGADYIV QVGDEKISEH
51  SINNAMQNEQ ADGGSPWRDA VFQSLQRAY LKQGA KLMI SVSSEIQQM
101  IVDDPNFHDA NGKFSHALLS QYLSQRHMS DQFVEEIRDQ FALQNLVSLV

```

```

151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKA SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPAHE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRAKEVR EEKNLLFEEA KDAVRQAYIR TEAAKLAENK AKEVLTQLNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLTGLP
451 APVIVEAQAV TPPEDIAAQL PPAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 835>:

m230-1.seq

```

1 ATGTTCCATT CCATCGAAAA ATACAGAACG CCCGCCCAAG TCCTTTTGGG
51 CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTGAGCAGC GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACAGAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG CGGAGCGCGC GCGGCCCTTC
201 GCGCGACGCG GTGTTCCAAT CCCTGCTGCA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAAATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGCTACCTTT CCCAACGCCA TATGCTGAA GACCAGTTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAACGCGCG TATTGGTTCG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACACAGGTC AACCGCACCA TCCGTTCGCA CACTTTCAAC CCCGACGAGT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA ATTTTATAAT
601 GCGAACAAA AAGACTATCT GCTGCCGAG GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAGGATT TTGCAGACAA GCAGACCGTC AGTGAAACGG
701 AAGTGAAAAA TGCATTTGAA GAGCGCGTGG CGGCTTTGCC GGCAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAACAA GGCAAAAGAA AAATTGGGCG
851 ACGATGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAAACTTGG CTGAGTAGGC AGGACGCGCA
951 AATGTCCGGT ATGCCCCGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCG TCCGCGCCCA AGAAGTCCGC GAAGAGAAAA CCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACTTGC CGAAAACAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GCGCAAGGCTG TTGACGTGAA ATGGTCGGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACCGGC AAACGGCAAA CCGCCTACG TCAGGCTGAT CGGTCTGCCG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GCGCAACAG CAGTCTGCCA
1451 ATACTTTTGA CTTGTTGATA CGTTATTTCA ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 836; ORF 230-1>:

m230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPPSRDA VFQSLQRAY LKQGAQLMGI SVSSEIQKI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSD QFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPQ AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLINSET
351 AWVVRAKEVR EEKTLFPAEA KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVKWE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEQAV TPPDDIAAQL PLAKQALAQQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDNG GQ*

```

m230-1/g230-1 96.3% identity in 512 aa overlap

```

          10      20      30      40      50      60
m230-1.pep MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISDHSINNAIQNEQ
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g230-1      MFHSIEKYRTPAQVLLGLIALTFVGFVSTVSHPGADYIVQVGDEKISEHSINNAMQNEQ
          10      20      30      40      50      60

          70      80      90     100     110     120
m230-1.pep ADGGGPPSRDAVFQSLQRAYLKQGAQLMGISVSSEIQKIIVDDPNFHDANGKFDHALLN
          |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:| |||:|
g230-1      ADGGGPPWRDAVFQSLQRAYLKQGAQLMGISVSSEIQKQMI VDDPNFHDANGKFSHALLS
          70      80      90     100     110     120

          130     140     150     160     170     180
m230-1.pep RYLSQRHMSDQFVEEIRDQFALQNLVNLVQNGVLVGDAQAEQLIRLTQVNRTIRSHFTN

```

g230-1	:	:	:	:	:	:
	QYLSQRHMS	EDQFVEE	IRDQFAL	QNLVSL	VQNGVL	VGDAQAEQLIRLTQVNRTIRSHFTFN
	130	140	150	160	170	180
m230-1.pep	190	200	210	220	230	240
	PDEFIAQVKVSEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
g230-1	190	200	210	220	230	240
	PDEFIAQVKASEADLQKFYNANKKDYLLPQAVKLEYVALNLKDFADKQTVSETEVKNAFE					
m230-1.pep	250	260	270	280	290	300
	ERVARLPANEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
g230-1	250	260	270	280	290	300
	ERVARLPAAHEAKPSFEQEKA AVENELKMKKAVADFNKAKEKLGDDAFNHPSSLAEAAKNS					
m230-1.pep	310	320	330	340	350	360
	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRAKEVR					
g230-1	310	320	330	340	350	360
	GLKVETQETWLSRQDAQMSGMPENLINAVFSDDVLKKKHNSVLTINSETAWVVRAKEVR					
m230-1.pep	370	380	390	400	410	420
	EEKTLFFAEAKDAVRQAYIRTEAAKLAENKAKDVLTLQNGGKAVDVKWSEVSVLGAQQAR					
g230-1	370	380	390	400	410	420
	EEKNLLFEEAKDAVRQAYIRTEAAKLAENKAKEVLTQNGGKAVDVKWSEVSVLGAQQAR					
m230-1.pep	430	440	450	460	470	480
	QSMPEAYAE LLKAKPANGKPAYVRLIGLPAPVIVEVQAVTPPDDIAAQLPLAKQALAAQQ					
g230-1	430	440	450	460	470	480
	QSMPEAYAE LLKAKPANGKPAYVRLTGLPAPVIVEAQAVTPPEDIAAQLPPAKQALAAQQ					
m230-1.pep	490	500	510			
	QSANTFDLLIRYFNGKIKQTKGAQSVDNGDGQX					
g230-1	490	500	510			
	QSANTFDLLIRYFNGKIKQTKGAQSVDNGDGQX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 837>:

a230-1.seq

```

1   ATGTTTCATT CCATCGAAAA ATACAGAACG CCCGCCAAG TCCTTTTGGG
51  CCTGATTGCA TTAACCTTCG TCGGCTTCGG GGTACGACAG GTATCCCATC
101 CGGGTGCCGA CTACATCGTC CAAGTGGGCG ACGAAAAAAT CAGCGACCAC
151 TCCATCAACA ACGCCATACA GAACGAACAG GCGGACGGCG GCGGCCCTTC
201 GCGCGACGCG GTGTTTCAAT CCCTGCTACA ACGCGCCTAC CTGAAACAGG
251 GCGCGAAGCT GATGGGCATT TCGGTTTCTT CCGAACAAAT CAAGCAGATT
301 ATCGTGGACG ATCCCAATTT CCACGACGCA AACGGCAAAT TCGACCACGC
351 GCTTTTAAAC CGTACCTTT CCCAACGTCA TATGCTGAA GACCAAGTTG
401 TCGAAGAAAT CCGCGATCAG TTTGCCTTGC AGAATTTGGT AAACCTCGTC
451 CAAAACGGCG TATTGGTCGG CGACGCGCAG GCGGAACAGC TGATCAGGCT
501 GACGACGGTC AACCGCACCA TCCGTTTCGA CACTTTCAAC CCCGACGAAT
551 TCATCGCCCA AGTCAAAGTG TCTGAAGCCG ATTTGCAGAA GTTTTATAAC
601 GCAAACAAAA AAGACTACCT GCTTCCCAA GCGGTCAAAT TGGAATATGT
651 CGCCTTGAAT CTGAAAGACT TTGCAGACAA ACAGACCGTC AGCGAAACAG
701 AAGTGAAAAA TGCCTTTGAA GAGCGCGTGG CGCGTTTGCC GGCAAATGAA
751 GCCAAACCTT CTTTCGAGCA GGAAAAAGCC GCCGTCGAAA ACGAATTGAA
801 AATGAAAAAG GCGGTTGCCG ACTTCAATAA GGCAAAAGAA AAGCTGGGCG
851 ATGACGCGTT CAACCATCCT TCCTCGCTTG CCGAAGCCGC CAAAACAGC
901 GGTTTGAAAG TCGAAACCCA AGAACTTGG CTGAGCAGGC AGGATGCGCA
951 AATGTCGGGT ATGCCCCGAA ACCTGATCAA TGCCGTATTC AGCGACGACG
1001 TATTGAAGAA AAAACACAAT TCCGAAGTGC TGACCATCAA CAGCGAAACC
1051 GCGTGGGTCTG TCCGCGCCAA AGAAGTCCGC GAAGAGAAAA CCCTGCCGTT
1101 TGCCGAAGCC AAAGACGCGG TACGTCAGGC TTATATCCGT ACCGAAGCCG
1151 CCAAACCTGC CGAAAAAAG GCAAAAGACG TGCTTACCCA ACTGAACGGC
1201 GCGAAGCGTG TTGACGTGAA ATGGTTCGAA GTGTCCGTTT TGGGCGCACA
1251 GCAGGCAAGG CAGTCCATGC CGCCCGAGGC TTATGCGGAA CTGCTGAAAG
1301 CAAAACGGCG AAACGGCAAA CCCGCCTACG TCAGGCTGAT CGGTCTGCGG
1351 GCACCCGTGA TTGTCGAAGT ACAGGCTGTA ACCCCGCCGG ATGATATCGC
1401 CGCACAGCTT CCGCTTGCAA AACAGGCTTT GGCGCAACAG CAGTCTGCCA
1451 ATACTTTCGA CTTGTTGATA CGTTATTTC ACGGCAAAAT CAAACAGACC
1501 AAAGGAGCGC AATCGGTCGA CAACGGCGAC GGTCAAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 838; ORF 230-1.a>:

a230-1.pep

```

1 MFHSIEKYRT PAQVLLGLIA LTFVGFVST VSHPGADYIV QVGDEKISDH
51 SINNAIQNEQ ADGGGPSRDA VFQSLQRAY LKQGAKLMGI SVSSEQIKQI
101 IVDDPNFHDA NGKFDHALLN RYLSQRHMSE DQFVEEIRDQ FALQNLVNLV
151 QNGVLVGDAQ AEQLIRLTQV NRTIRSHFTN PDEFIAQVKV SEADLQKFYN
201 ANKKDYLLPK AVKLEYVALN LKDFADKQTV SETEVKNAFE ERVARLPANE
251 AKPSFEQEKA AVENELKMKK AVADFNKAKE KLGDDAFNHP SSLAEAAKNS
301 GLKVETQETW LSRQDAQMSG MPENLINAVF SDDVLKKKHN SEVLTINSET
351 AWVVRakeVR EEKTLPFFAE KDAVRQAYIR TEAAKLAENK AKDVLTLQNG
401 GKAVDVkwSE VSVLGAQQAR QSMPEAYAE LLKAKPANGK PAYVRLIGLP
451 APVIVEVQAV TPDIDIAAQL PLAKQALAAQ QSANTFDLLI RYFNGKIKQT
501 KGAQSVNDGD GQ*

```

a230-1/m230-1 99.8% identity in 512 aa overlap

a230-1.pep	10	20	30	40	50	60
m230-1	10	20	30	40	50	60
a230-1.pep	70	80	90	100	110	120
m230-1	70	80	90	100	110	120
a230-1.pep	130	140	150	160	170	180
m230-1	130	140	150	160	170	180
a230-1.pep	190	200	210	220	230	240
m230-1	190	200	210	220	230	240
a230-1.pep	250	260	270	280	290	300
m230-1	250	260	270	280	290	300
a230-1.pep	310	320	330	340	350	360
m230-1	310	320	330	340	350	360
a230-1.pep	370	380	390	400	410	420
m230-1	370	380	390	400	410	420
a230-1.pep	430	440	450	460	470	480
m230-1	430	440	450	460	470	480
a230-1.pep	490	500	510			
m230-1	490	500	510			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 839>:

```
g231.seq
  1  atgtcaaaac gaaaatccat aaaccgtccg tatcaaaaac cggcggaact
 51  gccgccgttg caaaataatc cgccatttta ccgtaaaaac cgccgcctga
101  acttttttat cgcggcagac ggcggttgcg cgtctccgca aaaatgcagg
151  gcgcgcggtt ttcagacggc atttgccgtt caaggccgtg cgggtgtctt
201  accaaatgcc caaccattcg cccacggaat ccatccaatc cttattgcc
251  ccgcgcgtcc tgccctgccg gcggtacgcc cacggcgctt gcggattttt
301  agctttccac aatcctttgc gttccctttc cgctgaatt tgagcgctcg
351  catagtcggc aaaatccgcc ttatcctgct gttcttttagc ataactttta
401  taatgccacg ccgccccgtc ctgcacctgc atcaggttca aatcggtttt
451  gccggcggat acctgcgcca cttcgcgctg atagcggtcg gtttcaaaac
501  cacgtacact gactttccta ccctccgccg ccgcgcgcag gttgtcgcgc
551  gaacgtgtac cgtaagccctg tttcatctcc ggtgcgtcga tatacgccat
601  ccgaatttta tgtttcgcgc cgtcgccgtc gatgacgtga agggatcgcc
651  cgtcatagac tttggacacc gtgcctgtgt agctgtggcc ggatttcgcc
701  gatgcccgtc ggcgaacggg cgcgtcgaaa cccacgtccc ctgcagtgcc
751  gagtacgtcg agtacggcaa ccgccgtccg caccgcctca ctgtcatatc
801  ccgtataacc caacgcgccc aaaagcgaca gggcgacggg aagccatttc
851  atgatttttt taatctgcat atttttcaaa tgccgatgcc gtcgaacat
901  ctctga
```

This corresponds to the amino acid sequence <SEQ ID 840; ORF 231.ng>:

```
g231.pep
  1  MSKRKSINRP YQKPAELPPL QNPPFFYRKN RRLNFFIAAD GGCASPQKCR
 51  ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101  SFPQSFAFFP RLNLSVGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151  AGGYLRHFAL IAVGFKHTYT DFPTLRRRAQ VVARTCTVSL FHLRCVDIRH
201  PNFMFRAVAV DDVKGIIVID FGHRACVAVA GFRRCPSANG RVETHVPCSA
251  EYVEYGNRRP HRLTVISRIT QRAQKRQGDG KPFHDFNLH IFQMPMPSEH
301  L*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 841>:

```
m231.seq (partial)
  1  ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGCGGGAAC
 51  GCCGCCGTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
101  ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
151  CGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201  ACCAAATGCC CAACCATTCG GC....
```

This corresponds to the amino acid sequence <SEQ ID 842; ORF 231>:

```
m231.pep (partial)
  1  MSKRKSINRP YQKPAELPPL QNPPFFYRKN RRLNFFIAAD GGCASPQKCR
 51  ARGFQTAFV QGRAVSLPNA QPFG....
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 231 shows 98.6% identity over a 73 aa overlap with a predicted ORF (ORF 231.ng) from *N. gonorrhoeae*:

```
m231/g231
      10      20      30      40      50      60
m231.pep  MSKRKSINRPYQKPAELPPLQNPPFFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          |||
g231      MSKRKSINRPYQKPAELPPLQNPPFFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV
          |||
      10      20      30      40      50      60

      70
m231.pep  QGRAVSLPNAQPFG
          |||
g231      QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFFPRLNLSVGIVG
          70      80      90     100     110     120
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 843>:

a231.seq (partial)

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCTGA
101 ACTTTTTTAT CGNGGCAGAC GGCGGTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTCG GTGTGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCCGCCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCGGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGG CGCGTCGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCGTCCG CACCGCCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTT
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATC

```

This corresponds to the amino acid sequence <SEQ ID 844; ORF 217.a>:

a231.pep (partial)

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIXAD GGCASPQKCR
51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAL VAVGVEHADA DFPAFRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRAVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMMPSEH
301 I

```

m231/a231 98.6% identity in 73 aa overlap

	10	20	30	40	50	60
m231.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
a231	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIXADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
	70					
m231.pep	QSRVSLPNAQPFG					
a231	QSRVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFPFRLNLVSGIIG					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 845>:

g231-1.seq

```

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAAC CGGCGGAACT
51 GCCGCCGTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCTGA
101 ACTTTTTTAT CGCGGCAGAC GGCGGTGCG CGTCTCCGCA AAAATGCAGG
151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAGGCCGTG CGGTGTCTTT
201 ACCAAATGCC CAACCATTCG CCCACGGAAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCC GCGGTACGCC CACGGCGCTT GCGGATTTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAGTCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGGCGGAT ACCTGCGCCA CTTCGCGCTG ATAGCGGTCG GTTTCAAACa
501 CaCgTaCaat gagtttcgta ccctccGCCG ccgcgcgCAG GTTgtcgGC
551 GAACgTGtAC CGTAagcgtg TTtcatctcc GGTGcgtcGA TATACGCCaT
601 cCgAATTTta tGtttcgcgc cgtcgcCgtc gATGACGTGA AGGGtatcGC
651 CgtcATAGAC TTTGGACACC Gtgcctgcgt AGctGTGGCC GGATttcgc

```

This corresponds to the amino acid sequence <SEQ ID 846; ORF 231-1.ng>:

g231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QGRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF

```

101 SFPQSFAFFP RLNLVSGIVG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
 151 AGGYLRHFAL IAVGFKHTYN EFRTLRRRAQ VVARTCTVSV FHLRCVDIRH
 201 PNFMFRAVAV DDVKGIAVID FGHRACVAVA GFR

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 847>:

m231-1.seq

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG
 151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
 201 ACCAAATGCC CAACCATTCG CCCACGGCAT CCATCCAATC CTTATTGCC
 251 CGCCCGCTCC TGCCTGCTCG GCGGTACGCC CACGGCGCTT GCGGATTTTT
 301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCTGAATT TGAGCGTCGG
 351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
 401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
 451 GCCGACAGAA ACCTGCGCCA CTTCGCGCTG GTAGCGGTG GTATCGAACA
 501 CGCGCACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTCGCGC
 551 GAACGCGTGC CGTAAGCCTG TTTCATCTCC GGCGCGTGA TATACGCCAT
 601 CCGGATTTTG TGTTCGCGC CGTCGCGCTC GATAACGTGA AGGGTGTGCG
 651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
 701 GATGCTCGGC GCGGGGCGGG CGCGTCGGAA CCGCGCTCCC CTGCCGCGCC
 751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
 801 CCGTATAACC CAACGCACCC AAAAGCGACA GGGCGACGGG AAGCCATTTC
 851 ATGATTTTTT TAATCTGCAT ATTTTCAAA TGCCGATGCC GTCTGAACAT
 901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

This corresponds to the amino acid sequence <SEQ ID 848; ORF 231-1>:

m231-1.pep

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPOKCR
 51 ARGFQTAFV QSRVSLPNA QPFAHGIHPI LIAPAAPACS AVRPRRLRIF
 101 SFPQSFAFFP RLNLVSGIIG KIRLILLFFS ITFIMPRRPV LHLHQVQIGF
 151 ADRNLRHFAL VAVGIEHAHA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
 201 PDFVFRAVAV DNVKGVAVD FGHRACVAVA GFRRC SAAG RVGTRVPCRA
 251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMMPMSEH
 301 IGIGFQTAS*

g231-1/m231-1 87.0% identity in 262 aa overlap

	10	20	30	40	50	60
g231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPOKCRARGFQTAFV					
	10	20	30	40	50	60
g231-1.pep	QGRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFPQSFAFFPRLNLVSGIVG					
m231-1	QSRVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFPQSFAFFPRLNLVSGIIG					
	70	80	90	100	110	120
g231-1.pep	KIRLILLFFSITFIMPRRPVLHLHQVQIGFAGGYLRHFALIAVGFKHTYNEFRTLRRRAQ					
m231-1	KIRLILLFFSITFIMPRRPVLHLHQVQIGFADRNLRFHFAVAVGIEHAHADFPFRRRAQ					
	130	140	150	160	170	180
g231-1.pep	VVARTCTVSVFHLRCVDIRHPNFMFRAVAVDDVKGIAVIDFGHRACVAVAGFRXCPSANG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRAVAVDNVKGVAVIDFGHRACVAVAGFRRC SAAGG					
	190	200	210	220	230	240
g231-1.pep	CVETHVPCSAEYVVXGNRRPHR					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMMPMSEH					
	250	260	270	280	290	300

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 849>:

a231-1.seq

1 ATGTCAAAAC GAAAATCCAT AAACCGTCCG TATCAAAAC CGGCGGAAC
 51 GCCGCCGTTG CAAAATAATC CGCCATTTTA CCGTAAAAAC CGCCGCCTGA
 101 ACTTTTTTAT CGCGGCAGAC GGCGGTTGCG CGTCTCCGCA AAAATGCAGG

```

151 GCGCGCGGTT TTCAGACGGC ATTTGCCGTT CAAAGCCGTG CCGTGTCTTT
201 ACCAAATGCC CAACCATTCC CCCACGGCAT CCATCCAATC CTTATTGCCC
251 CCGCCGCTCC TGCCTGCCCG GCGGTACGCC CACGGCGCTT GCGGATTTT
301 AGCTTTCCAC AATCCTTTGC GTTCCCTTTC CGCCTGAATT TGAGCGTCGG
351 CATAATCGGC AAAATCCGCC TTATCCTGCT GTTCTTTAGC ATAACTTTTA
401 TAATGCCACG CCGCCCCGTC CTGCACCTGC ATCAGGTTCA AATCGGTTTT
451 GCCGACAGAA ACCTGCGCCA CTTCCGCTG GTAGCGGTCG GTGTCGAACA
501 CGCGGACGCT GACTTTCCTG CCTTCGCGCG CCGCGCGCAG GTTGTGCGCG
551 GAACGCGTGC CGTAAGCCTG TTTTCATCTC GCGCGCTCGA TATACGCCAT
601 CCGGATTTTG TGTTCGCGC CGTCGCCGTC GATAACGTGA AGGGTGTGCG
651 CGTCATAGAC TTTGGACACC GTGCCTGTGT AGCGGTGGCC GGATTTCGCC
701 GATGCTCGGC GCGGGCGGG GCGCTCGGAA CCCGCGTCCC CTGCCGCGCC
751 GAGTACGTCG AGTACGGCAA CCGCCGTCG CACCGCTCG CTGCCGTACC
801 CCGTATAACC CAACGCACCC AAAAGCGACA AGGCGACGGG AAGCCATTTC
851 ATGATTTTTT TAATCTGCAT ATTTTTCAAA TGCCGATGCC GTCTGAACAT
901 ATCGGAATCG GATTTCAGAC GGCATCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 850; ORF 231-1.a>:

a231-1.pep

```

1 MSKRKSINRP YQKPAELPPL QNNPPFYRKN RRLNFFIAAD GGCASPQKCR
51 ARGFQTAFV QSRAVSLPNA QPFAHGIHPI LIAPAAPACP AVRPRRLRIF
101 SFPQSFAFPF RLNLVSGIIG KIRLILFFS ITFIMPRRPV LHLHQVQIGF
151 ADRNLRHFAV VAVGVEHADA DFPAFRRRAQ VVARTRAVSL FHLRRVDIRH
201 PDFVFRVAV DNVKGVAVID FGHRACVAVA GFRRCSAAGG RVGTRVPCRA
251 EYVEYGNRRP HRLAAVPRIT QRTQKRQGDG KPFHDFNLH IFQMPMPSEH
301 IGIGFQTAS*

```

a231-1/m231-1 99.0% identity in 309 aa overlap

	10	20	30	40	50	60
a231-1.pep	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
m231-1	MSKRKSINRPYQKPAELPPLQNNPPFYRKNRRLNFFIAADGGCASPQKCRARGFQTAFV					
	10	20	30	40	50	60
a231-1.pep	70	80	90	100	110	120
	QSRAVSLPNAQPFAHGIHPILIAPAAPACPAVRPRRLRIFSFQSFAPFRLNLVSGIIG					
m231-1	QSRAVSLPNAQPFAHGIHPILIAPAAPACSAVRPRRLRIFSFQSFAPFRLNLVSGIIG					
	70	80	90	100	110	120
a231-1.pep	130	140	150	160	170	180
	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRHFAVAVGVEHADADFPFRRRAQ					
m231-1	KIRLILFFSITFIMPRRPVLHLHQVQIGFADRNLRHFAVAVGIEHAHADFPFRRRAQ					
	130	140	150	160	170	180
a231-1.pep	190	200	210	220	230	240
	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDQNVKGVAVIDFGHRACVAVAGFRRCSAAGG					
m231-1	VVARTRAVSLFHLRRVDIRHPDFVFRVAVDQNVKGVAVIDFGHRACVAVAGFRRCSAAGG					
	190	200	210	220	230	240
a231-1.pep	250	260	270	280	290	300
	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
m231-1	RVGTRVPCRAEYVEYGNRRPHRLAAVPRITQRTQKRQGDGKPFHDFNLHIFQMPMPSEH					
	250	260	270	280	290	300
a231-1.pep	310					
	IGIGFQTASX					
m231-1	IGIGFQTASX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 851>:

g232.seq

```

1 atgatgggca acagcctgat tgaatccggt acgtttgtcg ccatacctgtt
51 tggtcagatt ttgggaacgg cggttgccgg cgcgccgct tatattgtcg
101 ggatactggt ttgctgggtc gccgtcggag gaacggccgg cagcctgttt

```

530

```

151 atgccgtccg tacccgccaa ggctgccgat acccaaatcg agtggaatat
201 tgtccgtggt acaaaatccc tgctgcgtga aacgggtgcg cacaatcccc
251 tttttaccgc cattatcggc atctcgtggt tttggtttgt cggcgcggtt
301 tataccacgc aactgccgac ctttacccaa atccatttgg gcggcaacga
351 taatgttttt aacctgatgc ttgctttggt ttccatcggg attgccgccc
401 gttcgggtact gtgtgccaaag ttcggcaggg aacggctgat gttggcttgg
451 gtaacggttg gtgcgttggg ttcgacggtt tgcggcctgg ttttggtgtg
501 gctgacgcac ggacaccggt ttgaagggct gaacggcatt ttttggtttt
551 tatcgcaagg atgggcatac cccgtgatgg cggtgatgac gctgatcggc
601 tttttcggcg gattttttctc cgttccgctc tatacctggc tgcaaaccgc
651 cagcagcgag actttccgcg cccgcgcgct tgccgccaac aatatcgtta
701 acggcatctt tatggtttcc gccgcgctt tgagcgcggt attgctgttt
751 ttgtttgaca gcatttccct gctgtatctg attgtcgctt tgggcaatat
801 tccgttggcg gtatttttga ttaagcgcg aaggcggttt ttaggcgcg
851 cggcaatcag gaaaaaacct tga

```

This corresponds to the amino acid sequence <SEQ ID 852; ORF 232.ng>:

g232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGAPP YIVGILVLLV AVGGTAGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HNPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FGRERLMLAW
151 VTVGALGSTV CGLVLVWLTH GHRFEGLNGI FWFLSQGWAY PVMAMVTLIG
201 FFGGFFSVPL YTWLQTASSE TFRARAVAN NVNGIFMVSA AAVLSAVLLF
251 LFDSISLLYL IVALGNIPLA VFLIKRERRF LGAAAIRKKP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 853>:

m232.seq

```

1 ATGATGGGCA ACAGCCTGAT TGAATCGGGT ACGTTTGTCG CCATCTGTGT
51 CCGTCAGATT TTGGGAACGG CCGTGGCAGG TGTACCGCCT TATATTGTCTG
101 GGATACTGGT TTTGCTGGTC GCCGTCCGAG GCACGGTCGG CAGCCTGTGT
151 ATGCCGTCCG TACCCGCCAA GGCTGCCGAT ACACAAATTG AGTGAATAT
201 TGTCCGTGGC ACAAATCCCC TGCTGCGTGA AACGGTGCGG CACAAGCCCG
251 TTTTACCAGC CATTATCGGT ATTTCTGTGT TTTGGTTTGT CGGCGCGGTT
301 TATACCACGC AACTGCCGAC CTTTACCCAA ATCCATCTGG GCGGCAACGA
351 CAATGTTTTC AACCTGATGC TTGCTCTGTT TTCCATCGGT ATTGCCGCCG
401 GTTCGGTACT GTGTGCCAAG TTCAGCAKGG AACGCCTGAT GTTGCTTGG
451 GTAACGGTTG GTGCGTTGGG TTTGACGGTT TCGGCTTGG TTTTGGTGTG
501 GCTGACGCAC GGACACCGTT TTGAAGGGCT GAACGGCATT TTTTtGTTTT
551 TATCGCAAGG ATGGGCATAT CCCGTGATGG CCGTGATGAC GCTGATCGGC
601 TTTTTCGGCG GATTTTTTCTC CGTTCCGCTC TATACct (g) TG CAAACCGCCa
651 TAGCGAGaTT TCCGCGCCCG GCCGTTGCCG CCAACAATAT CGTTAACGGT
701 ATTTTATGAG TTTCCGCTGC CGTTTTGAGC GCGGTGTTGC TGTTTTGTG
751 TGACAGCATT TCCTTGTTGT ATCTGATTGT CGCTTTGGGC AATATTCCGT
801 TGTCGTATT TTTGATTAAG CGCGAAAGGC GGTTTTTAGG CGCGCGCGCA
851 ATCAGGAAAA AACCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 854; ORF 232>:

m232.pep

```

1 MMGNSLIESG TFVAILFGQI LGTAVAGVPP YIVGILVLLV AVGGTVGSLF
51 MPSVPAKAAD TQIEWNIVRG TKSLLRETVR HKPVFTAIIG ISWFWFVGAV
101 YTTQLPTFTQ IHLGGNDNVF NLMLALFSIG IAAGSVLCAK FSXERLMLAW
151 VTVGALGLTV CGLVLVWLTH GHRFEGLNGI FXFLSQGWAY PVMAMVTLIG
201 FFGGFFSVPL YTVQTAIARF PRPAVAANNI VNGIFMVSA VLSAVLLFLF
251 DSISLLYLIV ALGNIPLSVF LIKRERRFLG AAAIRKKP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 232 shows 94.1% identity over a 290 aa overlap with a predicted ORF (ORF 232.ng) from *N. gonorrhoeae*:

m232/g232

```

          10      20      30      40      50      60
m232.pep  MMGNSLIESGTFVAILFGQILGTAVAGVPPYIVGILVLLVAVGGTVGSLFMPSVPAKAAD
          |||||:|||||:|||||:|||||:|||||:
g232      MMGNSLIESGTFVAILFGQILGTAVAGAPPYIVGILVLLVAVGGTAGSLFMPSVPAKAAD

```

531

	10	20	30	40	50	60
	70	80	90	100	110	120
m232.pep	TQIEWNIVRGTKSLLRETVRHKPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
g232	TQIEWNIVRGTKSLLRETVRHNPVFTAIIGISWFWFVGAVYTTQLPTFTQIHLGGNDNVF					
	130	140	150	160	170	180
m232.pep	NLMLALFSIGIAAGSVLCAKFSXERLMLAWVTVGALGLTVCGLVLVWLTHGHRFEGLNGI					
g232	NLMLALFSIGIAAGSVLCAKFRERLMLAWVTVGALGSTVCGLVLVWLTHGHRFEGLNGI					
	190	200	210	220	230	
m232.pep	FXFLSQGWAYPVMAMVTLIGFFGGFFSVPLYT-VQTAIARFPRP-AVAANNIVNGIFMVS					
g232	FWFLSQGWAYPVMAMVTLIGFFGGFFSVPLYTWLQTASSETFRARAANAANNIVNGIFMVS					
	240	250	260	270	280	289
m232.pep	AAVLSAVLLFLFDSISLLYLIALGNIPLSVFLIKRERRFLGAAAIRKKPX					
g232	AAVLSAVLLFLFDSISLLYLIALGNIPLAFLIKRERRFLGAAAIRKKP					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 855>:

```

a232.seq
1  ATGTACGCTA AAAAAGGCGG TTTGGGACTG GTTAAAGCC GCCGTTTCGC
51  ACCTCTTTTC GCTACGCAGT TTCTCGGCGC GTTCAACGAC AATGTGTTCA
101 AAACCGCGCT GTTTGTGATG ATTGGGTTTT ACGGTTTGGG GCAAAACGGC
151 TTCTTGCCCTG CCGGACAGAT GTTGAAGTTG GGCGCGTTGC TGTATTATTT
201 GCCGTATTTTC CTGTTTTCCCT CGCTGTCGGG GCAGTTGGGT AACAAATTTC
251 ACAAGGCCGT TTTGGCGCGT TGGGCCAAGG TGCTGGAAAT GATCATTATG
301 GCGGTGGCGG CATACGGGTT TTATATCCGG TCTGCCCCGC TGCTTTTGGC
351 GTGTCTGTTT TGCATGGGCG CGCAATCGAC GCTGTTCCGG CCGCTGAAAT
401 ACGCCATCCT GCCCGATTAT CTCGACGACA AAGAGTTGAT GATGGGCAAC
451 AGCCTGATTG AATCGGGTAC GTTTGTGCGC ATCCTGTTCC GTCAGATACT
501 GGGGACTGCG GTGGCAGGTG TACCGCCTTA TATTGTCGGG ATACTGGTTT
551 TGCTGGTCGC CGTAGGAGGC ACGGTCGGCA GCCTGTTTAT GCCGTCCGTA
601 CCCGCCAAGG CTGCCGATAC ACAAATTGAG TGGAATATTG TCCGGGGTAC
651 AAAATCCCTG CTGCGTGAAA CCGTGCGGCA CAAGCCCGTT TTTACGCCCA
701 TTATCGGTAT TTCGTGGTTT TGGTTTGTGC GCGCGGTTTA TACCACGCAA
751 CTGCCGACCT TTACCCAAAT CCATCTAGGC GGCAACGACA ATGTTTTCAA
801 CCTGATGCTT GCCCTGTTTT CCATCGGTAT TGCCGCCGGT TCGGTACTGT
851 GTGCCAAGTT CAGCAGGGAA CGGCTGAGGT TGGCTTGGGT AACGGTTGGT
901 GCGTTGGGTT TGACGGTTTG CGGCTTGGTT TTGGTGTGGC TGACGCACGG
951 ACACCGTTTT GAAGGGCTGA ACGGCATTTT TTGGTTTTTA TCGCAAGGAT
1001 GGGCATATCC CGTGATGGCG GTGATGACGC TGATCGGCTT TTTCGGCGGA
1051 TTTTCTCCG TTCCGCTCTA TACCTGGCTG CAAACCGCCA GTAGCGAGAC
1101 TTTCCGCGCC CGCGCCGTTG CCGCCAACAA TATCGTTAAC GGTATTTTAA
1151 TGGTTTCCGC TGCCGTTTTG AGCGCGGTGT TGCTGTTTTT GTTTGACAGC
1201 ATTTCTTGT TGTATCTGAT TGTGCTTTG GGCAATATTC CGTTGTCCGT
1251 ATTTTGTGAT AAGCGCGAAA GCGGTTTTTT AGGCGCGGCG GCAATCAGGA
1301 AAAACCTTG A

```

This corresponds to the amino acid sequence <SEQ ID 856; ORF 232.a>:

```

a232.pep
1  MYAKKGGLGL VKSRREFAPLF ATQFLGAFND NVFKTALFVM IGFYGLGQNG
51  FLPAGQMLNL GALLFILPYF LFSSLSGQLG NKFDKAVLAR WAKVLEMIIM
101 AVAAYGFYIR SAPLLIACLF CMGAQSTLFG PLKYAILPDY LDDKELMMGN
151 SLIESGTFVA ILFGQILGTA VAGVPPYIVG ILVLLVAVGG TVGSLEMPSTV
201 PAKAADTQIE WNIVRGTKSL LRETVRHKPV FTAIGISWF WFGAVYTTQ
251 LPTFTQIHLG GNDNVFNLM LALFSIGIAAG SVLCAKFSRE RLRLAWVTVG

```

532

301 ALGLTVCGLV LVWLTHGHRF EGLNGIFWFL SQGWAYPVMA VMTLIGFFGG
 351 FFSVPLYTWL QTASSETFRA RAVAANNIVN GIFMVSAAVL SAVLLFLFDS
 401 ISLLYLIVAL GNIPLSVFLI KRERRFLGAA AIRKKP*

m232/a232 95.9% identity in 290 aa overlap

m232.pep					10	20	30
					MMGNSLIESGTFVAILEFGQILGTAVAGVPP		
a232	ACLFCMGAQSTLFGPLKYAILPDYLDKELMMGNSLIESGTFVAILEFGQILGTAVAGVPP						
	120	130	140	150	160	170	
m232.pep		40	50	60	70	80	90
		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
a232		YIVGILVLLVAVGGTVGSLFMPSVPAKAADTQIEWNIVRGTKSLLRETVRHKPVFTAIIG					
		180	190	200	210	220	230
m232.pep		100	110	120	130	140	150
		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSXERLMLAW					
a232		ISWFWFVGAVYTTQLPTFTQIHLGGNDNVFNLMMLALFSIGIAAGSVLCAKFSRERLRLAW					
		240	250	260	270	280	290
m232.pep		160	170	180	190	200	210
		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFXFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
a232		VTVGALGLTVCGLVLVWLTHGHRFEGLNGIFWFLSQGWAYPVMAVMTLIGFFGGFFSVPL					
		300	310	320	330	340	350
m232.pep		220	230	240	250	260	
		YT-VQTAIARFPRP-AVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
a232		YTWLQTASSETFRARAVAANNIVNGIFMVSAAVLSAVLLFLFDSISLLYLIVALGNIPLS					
		360	370	380	390	400	410
m232.pep		270	280	289			
		VFLIKRERRFLGAAAIRKKPX					
a232		VFLIKRERRFLGAAAIRKKPX					
		420	430				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 857>:

g233.seq

1	atgaaacgca	aaaatatcgc	gctgattccc	gccgccggca	tccgggtgcg
51	tttcggtgcg	gacaaaccca	agcaatatgt	cgaaatcgga	agcaaaaccg
101	ttttagaaca	tgtacttggg	atttttgaa	ggcatgaggc	cgtcgatttg
151	accgtcggtg	tcgtctcgcc	cgaagacacg	tttgccgata	aggttcagac
201	ggcatttcca	caggttcggg	tgtggaaaaa	cggtggacag	accgcgcgcg
251	aaactgtccg	caacggtgtg	gcaaaactgt	tggaaaccgg	tttggcggcg
301	gaaaccgaca	atattctggt	acacgatgcc	gcccgtgct	gcctgccgtc
351	tgaagctctg	gcgcggttga	tagaacaggc	gggcaacgcc	gccgaaggcg
401	ggattttggc	agttcccgtt	gccgatacgc	tcaagcgcgc	agaaagcgga
451	caaatcagtg	caactgtcga	ccgttcgggg	ctttggcagg	cgcaaacgcc
501	gcagcttttt	caagcgggtt	tgctgcaccg	cgcattggct	gcggaaaact
551	tgggcggcat	taccgatgaa	gcgtccgcgc	tggaaaaact	gggtgtgcgt
601	ccgctactga	tacagggcga	cgcgcgcaat	ttgaaactga	cgcagccgca
651	ggacgcatac	atcgtcaggc	tgctgctcaa	tgccgtctga	

This corresponds to the amino acid sequence <SEQ ID 858; ORF 233.ng>:

g233.pep

1	MKRKNIALIP	AAGIGVRFGA	DKPKQYVEIG	SKTVLEHVLG	IFERHEAVDL
51	TVVVVSPEDT	FADKVQTAFP	QVRVWKNNGQ	TRAETVRNGV	AKLLETGLAA
101	ETDNILVHDA	ARCCLPSEAL	ARLIEQAGNA	AEGGILAVPV	ADTLKRAESG

```
m233.seq (partial)
```

1	ATGAAGCGCA	AAAATATCGC	GCTGATTCCC	GCCGCCGGCA	TCGGGGCGCG
51	TTTCGGTGCG	GACAAACCCA	AGCAATATGT	CGAAATCGGA	AGCAAAACCG
101	TTTTAGAAC	TACGATTGGG	ATTTTTGAAC	GGCATGAGGC	CGTCGATTTG
151	ACCGTCGTTG	TCGTCTCGCC	CGAAGACACG	TTTGCCGATA	AGGTTCTAGAC
201	GGCATTTC	CAGGTTCTGGG	TGTGGA	CGGCGGACAG	ACCCGCGCCG
251	AAACCGTCCG	CAACGGTGTG	GCAAACTGT	TGGA	TTTGCGGCG
301	GAAACCGACA	ATATTCTGGT	ACACGATGCC	GCGCGTTGCT	GCCTGCCGTC
351	TGAAGCTTTG	ACGCGTTGA	TAGAACAGGC	GGGCAACGCC	GCCGAAGGCG
401	GGATTTTGGC	AATTCCCAT	GCCGATACG	TCAAGTGCGC	GGACGTTGGG
451	AACATT				

m233.pep (partial)

```

1  MKRVKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51 TVVVVSPEDT FADKVQTAFP QVRVWKNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAIPI ADTLKCADGG
151 NI....

```

Homology with a predicted ORF from *N. gonorrhoeae*

m233/g233

		10	20	30	40	50	60
m233.pep		MKRKNIALIPAAIGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT					
		:					
g233		MKRKNIALIPAAIGIGVRFGADKPKQYVEIGSKTVLEHVLGIFERHEAVDLTVVVVSPEDT					
		10	20	30	40	50	60
		70	80	90	100	110	120
m233.pep		FADKVQTAFFQVRVWKNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
g233		FADKVQTAFFQVRVWKNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL					
		70	80	90	100	110	120
		130	140	150			
m233.pep		TRLIEQAGNAAEGGILAIPIADTLKCADGGNI					
		: : : : : :					
g233		ARLIEQAGNAAEGGILAVPADTLKRAESGQISATVDRSGLWQAQTPQLFQAGLLHRLALA					
		130	140	150	160	170	180

a233.seq

1	ATGAAGCGCA	AAAATATCGC	GCTGATTCCC	GCCGCCGGCA	TCGGGGCGCG
51	TTTCGGTGCG	GACAAACCCA	AGCAATATGT	CGAAATCGGA	AGCAAAACCG
101	TTTTAGAACA	TACGATTGGG	ATTTTGAAC	GGCATTGAGC	CGTCGATTTG
151	ACCGTCTGTG	TCGTCTCGCC	CGAAGACAGC	TTTGCGGATA	AGGTTACAGC
201	GGCATTTCCTA	CAGGTTCTGGG	TGTGGAACAAA	CGGCGGACAG	ACCCGCGCCG
251	AAACTGTCCG	CAACGGTGTG	GCAAAATTGT	TGGAACCCGG	TTTGCGCGCG
301	GAAACCGACA	ATATTCTGTG	ACACGATGCC	GCGCGTTGCT	GCCTGCCGTG
351	TGAAGCTTTG	ACGCGTTTGA	TAGAACAGGC	GGGCAACGCT	CGCGAAGGTG
401	GGATTTTGGC	AATTCCCGTT	CGCGATACGC	TCAAGTGCGC	GGACGCTGGG
451	AACATTAGTG	CAACCGTCGA	GCGGACGAGC	CTTTGGCAGG	CGCAAACGCC
501	GCAGCTTTTC	CGCGCCGGGC	TGCTGCAACG	CGCATTGCTG	GCGGAAAAC
551	TGGACGGCAT	TACCCGATGA	CGCTCCGCCG	TGGAACAAAT	GGGCATCCGC
601	CCTTTGCTTG	TGCAGGGCGA	CGCGCGCAAT	TTGAAACTGA	CGCAGCCGCA
651	GGACGCATAC	ATCGTCAGGC	TGCTGCTCGA	TGCCGTCTGA	

This corresponds to the amino acid sequence <SEQ ID 862; ORF 233.a>:

```
a233.pep
1  MKRKNIALIP AAGIGARFGA DKPKQYVEIG SKTVLEHTIG IFERHEAVDL
51  TVVVVSPEDT FADKVQTAFF QVRVWKNNGGQ TRAETVRNGV AKLLETGLAA
101 ETDNILVHDA ARCCLPSEAL TRLIEQAGNA AEGGILAI PV ADTLKCADGG
151 NISATVERTS LWQAQTPQLF RAGLLHRLA AENLDGITDE ASAVEKLGIR
201 PLLVQGDARN LKLTQPQDAY IVRLLLDAV*
```

m233/a233 99.3% identity in 152 aa overlap

```

10      20      30      40      50      60
m233.pep  MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          |||
a233      MKRKNIALIP AAGIGARFGADKPKQYVEIGSKTVLEHTIGIFERHEAVDLTVVVVSPEDT
          |||
10      20      30      40      50      60

70      80      90      100     110     120
m233.pep  FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          |||
a233      FADKVQTAFFQVRVWKNNGGQTRAETVRNGVAKLLETGLAAETDNILVHDAARCCLPSEAL
          |||
70      80      90      100     110     120

130     140     150
m233.pep  TRLIEQAGNAAEGGILAIPIADTLKCADGGNI
          |||
a233      TRLIEQAGNAAEGGILAIPIADTLKCADGGNISATVERTSLWQAQTPQLFRAGLLHRLA
          |||
130     140     150     160     170     180

a233      AENLDGITDEASAVEKLGIRPLLQGDARNLKLTQPQDAYIVRLLLDAVX
          |||
190     200     210     220     230
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 863>:

```
g234.seq
1  atgaaaaccg tttccgcgcg catcgctttt gccgcgcgctg ccgtttcact
51  gaccggctgt gcgaccgagt cctcacgcag cctcgagggt gcaaaagtcg
101 cctcctgcaa tacgcaatat cacggtgttc gcaccccgat ttccgtcgga
151 acattcgaca accgctccag cttccaaaaa ggcattttct ccgacagtga
201 agaccgtctg ggcagccagg caaaaacccat cctggtaaca cacctgcaac
251 aaaccaaccg cttcaacgta ctgaaccgca ccaaccttag cgcattgaaa
301 caggaatccg gcatttcgag caaagcgagc aacctgaaag gcgcagatta
351 tgctggtacc ggcgatgtaa ccgaattcgg acgcagagat gtcggcgatc
401 atcagctctt cggcattttg ggctcgcgga aatcgcaaat cgcctatgca
451 aaagtggctc tgaatatcgt caacgtcaat acttccgaaa tcgtctattc
501 cacacagggc gcgggcgaat acgcactttc caaccgcgaa atcatcggtt
551 tcggcggcac ttccggctac gatgcgactt tgaacggcaa agttttagac
601 ttggcaatcc gcgaagcgt cgacaacttg gttcaggctg tcgacaacgg
651 cgcattggcaa tccaaccgtt aa
```

This corresponds to the amino acid sequence <SEQ ID 864; ORF 234.ng>:

```
g234.pep
1  MKTVSAAIAF AAAVSLTGC ATESSRSLEV AKVASCNTQY HGVRTPISVG
51  TFDNRSSFQK GIFSDSEDRL GSQAKTILVT HLQQTNRFNV LNRNTLSALK
101 QESGISGKAQ NLKGADYVVT GDVTEFGRRD VGDHQLFGIL GRGKSQIAYA
151 KVALNIVNVN TSEIVYSTQG AGEYALSRE IIGFGGTSY DATLNGKVL D
201 LAIREAVDNL VQAVDNGAWQ SNR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 865>:

```
m234.seq (partial)
1  ...GGCGCGGGCG AATACGCACT TTCCAACCGt GAAATCATCG GTTTCGGCGG
51  CACTTCCGGC TACGATGCGA CTTTGAACGG CAAAGTTTTA GACTTGGCAA
101 TCCGCGAAGC .gTCAACAGC CTGGTTCAGG CTGTTGACAA CGGCGCATGG
151 CAACCCAACC GTTAA
```

This corresponds to the amino acid sequence <SEQ ID 866; ORF 234>:

535

m234.pep (partial)
 1 ..GAGEYALSNR EIIGFGGTSG YDATLNGKVL DLAIREAVNS LVQAVDNGAW
 51 QPNR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 234 shows 94.4% identity over a 54 aa overlap with a predicted ORF (ORF 234.ng) from *N. gonorrhoeae*:

m234/g234

					10	20	30
m234.pep					GAGEYALSNREI	IGFGGTSGY	DATLNGKVL
g234	LGRGKSQIAYAK	VALNIVNVNT	SEIVYSTQ	GAGEYALSNREI	IGFGGTSGY	DATLNGKVL	
	140	150	160	170	180	190	

		40	50
m234.pep	DLAIREAVNSLVQ	AVDNGAWQPNRX	
		:	
g234	DLAIREAVDNLVQ	AVDNGAWQSNRX	
	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 867>:

a234.seq (partial)
 1 AACCGCACCT ATTTGAACGC ATTAAACAG GAATCCGGCA TTTCCGGCAA
 51 AGCGCATAAC CTGAAAGGCG CAAATTATGT CGNNACCGGC GATGTAACCG
 101 AATTCGGACG CANAGATGTC GGCGATCATC AGCTCTTCGG CATTTTGGGT
 151 CGCGGCAAAT CGCAAATCGC CTATGCAAAA GTGGCTCTGA ATATCGTCAA
 201 CGTCAATACT TCCGAAATCG TCTATTCCGC ACAGGGCGCG GGCGAATACG
 251 CACTTTCCAA CCGTGAAATC ATCGGTTTCG GCGGCACTTC CGGTACGAT
 301 GCGACTTTGA ACGGCAAAGT TTTAGACTTG GCAATCCGCG AAGCCGTCAA
 351 CAGCCTGGTT CAGGCTGTTG ACAACGGCGC ATGGCAACCC AACCGTTAA

This corresponds to the amino acid sequence <SEQ ID 868; ORF 234.a>:

a234.pep (partial)
 1 NRTYLNALKQ ESGISGKAHN LKGANYVXTG DVTEFGRXDV GDHQLFGILG
 51 RGKSQIAYAK VALNIVNVNT SEIVYSAQGA GEYALSNREI IGFGGTSGYD
 101 ATLNGKVLDL AIREAVNSLV QAVDNGAWQP NR*

m234/a234 100.0% identity in 54 aa overlap

					10	20
30						
m234.pep					GAGEYALSNREI	IGFGGTSGYD
a234	LGRGKSQIAYAK	VALNIVNVNT	SEIVYSAQGA	GAGEYALSNREI	IGFGGTSGYD	DATLNGKVL
	50	60	70	80	90	100

		40	50
m234.pep	DLAIREAVNSLVQ	AVDNGAWQPNRX	
		:	
a234	DLAIREAVNSLVQ	AVDNGAWQPNRX	
	110	120	130

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 869>:

g235.seq

1	atgaaacctt	tgattttagg	gcttgccgc	gtgttggtc	tgtctgctg
51	ccaagtctga	aaagctccc	acctcgacta	cacgtcattc	aaagaaagca
101	aaccggcttc	aattttggtg	gttcgccgc	tgaacgagtc	gcctgatgtc
151	aacggcactt	gggggatgct	ggcttcgacc	gccgcgccgc	tttccgaagc
201	cggctattac	gtctttccgc	cgcagctcgt	ggaggaacaac	ttcaaaagaa
251	acggcttgac	caatgcgcc	gatattcacg	caggtccggcc	ggaaaaactg
301	catcaaattt	tcggcaatga	tcggtttttg	tacattacgg	ttaccgaata
351	cggcacttca	tatcaaattt	tagacagcgt	gacgaccgta	tcgcctaaag
401	cacggctggg	cgattcccgc	aacgggaaag	agtgtgtgtc	gggttcggcc
451	agcatccgcg	aaggcagcaa	caacagcaac	agcggcctgc	tgggggcttt
501	ggtcggcgca	gtggccaatc	agattgccaa	cagcctgacc	gaccgcggtt
551	atcaggtttc	caaaacgcgc	gcatacaacc	tactgtcgcc	ctattcccgc
601	aacggtatct	tgaaaggctc	gagattcgtc	gaagagcagc	ccaaataa

g235.ppe

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 871>:

m235.seq

1	ATGAAACCTT	TGATTTTAGG	GCTTGCCGCC	GTGTGGCGC	TGCTGCGCTG
51	CCAAGTTCAA	AAAGCGCCCG	ATTTGCGACTA	CACGTCATTG	AAGGAAAGCA
101	AACCGGCTTC	AATTTTGGTG	GTTCGCGCGC	TGAACGAATC	GCCCGATGTC
151	AACGGACAT	GGGTTGTACT	GGTTCGAC	CGCGCGCCG	TTTCCGAAGC
201	CGGCTATTAC	GTCTTCCCG	CCGCAGTCGT	GGAGGAAACC	TTCAAAACAA
251	ACGGCTTGAC	CAATGCCGCC	GATATTCACG	CCGTCCGGCC	GGAAAACTG
301	CATCAGATT	TCGGCAATG	TGCGTTTGT	TACATTACGG	TTACCGAATA
351	CGGCACCTCA	TATCAAATTT	TAGACAGCTG	GACGACCCTA	TCCGCGAAAG
401	CACGGCTGGT	CGATTCCCGC	AACGGAAG	AGTTGTGGTC	GGTTCCGGCC
451	AGCATCCGCG	AAGGCAGCAA	CAACAGCAAC	AGCGCCTGT	TGGGGGCTTT
501	GGTCAGCGCA	GTGGTCAATC	AGATTGCCAA	CAGCGTGACC	GACCGCGTAT
551	ATCAGGTTTC	CAAAACCGCC	GCATACAAC	TGCTGTCCGC	CATTCTCTCC
601	AACGGCATCT	TGAAAGGTC	GAGATTCGTT	GAAGAGCAGC	CCAATAAA

m235 . pep

1	<u>MKPLILGLAA</u>	<u>VLALSACQVQ</u>	KAPDFDYTSF	KESKPASILV	VPPLNESPDV
51	NGTWGVLAST	AAPLSEAGYY	VFPAAVVEET	FKQNGLTNAA	DIHAVRPEKL
101	HQIFGNDAVL	YITVTEYGTS	YQILDSVTTV	SAKARLVDSR	NGKELWSGSA
151	SIREGSNNNS	SGLLGALVSA	VVNQIANSLT	DRGYQVSKTA	AYNLLSPYSH
201	NGILKGPRFV	EEQPK*			

Homology with a predicted ORF from *N. gonorrhoeae*

m235/g235

	10	20	30	40	50	60
m235.pep	MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST					
	: :					
g235	MKPLILGLAAVLALSACQVRKAPDLDYTSFKESKPASILVVPPLNESPDVNGTWGMLAST					
	10	20	30	40	50	60
	70	80	90	100	110	120
m235.pep	AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	: :					
g235	AAPISEAGYYVFPAAVVEETFKENGLTNAADIHAVRPEKLHQIFGNDAVLYITVTEYGTS					
	70	80	90	100	110	120
	130	140	150	160	170	180

537

```

m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           |||||||
g235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130      140      150      160      170      180

           190      200      210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           |||||||
g235      DRGYQVSKTAAYNLLSPYSRNGILKGPRFVEEQPKX
           190      200      210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 873>:

```

a235.seq
1  ATGAAACCTT TGATTTTAGG GCTTGCCGCC GTGTTGGCGC TGTCTGCCTG
51  CCAAGTCAA AAAGCGCCCG ATTTGCGACTA CACGTCATTC AAGGAAAGCA
101 AACCGGCTTC AATTTTGGTG GTTCCGCCGC TGAACGAATC GCCCGATGTC
151 AACGGAACAT GGGGTGTACT GGCTTCGACC GCCGCGCCGC TTTCCGAAGC
201 CGGCTATTAC GTCTTCCCGC CCGCAGTCGT GGAGGAAACC TTCAAACAA
251 ACGGCTTGAC CAATGCCGCC GATATTCACG CCGTCCGGCC GGAAAACTG
301 CATCAGATTT TCGGCAATGA TCGGGTTTTG TACATTACGG TTACCGAATA
351 CGGCACTTCA TATCAAATTT TAGACAGCGT GACGACCGTA TCCGCCAAAG
401 CACGGCTGGT CGATCCCCGC AACGGAAGAG AGTTGTGGTC GGGTTCGGCC
451 AGCATCCGCG AAGGCAGCAA CAACAGCAAC AGCGGCCTGT TGGGGGCTTT
501 GGTCAAGCGA GTGGTCAATC AGATTGCCAA CAGCCTGACC GACCGCGGTT
551 ATCAGGTTTC TAAACCGGCC GCATACAACC TGCTGTCGCC CTATTCTCAC
601 AACGCATCT TGAAAGGTCC GAGATTCGTC GAAGAGCAGC CCAATAA

```

This corresponds to the amino acid sequence <SEQ ID 874; ORF 235.a>:

```

a235.pep
1  MKPLILGLAA VLALSACQVQ KAPDFDYTSF KESKPASILV VPPLNESPDV
51  NGTWGVLAST AAPLSEAGYY VFPAAVVEET FKQNGLTNAA DIHAVRPEKL
101 HQIFGNDAVL YITVTEYGTS YQILDSVTTV SAKARLVDSR NGKELWSGSA
151 SIREGSNNSN SGLLGALVSA VVNQIANSLT DRGYQVSKTA AYNLLSPYSH
201 NGILKGPRFV EEQPK*

```

m235/a235 100.0% identity in 215 aa overlap

```

           10      20      30      40      50      60
m235.pep  MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           |||||||
a235      MKPLILGLAAVLALSACQVQKAPDFDYTSFKESKPASILVVPPLNESPDVNGTWGVLAST
           10      20      30      40      50      60

           70      80      90      100     110     120
m235.pep  AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAVRPEKLHQIFGNDAVLYITVTEYGTS
           |||||||
a235      AAPLSEAGYYVFPAAVVEETFKQNGLTNAADIAVRPEKLHQIFGNDAVLYITVTEYGTS
           70      80      90      100     110     120

           130     140     150     160     170     180
m235.pep  YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           |||||||
a235      YQILDSVTTVSAKARLVDSRNGKELWSGSASIREGSNNSNSGLLGALVSAVVNQIANSLT
           130     140     150     160     170     180

           190     200     210
m235.pep  DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           |||||||
a235      DRGYQVSKTAAYNLLSPYSHNGILKGPRFVEEQPKX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 875>:

g236.seq

```

1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCCGCACAG CGTTTGCAGA
51  CGGTTTCATA ACCTGCAACC GCGCCACAT CCGGGGTGTA ATGCCAGCAG
101 CGTTCGCATT TTTCGCCGTC GCTGGCTTTG GCGGCAACGG CAAGTTCATC
151 ACCGACTTTC ACTTCTGCTT TAGACACCAG CAGGGCAAAG CGCAATTCCT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTCCGGCGC GGTAAATTCG
251 GCTTCCGCCT GCAAaggacga accgacagTT TTGTcggcGC GCAAAGGCTC
301 GAtagcggcg gTtACTGCTT CGCGCGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAGTTC GGCTTCGGCT TTTCGTTGA TGGCCGGGAA CTCGTGCCAA
401 GTATGGAAGA GGACGCTGTC TTCTTCGCCG CCGCCGATGA TGTCCCACGC
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTCGCGC TCGGCGGGC GCGGCTGTGC
551 GCTTTGGTGG TGTAGAGGCG GTCTTTCAGG ATGTCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACAATGTC TTTCACGGCG AAGTGAAGG
651 CATAGCGCGG ATAGTAACCG CCTGCCAAAC GCTCTTGCA GCGCCGCGCC
701 AATACCAAGG CGTAGCGGTC GATTTCCACC ATATCCGCCT GTTGCACGGC
751 ATCTTCAATC GGATTAAAGT CGCTCAAATT GGCAAacagG AAGCTCAAGG
801 TATTGCGGAT GCGGCGGTAG CTTTCGGTAA CGCGTTTGAG GATTTCTTTG
851 GAAatcgCCA ATtcgccgct gTAATCGGTG GATCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAATTCGT TATAGACTTC CTGCGGCGCG ACGACGTTGC
951 CGATGGATTG CGACATTTTG CGGCCGTTTT GGTCAACCAC GAAACCGTGG
1001 GTCAGCAGCT GTTTATACGG TCGCGTCCC ATGGATGA

```

This corresponds to the amino acid sequence <SEQ ID 876; ORF 236.ng>:

g236.pep

```

1  MARFAFSADI LRTAFADGFI TCNRAHIAGV MPAAFAFFAV AGFGGNGKFI
51  TDFHFCFRHQ QGKAQFFAQs IQIAGHFFRR GNFGFRLQGR TDSFVGAQRL
101 DSGGYCFARF ADCRPFFHQF GFGFFVDGRE LVPSMEEDAV FFAAADVPR
151 FFAGEAQNRC NQENQAARDV VQGLLRAAG AAVGFGGVEA VFQDVEVERA
201 QVFRAERNNV FHGEVEGIAR IVTACQTLQ PPRQYQGVAV DFHHIRLLHG
251 IFNRIKVAQI GKQEAQGIAD AAVAFGNAFE DFFGNRQFAA VIGGCRPQAG
301 DVRAEFVIDF LRRDDVADGF RHFAAVLVNH ETVGQQLFIR CASHG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 877>:

m236.seq (partial)

```

1  ..TTGCACGGAC GAACCGACGG TTTTGTGCGC GCGCAAAGGC TCGATGGCGG
51  CGGTTACCGC TTCGCGGGCT TCGCGGATTG CCGTCCATTT TTTCACCAGT
101 TCGGCTTCGG TTTTTCGTT GATGGTCGGG AACTCGTGCC AAGTATGGAA
151 GAGGACGCTG TcKtCTTCGC CGCCGCCGwT GAyGTCCAC GCTTCTTCGC
201 CGGTGAAGCA CAAAATCGGT GCAATCAAGA GAACCAAAC GCGTGTGATG
251 TGATACAGGG CAGTTTGTGC GCTGCGGCGT GCATGGCTGT CTGCTTTGGT
301 GGTGTAGAGG CGGTCTTCA GGATGTCGAG GTAGAACGCA CCCAAGTCTT
351 CCGAGCAGAA AGAAACA-TG TCTTTTACGG CAAAGTGGaA kGCATAACGC
401 GGATAGTAAT CGCCTGCCAG ACACCTTGC AGCTGACGTG CCAATACCAC
451 GGCGTAGCGG TCGATTCCA CCATATCCGC CTGTTGCACG GCATCTTCAA
501 TCGGATTAAA GTCGCTCAAG TTGGCAAACA AAAAGCTCAA GGTATTGCGG
551 ATACGGCGGT AgCTTTCGGT TACGCGTTTG AGGATTCTT TGGAAATCGC
601 CAATTCGCCG CTGTAATCGG TAGATGCCGC CCACAGGCGC AGGATGTCTG
651 CGCCGAATTC GTTATAAACC TCTTGCGGTG CAACGACGTT GCCGATGGAT
701 TTCGACATTT TTTTGCCTTC GCCGTCGACA ACGAAACCAT GGGTCAGCAG
751 CTGTTTATAC GGCGCGCGAC CCATTGA

```

This corresponds to the amino acid sequence <SEQ ID 878; ORF 236>:

m236.pep (partial)

```

1  ..LHGRTDGFVG AQRLDGGGYR FAGFADCRPF FHQFGFGFFV DGRELVPSME
51  EDAVXFAAAX DVPRFFAGEA QNRCNQENQT ACDVIQSLC AAACMAVCFG
101 GVEAVFQDVE VERTQVFAE RNxVFYgKVE XITRIVIAQ TLLQLTCoYH
151 GVAVDFHHIR LLHGIFNRIK VAQVGKQKAQ GIADTAVAFG YAFEDFFGNR
201 QFAAVIGRCR PQAQDVCAEF VINLLRCNDV ADGFRHFFAF AVDNETMGQQ
251 LFIRRATH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 236 shows 82.9% identity over a 258 aa overlap with a predicted ORF (ORF 236.ng) from *N. gonorrhoeae*:

m236/g236

[illegible]

```
a236.seq
1  ATGGCGCGTT TCGCCTTCTC CGCCGACATT CTCTGCACAG CGTTTGCAGA
51  CGGTTTCATG GCCTGCAACC GCGCCCACAT CGCGGGTGTA GTGCCAGCAG
101 CGTTTCGATT TTTACCATTG ACTGGCTTTA GCGGCAACGG CAAGTTCGCT
151 GCCTACTTTT ACCTTCGCTT TAGACACCAG CAAAGCAAAG CGCAATTCTT
201 CGCCCAAAGC ATTCAGATAG CCGGCCATTT CTTCCGGCGC GGTAATTTTCG
251 GCTTCGGCTT GCAAGGACGA ACCGACGGTT TTGTCGGCGC GCAAAGGCTC
301 GATGGCGGCG GTTACCCTT  CGCGGGCTTC GCGGATTGCC GTCCATTTTT
351 TCACCAGTTT GGCTTCGGCT TTTTCGTTGA TGGTCCGGAA CTCGTGCCAA
401 GTATGAAAAA GCACGCTGTC TTCTGCGCCG CGCCCGATGA TGTCACACGT
451 TTCTTCGCCG GTGAAGCACA AAATCGGTGC AATCAAGAGA ACCAGGCTGC
501 GCGTGATGTG GTACAGGGCG GTTTGCGCGC TCGCGCGGGC GCGGCTGTCTG
551 GCTTTGGTGG TATAGAGGCG GTCTTTCAGG ATATCGAGGT AGAACGCGCC
601 CAAGTCTTCC GAGCAGAAAG AAACCATTTT TTTCACGGCA AAGTGGAAGG
651 CATAACGCGG ATAAAAATCA CGGGCAACGC GTTCTTGCAG CCGCCTTGCC
701 AACACCAAGG CATAGCGGTC GATTTCCACC ATTCCGCCT GTTGCACGGC
751 ATCTTCAATA GGATTGAAGT CGCTCAAGTT GGCAAACAAA AAGCTCAAGG
801 TATTGCGGAT ACGGCGGTAG CTTTCGGTTA CGCGCTTGAG GATTTCCTTG
851 GAAATCGCCA ATTGCGCGCT GTAATCGGTG GATGCCGCCC ACAGGCGCAG
901 GATGTCCGCG CCGAACTCGT TATACACTTC TTGCGCGCGC ACGACGTTGC
951 CGATGGATTT CGACATTTTG CGCCCGTTTT GATCCACCAC GAAACCATGG
1001 GTCAGCAGCT GTTTGTACGG CGCGCGACCC ATTGA
```

a236.pep	1	MARFAFSADI	LCTAFADGFM	ACNRAHIAGV	VPAAFAFFT I	TGFSNGKFL
	51	AYFHCFRHHQ	QSKAQFFAQS	IQIAGHFFRR	GNFGFGLQGR	TDGFVGAQRL
	101	DGGYFAFRAGF	ADCRPFHQF	GGGFFVDGRE	LVPSMEKHAV	FCAAADVPR
	151	FFAGEAQNRC	NQENQAARDV	VQGGLRAAAG	AAVGFGGIEA	VFQDIEVERA
	201	QVFRAERNHF	FHGKVEGTR	IKITGNAFLQ	PPCQHQGIAY	DFHHIRLLHG
	251	IFNRIEVAQV	GKQKAQGIAD	TAVAFGYALE	DTFGNRQFAA	VIGGCRPQAO
	301	DVRAELVIHF	LRRDDVADGF	RHFAPVLIHH	EFFMGOLFVR	RATH*

m236/a236 81.0% identity in 258 aa overlap

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 881>:

This corresponds to the amino acid sequence <SEQ ID 882; ORF 237.ng>:

g237.pep
1 MRDKVGGNIA LPAPRIFDSN IGKLRKNFKH ILADKLGHTR RIVDKFVILT
51 AEQPAVRAE AVIIQNMAVV AYCHIVADKP FCARAOGFGG NNKGADGNRL

541

```

101 AFQRPEYRVQ TDISIDGIDH IFTLDAAFGR VNQPTVLIRF DARHRGLEN
151 LRAFGSGAG NTQRVIERMK MPQGIELCA LVHIAVKLLF QLGFIPKLIM
201 TRTVMLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAGVVADNL PATPAGRAEA DTCGFQNDGF
301 MSVFRQRQCG TOTAQTAADN AGFGFQTALE FRINSMRINR TKIIRROIIFL
351 KIRANHCVCF IGYIFGRNDT DCRAISSKQK IG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 883>:

m237.seq

```

1 ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCCC CACGAATATT
51 CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG TCATaCGCTC AGGATTGTCTG ATAAACTCGT TATCCTTACC
151 GCCGAAAAGC AGTCTGCCGT CCGCGCTGAG GCGTAATAA TCCAAAATAT
201 GGCGTTGTGC GCATACTGCC ATATTGTTAC GGATAAGCCC TTTGCGCGC
251 GCCCCAAGG GTTCGGTCGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGTTCCAAA GGCCGAATA TCGGGTTCAA ACCTGCATAA GTATTGACAG
351 CATAGACCAC ATTTTTCAC TCGACGCTGC CTTGCGGCGT GTAAACCAGC
401 CAACCGTTTT GATGCGGTTT GATGCACGTC ATCGGGGATT GCTCGAAAAAT
451 CTGCGCACCG GCTTCGGCAG CGGCACGAGC GATGCCCAA GTGTAAGTGA
501 GCGGATGCAG GTGTCCGAT AAGGGTCTGA ATTGTGCCCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGTTT CAACTCGGCT TTATCCCAA GTTGATAATG
601 ACTCGCACCG TAATGCCGTT GGGCGTGTTC ATGCCACTGC TGCAACTCTT
651 CCAATGCTG CGGACGACG GCAACCGTGG CATAACCGCG CTGCCAATCA
701 CAATCGACGG CATGTTTTCG GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCCTG CTCCAAGCCG ACCTGTTTTT
801 CAATTTCCCC CATACCGCAG nCGTAATCGC TGATAACCTG CCCGCCACTC
851 CGTCCCAGC CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAC GGCATTGAAG TTtCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTT TGTTTGCTTT ATCAGGTGTA TTTTCGGACG
1101 GAATGATACA GGCTGTCGGG CCATATCGTC CAwACAGAAA ATCGGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 884; ORF 237>:

m237.pep

```

1 MRDKVGGNVA LPAPRIFFDF IGKLRKNFKH ILADKLGH TL RIVDKLVILT
51 AEKQSAVRAE AVIIQNMAVV AYCHIVTDKP FCARPQGFGR NKGADSNRL
101 AFQRPEYRVQ TCISIDSIDH IFALDAAFGR VNQPTVLMRF DARHRGLEN
151 LRTGFGSGTS DAQSVSERMQ VSGXGVELCP LVHIAVKLLF QLGFIPKLIM
201 TRTVMLGVF MPLLQLFPML RTDGNRGITA LPITIDGMFA DAFVHQFDRL
251 QRLLPKPLRL LQADLFFNFP HTAXVIADNL PATPSRRAET DTRGFQHNRF
301 MSLLRQGQCS AQTTSQAADD TGIGFQTALK FRINSMRINR TEIIRROIIFL
351 KIRANHCVCF IRCIFGRNDT GCRAISSXQK IG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 237 shows 86.1% identity over a 382 aa overlap with a predicted ORF (ORF 237.ng) from *N. gonorrhoeae*:

m237/g237

```

              10      20      30      40      50      60
m237.pep      MRDKVGGNVALPAPRIFFDFDIGKLRKNFKHILADKLGH TL RIVDKLVILTAEKQSAVRAE
              |||||:|||||:|||||
g237           MRDKVGGNIALPAPRIFDSNIGKLRKNFKHILADKLGH TRRIVDKFVILTAEKQPAVRAE
              10      20      30      40      50      60

              70      80      90      100     110     120
m237.pep      AVIIQNMAVVAYCHIVTDKPF CARPQGFGRNKGADSNRLAFQRPEYRVQTCISIDSIDH
              |||||:|||||:|||||:|||||:|||||
g237           AVIIQNMAVVAYCHIVADKPF CARAQFGGNNKGADGNRLAFQRPEYRVQTDISIDGIDH
              70      80      90      100     110     120

              130     140     150     160     170     180
m237.pep      IFALDAAFGRVNQPTVLMRFDARHRGLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP

```

	: : : :
g237	I F T L D A A F G R V N Q P T V L I R F D A R H R G L L E N L R A G F G S G A G N T Q R V I E R M K M P G Q G I E L C A
	130 140 150 160 170 180
m237.pep	190 200 210 220 230 240
	L V H I A V K L L F Q L G F I P K L I M T R T V M P L G V F M P L L Q L F P M L R T D G N R G I T A L P I T I D G M F A
g237	
	L V H I A V K L L F Q L G F I P K L I M T R T V M P L G V F M P L L Q L F P M L R T D G N R G I T A L P I A I D G M F A
	190 200 210 220 230 240
m237.pep	250 260 270 280 290 300
	D A F V H Q F D R L Q R L L P K P L R L L Q A D L F F N F P H T A X V I A D N L P A T P S R R A E T D T R G F Q H N R F
g237	
	D A F V H Q F D R L Q R L L P K P L R L L Q A D L F F N F P H T A G V V A D N L P A T P A G R A E A D T C G F Q N D G F
	250 260 270 280 290 300
m237.pep	310 320 330 340 350 360
	M S L L R Q G Q C S A Q T T Q S A A D D T G I G F Q T A L K F R I N S M R I N R T E I I R R Q I F L K I R A N H C V C F
g237	: : : : : : : : : : : : : : : : : :
	M S V F R Q R Q C G T Q T A Q T A A D N A G F G F Q T A L E F R I N S M R I N R T K I I R R Q I F L K I R A N H C V C F
	310 320 330 340 350 360
m237.pep	370 380
	I R C I F G R N D T G C R A I S S X Q K I G X
g237	
	I G Y I F G R N D T D C R A I S S X Q K I G X
	370 380

```
a237.seq
1   ATGCGGGACA AGGTTGGCGG TAATGTCGCA CTCCCCGCC CACGAATATT
51  CGATTTTGAC ATCGGCAAGC TGCGGAAAAA CTTTAAGCAT ATCTTGGCGG
101 ACAAGCTCGG GCATACGCGC GGGATTGTCTG ATAAACTCGT TATCTTACC
151 GCCGAAAAAGC TGTCTGCCGT CCGCGCTGAG CGGTAATAAA TCCAAAATAT
201 GACGGTTGTC GCATACTGCC ATATTGTTGC GGATAAGCCC TTTTGCACGC
251 GCGCCCAAGG GTTCTGTGGC AATAATAAAG GTGCTGACAG CAATCGCCTT
301 GCGCTCCAAA GGCTTGAATA TCGGATTCAA ACCGGCATAA GTATTGACGG
351 CGTACACCAG ATTTTGTGAT TCGACGCTGC CTTCGGGGGT GTAAACCAGC
401 CAACCGTTTT GATAAGGTTT AATGCGTATC ATGGGAGAAT GCTCAAAAAT
451 CTTCGTACCA GCTTCGGCAG CGGCGCGGGC GATGCCCAAC GTGTAATTGA
501 GCGGATGGAG ATGCCCCGGAC AAGGGATCGA ACTGTGCGCC TTGGTACATA
551 TCGCTGTCAA GCTGCTGCTT CAGTTTCACTG TTAATCCCAG GTTGATAATG
601 AGTTGCACCG TAATATTTTT GGGCGTGCTC ATGCCATTGT GTCAATTCCT
651 CCAATGCTG CGAACGGATG GCAACCGTGG CATAACCGCG CTGCCAATCG
701 CAATCAATGG CATGTTTGC GACGCGTTCG TCCACCAGTT CGACCGCCTG
751 CAAAGACTGT TGCCAAAACC ATTGCGCTTG CTCCAAACCG ACCTGTTTTT
801 CAATTTCCTC CATACCGCAG GCGTAATCTG TGATAACCTG CCCGCCACTT
851 CGTCCCGACG CGCCGAAACC GATACGCGCG GCTTCCAACA CAACCGTTTC
901 ATGTCCCTGC TCCGCCAAGG GCAATGCAGT GCACAAACCA CTCAATCCGC
951 CGCCGATGAT ACAGGTATCG GTTTTCAGAG GCATTGAAG TTTCGGATAA
1001 ACAGTATGAG GATTAACCGA ACTGAAATAA TAAGAAGGCA GATATTCTTG
1051 AAAATCAGGG CGAATCATTG TGTTTGCTTT ATCGGGTATA TTTTCGGACG
1101 GAATGATACA GGCTGTCTGAG CCATATCGTC CAAACAGAAA ATCGGTTGA
```

a237.pap

1	MRDKVGGNVA	LPAPRIFFDFD	IGKLKRNFKH	ILADKLGHTR	GIVDKLVILT
51	AEKQSAVRAE	AVIIQNMTVQ	AYCHIVADPK	FCTRAQGFCC	NNKGADSNRL
101	ALQRLLEYRIQ	TGISIDGVHQ	IFAFDAAFGG	VNQPTVLFRG	NAYHGRMLKN
151	LRTSFGSGAG	DAQRVIERME	MPGGQIELCA	LVHIAVKLLL	QFSVIPELIM
201	<u>SCTVIFLGLV</u>	<u>MPLLQFFPML</u>	RTDGNRGITA	LPIAINGMFA	DAFVHQFDRL
251	QRLLPKPLRL	LQTDLFFNFL	HTAGVIADNL	PATPSRAART	DTRGFQHNRF
301	MSLLRQGCQS	AQTTQSAADD	TGIGFQTALK	FRNSMRINR	TEIIRQIFL
351	KIRANHCVCF	IGYIFGRNDT	GCAISSKQK	IG*	

543

m237/a237 85.6% identity in 382 aa overlap

	10	20	30	40	50	60
m237.pep	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTLRIVDKLVILTAEKQSAVRAE					
a237	MRDKVGGNVALPAPRIFDFDIGKLRKNFKHILADKLGHTRGIVDKLVILTAEKQSAVRAE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m237.pep	AVIIQNMVAVYCHIVTDKPFPCARQGFGRNNKGADSNRLAFQRPYRVQTCISIDSIDH					
a237	AVIIQNMVAVYCHIVADKPFCTRAQGFGRNNKGADSNRLALQRLRYRIQTGISIDGMVHQ					
	70	80	90	100	110	120
	130	140	150	160	170	180
m237.pep	IFALDAAFGRVNQPTVLMRFDARHRLLENLRTGFGSGTSDAQSVSERMQVSGXGVELCP					
a237	IFAFDAAFGGVNQPTVLIRFNAYHGRMLKNLRTSFGSGAGDAQRVIERMEMPGQGIELCA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m237.pep	LVHIAVKLLFQLGFIPKLIMTRTVMLGVFMPLLQLFPMLRTDGNRGITALPITIDGMFA					
a237	LVHIAVKLLQLFSVIPELIMSCVIFLGVLMPLLQFFPMLRTDGNRGITALPIAINGMFA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m237.pep	DAFVHQFDRLQRLPKPLRLLQADLFFNFPHTAXVIADNLPATPSRRAETDTRGFQHNRF					
a237	DAFVHQFDRLQRLPKPLRLLQDLFFNFLHTAGVIADNLPATPSRRAETDTRGFQHNRF					
	250	260	270	280	290	300
	310	320	330	340	350	360
m237.pep	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
a237	MSLLRQGQCSAQTTQSAADDTGIGFQTALKFRINSMRINRTEIIRRQIFLKIRANHCVCF					
	310	320	330	340	350	360
	370	380				
m237.pep	IRCFGRNDTGCRAISSXQKIGX					
a237	IGYIFGRNDTGCRAISSXQKIGX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 887>:

g238.seq

```

1  atgaatttgc ctattcaaaa attcatgatg ctgttggcag cggcaatatc
51  gatgctgcat atccccatta gtcatgcgaa cggtttggat gcccgtttgc
101 gcgatgatat gcaggcaaaa cactacgaac cgggtggcaa ataccatctg
151 tttggtaatg ctgcggcgag tgtaaaaaat cgggtttgag ccgtccaaac
201 atttgatgca actgcggtcg gccccatact gcctattaca cacgaacgga
251 caggatttga aggtgttatc ggctatgaaa cccatttttc aggacacgga
301 cacgaagtac acagtccggt cgataatcat gattcaaaaa gcatttctga
351 tttcagcggc ggcgtagacg gcggttttac cgtttacca cttcatcgga
401 cagggtcgga aatacatccc gcagacggat atgacgggcc tcaaggcggc
451 gggtatccgg aaccacaagg ggcaagggat atatacagct accatatcaa
501 aggaacttca accaaaacaa agataaacac tggtccgcaa gccctttttt
551 cagaccgctg gctaaaagaa aatgccggtg ccgcttcagg ttttctcagc
601 cgtgcgggat aagcaggaaa actgatatgg gaaaacgacc ccgataaaaa
651 ttggcgggct aaccgatgg atgatattcg cggcatcgtc caaggtgcgg
701 ttaatccttt ttaacgggt tttcaaggg tagggattgg ggcaattaca
751 gacagtgcgg taagcccggc cacagataga gccgctcagc agactctaca
801 aggtattaat gatttaggaa atttaagtcc ggaagcacia cttgccgccg

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544

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851 cgagcctatt acaggacagt gcctttgcgg taaaagacgg catcaattcc
901 gccagacaat gggctgatgc ccatccgaat ataacagcaa cagcccaaac
951 tgcccttgcc gtagcagagg ccgcaggtac ggtttggcgc ggtaaaaaag
1001 tagaacttaa cccgaccaa tgggattggg taaaaatac cggctataaa
1051 aaacctgctg cccgccatat gcagactgta gatggggaga tggcaggggg
1101 gaatagaccg cctaaatcta taacgtcggg aggaaaagct aatgctgcaa
1151 cctatcctaa gttgggtaat cagctaaatg agcaaaactt aaataacatt
1201 gcggctcaag atccaagatt gagtctagct attcatgagg gtaaaaaaaa
1251 ttttccaata ggaactgcaa cttatgaaga ggcagataga ctaggtaaaa
1301 tttgggttgg tgagggtgca agacaaacta gtggaggcgg atgggttaagt
1351 agagatggca ctcgacaata tcggccacca acagaaaaaa aatcacaatt
1401 tgcaactaca ggtattcaag caaattttga aacttatact attgattcaa
1451 atgaaaaaag aaataaaatt aaaaatggac atttaaatat taggtaa

```

This corresponds to the amino acid sequence <SEQ ID 888; ORF 238.ng>:

g238.pep

```

1 MNLPIQKFMM LLAAAI SMLH IPISHANGLD ARLRDDMQAK HYEPPGKGYHL
51 FGNARGSVKN RVCAVQTFDA TAVGPILPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDNH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP ADGYDGPQGG
151 GYPEPQGARD IYSYHIKGTs TKTKINTVPQ APFSDRWLKE NAGAASGFLS
201 RADEAGKLIW ENDPDKNWRa NRMDDIRGIV QGAVNPFLTg FAGVGIGAIT
251 DSAVSPVTDt AAQQTlQGIN DLGNLSPEAQ LAAASLLQDS AFAVKDGINS
301 ARQWADAHPN ITATAQTALA VAEAAGTVWR GKKVELNPTK WDWVKNTGYK
351 KPAARHMQTV DGEMAGGNRP PKSITSEGKA NAATYPKLVN QLNEQNLNNI
401 AAQDPRLSLA IHEGKKNFPI GTATYEEADR LGKIWVGEGA RQTSGGGWLS
451 RDGTRQYRPP TEKKSQFATT GIQANFETYt IDSNEKRNKI KNGHLNIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 889>:

m238.seq

```

1 ATGAATTTGC CTATTCAAAA ATTCATGATG CTGTTTGcAG CAGCAATATC
51 GTTGCTGCAA ATCCCCATTA GTCATGCGAA CGGTTTGGAT GCGCGTTTGC
101 GCGATGATAT GCAGGCAAAA CAcTACGAAC CGGGTGGTAA ATACCATCTG
151 TTTGGTAATG CTCGCGGCAG TGTTAAAAAG CGGGTTTACG CCGTCCAGAC
201 ATTTGATGCA ACTGCGGTCA GTCCTGTACT GCCTATTACA CACGAACCGA
251 CAGGGTTTGA AGGTGTTATC GGTTATGAAA CCCATTTTTC AGGGCACGGA
301 CATGAAGTAC ACAGTCCGTT CGATCATCAT GATTCAAAAA GCATTCTGA
351 TTTcAGCGGC GGTGTAGACG GCGGTTTtAC TGTTTACCAA CTTCATCGAA
401 CAGGGTCGGA AATCCATCCG GAGGATGGAT ATGACGGGCC GCAAGGCAGC
451 GATTATCCGC CCCCcGGAGG AGCAAGGGAT ATATACAGCT ATTATGTCAA
501 AGGAACtTCA ACAAAAACAA AGACTAATAT TGTCCCTCAA GCGCCATTTT
551 CAGACCGTTG GCTAAAAGAA AATGCCGGTG CCGCCTCTGG TTTTTTCAGC
601 CGTGCGGATG AAGCAGGAAA ACTGATATGG GAAAGCGACC CCAATAAAAA
651 TTGGTGGGCT AACCGTATGG ATGATGTTcG CGGCATCGTC CAAGGTGCGG
701 TTAATCCTTT TTTAATGGGT TTTCAAGGAG TAGGGATTGG GGCAATTACA
751 GACAGTGCAG TAAGCCCGGT CACAGATACA GCCGCGCAGC AGACTCTACA
801 AGGTATTAAT GATTTAGGAA AATTAAGTCC GGAAGCACA CTTGCTGCCG
851 CGAGCCTATT ACAGGACAGT GCTTTTGCGG TAAAAGACGG TATCAACTCT
901 GCCAAACAAT GGGCTGATGC CCATCCAAAT ATAACAGCTA CTGCCCCAAC
951 TGCCCTTTCC GCAGCAGAGG CCGCAGGTAC GGTTTGGAGA GGTAAAAAAG
1001 TAGAACTTAA CCCGACTAAA TGGGATTGGG TTAAAAATAC CGGTTATAAA
1051 AAACCTGCTG CCCGCCATAT GCAGACTTTA GATGGGGAGA TGGCAGGTGG
1101 GAATAAACCT ATTAATCTT TACCAAACAG TGCCGCTGAA AAAAGAAAAC
1151 AAAATTTTGA GAAGTTTAAT AGTAACTGGA GTTCAGCAAG TTTTGATTCA
1201 GTGCACAAAA CACTAACTCC CAATGCACCT GGTATTTTAA GTCCTGATAA
1251 AGTTAAACT CGATACACTA GTTTAGATGG AAAAATTACA ATTATAAAAG
1301 ATAACGAAAA CAACTATTTT AGAATCCATG ATAATTCACG AAAACAGTAT
1351 CTTGATTCAA ATGGTAATGC TGTGAAAACC GGTAAATTAC AAGGTAAGCA
1401 AGCAAAAGAT TATTTACAAC AACAAACTCA TATCAGGAAC TTAGACAAAT
1451 GA

```

This corresponds to the amino acid sequence <SEQ ID 890; ORF 238>:

m238.pep

```

1 MNLPIQKFMM LFAAAISLLQ IPISHANGLD ARLRDDMQAK HYEPPGKGYHL
51 FGNARGSVKK RVYAVQTFDA TAVSPVLPIT HERTGFEGVI GYETHFSGHG
101 HEVHSPFDHH DSKSTSDFSG GVDGGFTVYQ LHRTGSEIHP EDGYDGPQGS

```

Homology with a predicted ORF from *N. gonorrhoeae*

m238/g238

m238.pep	MNLPIQKFMMLFAAAISLLQIPI	SHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK			
g238	MNLPIQKFMMLLAAAISMLHIPI	SHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN			
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEGVIGYETHFSGHGHEVHSPFDHHD	SKSTSDFSG			
g238	RVCAVQTFDATAVGPILPITHERTGFEGVIGYETHFSGHGHEVHSPFDNH	DSKSTSDFSG			
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS	DYPPPGGARDIYSYVVKGTSTKTKTNIVPQ			
g238	GVDGGFTVYQLHRTGSEIHPADGYDGPQGGGYEPQGARDIYSYHIKGTSTKTKINTVPQ				
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPNKNWWANRMD	DVRGIVQGA	VNPFLMG		
g238	APFSDRWLKENAGAASGFLSRADEAGKLIWENDPDKNWRANRMD	DIRGIVQGA	VNPFLTG		
m238.pep	FQGVGIGAITDSAVSPVTD	TAAQQTLOGINDLGKLSPEAQLAAASLLQDS	SAFAVKD	GINS	
g238	FQGVGIGAITDSAVSPVTD	TAAQQTLOGINDLGNLSPEAQLAAASLLQDS	SAFAVKD	GINS	
m238.pep	AKQWADAHPNITATAQTALSA	AEAAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHM	QTL		
g238	ARQWADAHPNITATAQTALAVAEAAAGTVWRGKKVELNPTKWDWVKNTGYKKPAARHM	QTV			
m238.pep	DGEMAGGNKPIKSLPNSAAEKRKQNF	EKFNSNWSSASFDSVHKLTLPNAPGILSPDKVKT			
g238	DGEMAGGNRPPKSI-TSE	GKANAAATYPKLVNQLNEQNLNNIAAQDPRLSLAIHEGKKNFP			
m238.pep	RYTSLDGKITIIKDNENNYFRI	HDNSRKQYLD	SNGNAVKTGNLQ	GKQAKDY	LQQQTHIRN
g238	IGTATYEEADRLGKIWVGEGARQ	TSGGGWLSRDGTRQYRPPTEKKSQFATTGIQANFETY			

This corresponds to the amino acid sequence <SEQ ID 892; ORF 238.a>:

m238/a238 91.9% identity in 385 aa overlap

	10	20	30	40	50	60
m238.pep	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKK					
a238	MNLPIQKFMMLFAAAISLLQIPISHANGLDARLRDDMQAKHYEPGGKYHLFGNARGSVKN					
	10	20	30	40	50	60
m238.pep	RVYAVQTFDATAVSPVLPITHERTGFEIGYETHFSGHGHEVHSPFDHHD	70	80	90	100	110
a238	RVYAVQTFDATAVGPILPITHERTGFEIGYETHFSGHGHEVHSPFDNHD	70	80	90	100	110
	130	140	150	160	170	180
m238.pep	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS					
a238	GVDGGFTVYQLHRTGSEIHPEDGYDGPQGS					
	130	140	150	160	170	180
m238.pep	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPKNKWWANRMD	190	200	210	220	230
a238	APFSDRWLKENAGAASGFFSRADEAGKLIWESDPKNKWWANRMD	190	200	210	220	230
	250	260	270	280	290	300
m238.pep	FOGVGIGAITDSAVSPVTD					

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```

|||||
a238      FQGVGIGAITDSAVSPVTDTAQQTLQGINHLGNLSPEAQLAAATALQDSFAVKGINS
          250      260      270      280      290      300

          310      320      330      340      350      360
m238.pep  AKQWADAHPNITATAQTALSAEEAAGTVVRGKKVELNPTKWDVWKNTGYKKPAARHMQTL
          |||||
a238      ARQWADAHPNITATAQTALAVAEAAATTVWGGKKVELNPTKWDVWKNTGYKTPAVRTMHTL
          310      320      330      340      350      360

          370      380      390      400      410      419
m238.pep  DGEMAGGNKPIKSLP-NSAAEKRKQNFEFNSNWSSASFDSVHKTLTPNAPGILSPDKVK
          |||||
a238      DGEMAGGNRPPKSITSNSKADASTQ

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 893>:

```

g239.seq
1  atgttccacc ataaaggatg tgcccgaaac cggcggatgg aggttttgtt
51  tttctgccgc cgccctgatc gcttcgtgat tcgccaaacg cgccctgttgc
101 agcctcattt gcgcataatc ctgctccaag gcgatttcct gttttttcgc
151 cttgtccaaa gctgtgaagt tgagcctgta ctgggttttc agcatcaca
201 cggaaaaagc ggaaacgcac accgcaagca gcagaaagaa attcgatttg
251 ttcattgccg ttcagacgtt tttctctgtt attattccgg tatcgaccg
301 gcagtcggct ccgccacacg caaaactgcg ctccctcgcc tcgggttggc
351 ggcaatttcc gcttcaccgc gctttaatgc cctgccacg attttcaggg
401 gcggatcggg caaatccgct tctctgaccg ccgccagct cggcaggggc
451 tcgtgttgcg aatatttttt gacaaactgc ttcacaatgc ggtcttccaa
501 cgaatggaaa gcaatgaccg ccaaaccgcc gccctctttc agacggcaca
551 tgacctgcgg caataccgcc cctacttctt caagctcgcg gttataaag
601 atgcggattg cctggaaggc gcgcgtcgca ggatcctgcc cccgctcgcg
651 agtacggacg ttttgtgcca cgatctgcgc cagcttgcgg gttgtatcga
701 ttggactttc cgcccgttgc gcgacaatgg cgcgcacaat ctggcggcta
751 aaccgctctt caccataa

```

This corresponds to the amino acid sequence <SEQ ID 894; ORF 239.ng>:

```

g239.pep
1  MFHHKGIARN RRMEVLFFCR RPDRFVIRQT RLLQPHLR II LLQGDFFFR
51  LVQSCEVEPV LVLLHHNGKS GNAHRKQKKE IRFVHCRSDV FLCYYSIGIP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPT IFRGGSGKSA SLTAAQLGRG
151 SCCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARTIWR
251 NRSSP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 895>:

```

m239.seq
1  ATGCTCCACC ATAAAGGTmy kGCCCCGAAAC CGGCKGATGG AGGTTTTGT
51  TTTCTGCCGC CGCCCTGATC GCTTCGTGGT TCGCCAAACG CGCCTGTTGC
101 AGCCTCATTT GCGCATAATC CTGCTCCAAG GCGATTTCCT GTTTTTTCGC
151 CTTATCCAAA GCTGTGAAAT TGAGCCTGTA CTGGTTTTGC TGCATCACAA
201 CGGAAAAAGC GGAAACGCAC ACCGCAAGCA GCAGAAGGAA ATTC AATTG
251 TTCATTGCCA TTCAGACGTT TTTCTCTGTG ATTGTTCCGG TATCGGACCG
301 GCAGTCCGCT CCGCCACACG CAAAACCGCA CTTCTCGCCC TCGGATTGGC
351 GGCAATTTCC GCCTCACCAG GCTTTAATGC CCTGCCACG ATTTTCAGGG
401 GCAGCTCGGG CAAATCCGCT TCCCTGACCG CCGCCAGCG CGGCAGGGGC
451 GCGTGTGCG AATATTTTTC GACAAACTGC TTCACAATGC GATCTTCCAA
501 CGAATGGAAA GCAATGACCG CCAAACGTCC GCCCTCTTTC AGACGACACA
551 TGACCTGCGG CAATACTGCC CTA CTCTT CAAGCTCGCG GTTAATAAAG
601 ATGCGGACCG CCTGGAAGGT GCGCGTCGCA GGATCTGCC CCCGCTCGCG
651 AGTACGACG TTTTGTGCCA CGATCTGCGC CAGCTTGCAG GTTGATCGA
701 TTGGACTTTC CGCCC GTTGC GCAACAATGG CGCGCGCAAT cCGGCGGCTa
751 AACCCTCTT cACCATAA

```

This corresponds to the amino acid sequence <SEQ ID 896; ORF 239>:

Homology with a predicted ORF from *N. gonorrhoeae*

m239/g239

		10	20	30	40	50	60
m239.pep		MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRIILLQGDFLFFRLIQSCEIEPV					
		: : : : : : : : : : :					
g239		MFHHKGIARNRRMEVLFFCRRPDRFVIRQTRLLQPHLRIILLQGDFLFFRLVQSCEVEPV					
		10	20	30	40	50	60
		70	80	90	100	110	120
m239.pep		LVLLHHNGKSGNAHRKQQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
		: : : : : : : : :					
g239		LVLLHHNGKSGNAHRKQQKEIRFVHCRSDVFLCYYSIGIGPAVRSATRKTALLALGLAAIS					
		70	80	90	100	110	120
		130	140	150	160	170	180
m239.pep		ASPGFNALPTIFRGSSGKSASLTAAQGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
		: : : : : : : : :					
g239		ASPGFNALPTIFRGSSGKSASLTAAQLGRGSCCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
		130	140	150	160	170	180
		190	200	210	220	230	240
m239.pep		RRHMTCGNTAPTSSSSRLIKMRTAWKVVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
		: : : : : : : : :					
g239		RRHMTCGNTAPTSSSSRLIKMRIAWKVVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
		190	200	210	220	230	240
		250					
m239.pep		ATMARAI RRLNRSSPX					
		:					
g239		ATMARTIWRRLNRSSPX					
		250					

a239.seq

1	ATGCTCCACC	ATAAAGGTAT	TGCCCCGAAAC	CGGCGGATGG	AGGTTTTGTT
51	TTTCTGCCGC	CGCCCTGATC	GCTTCGTGGT	TCGCCAAACG	CGCCTGTTGC
101	AGCCTCATTT	GCGCTAATAC	CTGCTCCAAG	GCGATTTCCT	GTTTTTTCGC
151	CTTATCCAAA	GCTGTGAAGT	TGAGCCTAGT	CTGGTTTTTC	TGCATCACAA
201	CGGAAAAAAG	GGAACGCGAC	ACCGCAAGCA	CGAGAAGGAA	ATTCAATTGT
251	TTCATTGCCA	TTCAGACGTT	TTTCTCTGTG	ATTGTTCCGG	TATCGGACCG
301	GCAGTCCGCT	CCGCCACACG	CAAACCGCA	CTTCTCGCCC	TCGGATTGGC
351	GGCAATTTC	GCCTCACC	GCTTTAATGC	CCTGCCCGCG	ATTTTCAGGG
401	GCGGCTCGGG	CAAAATCCGCT	TCCCTGACCG	CCGCCACGCG	CGGCAGGGGG
451	GCGTGTTCGG	AATATTTTTT	GCAAAACTGC	TTCACAATGC	GGTCTTCCAA
501	CGAATGGAAA	GCAATGACCG	CCAAACGTCC	GCCCTCTTTC	AGACGACACA
551	TGACCTGCGG	CAATACTGCC	CCTACTTCTT	CAAGCTCGCG	GTTAATAAAG
601	ATGCGGATTG	CCTGGAAGGT	GCGCGTCGCA	GGATCTGCC	CCCGCTCGCG
651	AGTACGGAGC	TTTTGTGCCA	CGATCTGCGC	CAGCTTGCGG	GT'TGATCGA
701	TGGAGCTTTC	CGCCCCTTGC	GCAACAATGG	CGCGCGCAAT	CTGGCGGCTA
751	AACCGCTCTT	CACCATAA			

This corresponds to the amino acid sequence <SEQ ID 898; ORF 239.a>:

```
a239.pep
  1 MLHHKGIARN RRMEVLFFCR RPDRFVVRQT RLLQPHLRRI LLQGDFFLFFR
 51 LIQSCEVEPV LVLLHHNGKS GNAHRKQQKE IQFVHCHSDV FLCDCSGIGP
101 AVRSATRKTA LLALGLAAIS ASPGFNALPA IFRGGSGKSA SLTAAQRGRG
151 ACCEYFLTNC FTMRSSNEWK AMTAKRPPSF RRHMTCGNTA PTSSSRLIK
201 MRIAWKVRVA GSCPRSRVRT FCATICASLR VVSIGLSARC ATMARAIWRL
251 NRSSP*
```

m239/a239 97.3% identity in 255 aa overlap

m239.pep	10	20	30	40	50	60
	MLHHKGXARNRXMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFFLFFRLIQSCEIEPV					
a239	MLHHKGIARNRRMEVLFFCRRPDRFVVRQTRLLQPHLRRIILLQGDFFLFFRLIQSCEVEPV					
	10	20	30	40	50	60
m239.pep	70	80	90	100	110	120
	LVLLHHNGKSGNAHRKQQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
a239	LVLLHHNGKSGNAHRKQQKEIQFVHCHSDVFLCDCSGIGPAVRSATRKTALLALGLAAIS					
	70	80	90	100	110	120
m239.pep	130	140	150	160	170	180
	ASPGFNALPTIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
a239	ASPGFNALPAIFRGSSGKSASLTAAQRGRGACCEYFLTNCFTMRSSNEWKAMTAKRPPSF					
	130	140	150	160	170	180
m239.pep	190	200	210	220	230	240
	RRHMTCGNTAPTSSSRLIKMRATAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
a239	RRHMTCGNTAPTSSSRLIKMRIAWKVRVAGSCPRSRVRTFCATICASLRVVSIGLSARC					
	190	200	210	220	230	240
m239.pep	250					
	ATMARAIIRRLNRSSPX					
a239	ATMARAIWRLNRSSPX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 899>:

```
g240.seq
  1 atgatagaag tcatacat tttctcgccgcc gaaacgcgca gacagtttgc
 51 ttgtgccgac gttggacgat ttctgcataa tgccgcgcac atccaaagag
101 gggtaaacaat gggatcatc gcgcacggga gacggtccga ttttataagg
151 ctgcgtattc agccgttcgt tcaaatacgg tttgcccgcga tccaatgcct
201 tcgcaatcac gaacggtttg attgccgaac caggttcgat catatcgggt
251 acggcacggg tgccgcgctg ttcgctgtct gcccgccggg gtctgttggg
301 atcgtaggcg ggcgtattgg ccaaggcgag gatttcccc gtgcgggcat
351 ccaaaaccac caccgttcg gcttttgcct gatggtattc gaccgccttg
401 ttcaactctt cataggccaa ggtctgaatc ctctgatcga gggaaaggat
451 gatgtctttg ccgttttgcg gtgctttatt gcgcggggag tccaagctgt
501 ccacaatatt gccctgccgg tcccgcaaaa caacttccgc gccgtcttcg
551 ccatacaggc tgtcttcaag cgaaagttcc aaaccttcct gacctttgcc
601 gtcaatatcg gtaaatccga tgacgtgtgc aaacaggttg cccatcgggt
651 aatggcggtt taa
```

This corresponds to the amino acid sequence <SEQ ID 900; ORF 240.ng>:

```
g240.pep
  1 MIEVIHFFGA ETRRQFACAD VGRFLHNAAH IQRGVNMGII AHGRRSDFIR
 51 LRIQPFVQIG FARIQCLRNH ERFDCRTRFD HIGYGTVA PLFAVCPAGSVG
101 IVGGRIGQGE DFPRAGIQNH HRS GFCLMV FDRLVQLFIGQ GLNPLIEGKD
151 DVFAVLRCFI ARGVQAVHNI ALPVPQNNFR AVFAIQAVFK RKFQTFLTFA
```

550

201 VNIGKSDDVC KQVAHRVMAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 901>:

```

m240.seq
1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCGGCT TTTGCCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTAKTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAA CAGGTTGCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 902; ORF 240>:

```

m240.pep
1   MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
51  RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
101 VGGRIQGED FPRAGIQXHH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
151 VFAVFRGFXA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTLFTFAV
201 NIGKSDDVCK QVAHRVMAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 240 shows 94.5% identity over a 220 aa overlap with a predicted ORF (ORF 240.ng) from *N. gonorrhoeae*:

```

m240/g240

      10      20      30      40      50      59
m240.pep MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIG
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      MIEVIHFFGAETRRQFACADVGRFLHNAAH IQRGVNMGIIAHGRRSDFIRLRIQPFVQIG
      10      20      30      40      50      60

      60      70      80      90      100     110     119
m240.pep FARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIQGEDFPRAGIQXH
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      FARIQCLRNHERFDCRTRFDHIGYGTVAPLFAVCPAGSVGIVGGRIQGEDFPRAGIQNH
      70      80      90      100     110     120

      120     130     140     150     160     170     179
m240.pep HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFR
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      HRSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVLRFCFIARGVQAVHNIALPVPQNNFR
      130     140     150     160     170     180

      180     190     200     210     220
m240.pep AVFAMQAVFKRKQTLFTFAVNIGKSDDVCKQVAHRVMAFX
      ||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g240      AVFAIQAVFKRKQTLFTFAVNIGKSDDVCKQVAHRVMAF
      190     200     210     220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 903>:

```

a240.seq
1   ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
51  TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG

```


551

```

251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AAACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTATTGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAGGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 904; ORF 240.a>:

```

a240.pep
  1 MIEVIHFFGT ETRRQFACAD VGRFLHDAAH IQRGVNMGIA HGRRSDFIRL
  51 RIQPFVQIGF ARIQCLRNHK RFDCRTGFDH IGYGTVAPLF AVCPAGPVGI
 101 VGGRIGQGED FPRAGIQNH RSGFCLMVFD RLVQLFIGQG LNPLIEGKDD
 151 VFAVFRGFIA RGVQAVHNIA LPVPQNDFRA VFAMQAVFKR KFQTFLTFAV
 201 NIGKSDDVCK QVAHRVMAF*

```

m240/a240 99.1% identity in 219 aa overlap

```

              10      20      30      40      50      60
m240.pep    MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF
              |||
a240         MIEVIHFFGTETRRQFACADVGRFLHDAAH IQRGVNMGIAHGRRSDFIRLRIQPFVQIGF
              10      20      30      40      50      60

              70      80      90      100     110     120
m240.pep    ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQXHH
              |||
a240         ARIQCLRNHKRFDCRTGFDHIGYGTVAPLFAVCPAGPVGIVGGRIGQGEDFPRAGIQNH
              70      80      90      100     110     120

              130     140     150     160     170     180
m240.pep    RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFXARGVQAVHNIALPVPQNDFRA
              |||
a240         RSGFCLMVFDRLVQLFIGQGLNPLIEGKDDVFAVFRGFIARGVQAVHNIALPVPQNDFRA
              130     140     150     160     170     180

              190     200     210     220
m240.pep    VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX
              |||
a240         VFAMQAVFKRKFQTFLTFAVNIGKSDDVCKQVAHRVMAFX
              190     200     210     220

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 905>:

```

g241.seq
  1 ATGATAGAAG TCATACATTT CTTCCGGCACC GAAACGCGCA GACAGTTTGC
  51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
 101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
 151 CGTATTTCAGC CGTTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
 201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
 251 GCACGGTTGC GCCGCTGTTC GCTGTCTGCC CGGCCGGGCC TGTGTTGGATC
 301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
 351 AACCACCAC CGTTCGGGCT TTTGCCTGAT GGTATTTCGAC CGCCTTGTTT
 401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
 451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
 501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
 551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
 601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
 651 GGCGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 906; ORF 241.ng>:

```

g241.pep
  1 MPTRPTRAAN PPTPTTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS

```

552

```

51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSQ RQSVVMTVR
101 TVDMTVCDL IGCIHAFAFN SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFPGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 907>:

m241.seq (partial)

```

1  ..CGGCAATCAG TGGTGGTGAT GACCGTGCGG GCCGTGGACA TGACCGTGTG
51  CGATTTCCTC ATCGGATGCA TCGCGCACGC TTTCAACTGT AGCCTTAAAG
101 CGGATTTTCA TGCCTGCCAA AGGATGGTTG CCGTCCACCA CCGCCTTGCC
151 GTCGGCAACA TCGGTTACAC GATAGACGAC AACATCGCCG GTTTCAGGAT
201 CGTCGGCTTC AAACATCATG CCGACTTCGA CTTCAACAGG GAACACGCCC
251 GCATCTTCGA TACGGACCAA CTCCGGATCC TGCTCGCCA ACGCATCGTC
301 GGGCGACAGC GCCACATCGA CCGTATCGCC GGCATCCTTA CCGTGCAACG
351 CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT AACCGCCGTG CAGATACGCA
401 ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA TTGTGGCAT CATACTCTC
451 ATAATGCAGC GAAACCACGG AATTTTTCAC GATAGCCATA TTTGTCCTTT
501 CAGGAACAGC AGATTAATTA CAGGCGCATT CTAA

```

This corresponds to the amino acid sequence <SEQ ID 908; ORF 241>:

m241.pep (partial)

```

1  ..RQSVVMTVR AVDMTVCDL IGCIHAFAFN SLKADFHACQ RMVAVVHRLA
51  VGNIGYTIDD NIAGFRIVGF KHHADDFNR EHARIFDTDQ LRILLAERIV
101 GRQRHIDRIA GILTVQRLFH QRENAVVTAV QIRNRFPGFV QKLIVGIIHL
151 IMQRNHGIFH DSHICPFRNS RLITGAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 241 shows 91.5% identity over a 177 aa overlap with a predicted ORF (ORF 241.ng) from *N. gonorrhoeae*:

m241/g241

m241.pep				10	20	30
				RQSVVMTVR	AVDMTVCDL	IGCIHAFAFN
g241	QPTYLLHPSN	KMPSETEQTL	FRRHQIPPSQ	RQSVVMTVR	TVDMTVCDL	IGCIHAFAFN
	70	80	90	100	110	120
m241.pep		40	50	60	70	80
		SLKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVGF	KHHADDFNR
g241	SFKADFHACQ	RMVAVVHRLA	VGNIGYTIDD	NIAGFRIVRF	KHHTDLDFNR	ERARIFNTDQ
	130	140	150	160	170	180
m241.pep		100	110	120	130	140
		LRILLAERIV	GRQRHIDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFPGFV
g241	LRIMLTERIV	GRKRHFDRIA	GILTVQRLFH	QRENAVVTAV	QIRNRFPGFI	QKLIVGIIHL
	190	200	210	220	230	240
m241.pep		160	170			
		IMQRNHGIFH	DSHICPFRNS	RLITGAFX		
g241	IMQRNHGIFC	NSHICPFRNS	RLITGAFX			
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 909>:

a241.seq

```

1  ATGCCAACAC GTCCAACCTG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCAGC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCCTT TTCAGACGGC

```

553

```

251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCTCT ATCGGATGCA TCGCGCACAC
351 TTTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACCGCCGTG CAGATACGCA ATCGGTTCTT CGGTTTTGTC CAAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCCTCAC
751 GATAGCCATA TTTGTCCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTAA

```

This corresponds to the amino acid sequence <SEQ ID 910; ORF 241.a>:

```

a241.pep
  1 MPTRPTRAAK HPTPPTWLQT AYCPRPPYRP PSVQTHTPHE PASSTCAAKS
 51 ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVMTVR
101 TVDMTVCDL IGCIHTFNR SLKADFHACQ RMVAVHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDNR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241/a241 96.0% identity in 177 aa overlap

```

                                10      20      30
m241.pep                                RQSVVMTVRVDMTVCDLIGCIAHAFNC
                                |||||:|||||:|||||:||
a241      QPTYLLHPSNKMPSMEQTLFRRHQIPPSCRQSVVMTVRTVDMTVCDLIGCIAHTFNR
              70      80      90      100     110     120

              40      50      60      70      80      90
m241.pep      SLKADFHACQRMVAVHRLAVGNIGYTIDNIAAGFRIVGFKHHADFDNRHARIFDNDQ
              |||||:|||||:|||||:|||||:|||||:||
a241      SLKADFHACQRMVAVHRLTVGNIGYTIDNIAAGFRIVGFKHHADFDNRHARIFDNDQ
              130     140     150     160     170     180

              100     110     120     130     140     150
m241.pep      LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              |||||:|||||:|||||:|||||:|||||:||
a241      LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL
              190     200     210     220     230     240

              160     170
m241.pep      IMQRNHGIFHDSHICPFRNSRLITGAFX
              |||||:|||||:|||||:||
a241      IMQRNHGILHDSHICPFRNSRLITGAFX
              250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 911>:

```

g241-1.seq
  1 ATGATAGAAG TCATACATTT CTTCGGCACC GAAACGCGCA GACAGTTTGC
 51 TTGTGCCGAC GTTGGACGAT TTCTGCATGA TGCCGCGCAC ATCCAAAGAG
101 GGGTAAACAT GGGTATCGCG CACGGGAGAC GGTCCGATTT TATAAGGCTG
151 CGTATTCAGC CGTTCGTTCA AATCGGTTTT GCCCGCATCC AATGCCTTCG
201 CAATCACAAA CGGTTTGATT GCCGAACCGG GTTCGATCAT ATCGGTTACG
251 GCACGGTTGC GCCGCTGTTT GCTGTCTGCC CGGCCGGGCC TGTGGGATC
301 GTAGGCGGGC GTATTGGCCA AGGCGAGGAT TTCCCCCGTG CGGGCATCCA
351 AACCACCAC CGTTCCGGCT TTTGCTGAT GGTATTCGAC CGCCTTGTTT
401 AACTCTTCAT AGGCCAAGGT CTGAATCCTC TGATCGAGGG AAAGGATGAT
451 GTCTTTGCCG TTTTTCGGGG CTTTaktGCG CGGGGAGTCC AAGCTGTCCA
501 CAATATTGCC CTGCCGGTCC CGCAAAACGA CTTCCGCGCC GTCTTCGCCA
551 TGCAAGCTGT CTTCAAGCGA AAGTTCCAAA CCTTCCTGAC CTTTGCCGTC
601 AATATCGGTA AATCCGATGA CGTGTGCAAA CAGGTTGCCC ATCGGGTAAT
651 GCGGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 912; ORF 241-1.ng>:

554

g241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMVTR
101 TVDMTVCDL IGCIAHAFNR SFKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVRF KHHTDLDFNR ERARIFNTDQ LRIMLTERIV GRKRHFDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFI QKLIVGIIHL IMQRNHGIFC
251 NSHICPFRNS RLITGAF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 913>:

m241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCTGCAAAC CCTCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC
101 AAACGCGTAC ACCGCGTGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTC TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAACGGA ACAAACCCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CGGCAATCAG TGGTGGTGAT GACCGTGCGG
301 GCGGTGGACA TGACCGTGTG CGATTTCTCT ATCGGATGCA TCGCGCACGC
351 TTTCAACTGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTGCC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCCG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTTCAACAGG GAACACGCCC GCATCTCGA TACGGACCAA CTCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGACAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTCTT CGGTTTGTG CAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTTTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTAATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 914; ORF 241-1>:

m241-1.pep

```

1  MPTRPTRAAN PPTPTTWLQT AYCPRPYPYR PSVQTRTPRE PASSTCAAKS
51  ANRRENSHNA QPTYLLHPSN KMPSETEQTL FRRHQIPPSC RQSVVVMVTR
101 AVDMTVCDL IGCIAHAFNC SLKADFHACQ RMVAVVHRLA VGNIGYTIDD
151 NIAGFRIVGF KHHADDFNR EHARIFDQDQ LRILLAERIV GRQRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGIFH
251 DSHICPFRNS RLITGAF*

```

m241-1/g241-1 93.3% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTRTPREPASSTCAAKSANRRENSHNA					
g241	MPTRPTRAANPPTPTTWLQTAYCPRPPYRPPSVQTHTPHEPASSTCAAKSANRRENSHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMVTRAVDMTVCDLIGCIAHAFNC					
g241	QPTYLLHPSNKMPSSETEQTLFRRHQIPPSCRQSVVVMVTRVDMTVCDLIGCIAHAFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQRMVAVVHRLAVGNIGYTIDNIAAGFRIVGFKHHADDFNREHARIFDQDQ					
g241	SFKADFHACQRMVAVVHRLAVGNIGYTIDNIAAGFRIVRFKHHADDFNREHARIFDQDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
g241	LRIMLTERIVGRKRHFDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFIQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
g241	IMQRNHGIFCNSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 915>:

a241-1.seq

```

1  ATGCCAACAC GTCCAACCTCG CGCCGCAAAG CATCCAACCC CGCCAACCTG
51  GCTTCAGACG GCATACTGCC CTCGTCCGCC ATATCGTCCG CCGTCCGTGC

```

555

```

101 AAACGCATAC ACCGCATGAA CCGGCTTCCT CAACCTGCGC GGCAAAATCA
151 GCGAACCGAC GGGAAAATTT TCATAATGCC CAACCGACAT ACCTTCTCCA
201 TCCATCAAAC AAAATGCCGT CTGAAATGGA ACAAACCTT TTCAGACGGC
251 ATCAGATACC TCCAAGCTGC CCGCAATCAG TGGTGGTGAT GACCGTGCGG
301 ACCGTGGACA TGACCGTGTG CGATTTCCCTC ATCGGATGCA TCGCGCACAC
351 TTCAACCGT AGCCTTAAAG CGGATTTTCA TGCCTGCCAA AGGATGGTTG
401 CCGTCCACCA CCGCCTTACC GTCGGCAACA TCGGTTACAC GATAGACGAC
451 AACATCGCGG GTTTCAGGAT CGTCGGCTTC AAACATCATG CCGACTTCGA
501 CTCAACAGG GAACACGCCC GCATCTTCAA TACGGACCAA CTCCGGATCC
551 TGCTCGCCGA ACGCATCGTC GGGCGAAAGC GCCACATCGA CCGTATCGCC
601 GGCATCCTTA CCGTGCAACG CCTCTTCCAC CAAAGGGAAA ATGCCGTCGT
651 AACC GCCGTG CAGATACGCA ATCGGTTCTT CGGTTTGTG CAAAGCTGA
701 TTGTTGGCAT CATACTCTC ATAATGCAGC GAAACCACGG AATTCTTCAC
751 GATAGCCATA TTTGTCTTT CAGGAACAGC AGATTATTA CAGGCGCATT
801 CTA

```

This corresponds to the amino acid sequence <SEQ ID 916; ORF 241-1.a>:

a241-1.pep

```

1  MPTRPTRA AK HPTPPTWLQT AYCPRPYPYR PSVQTHTPHE PASSTCAAKS
51  ANRRENFHNA QPTYLLHPSN KMPSEMEQTL FRRHQIPPSC RQSVVVM TVR
101 TVDMTVCDFL IGCIAHTFNR SLKADFHACQ RMVAVHHRLT VGNIGYTIDD
151 NIAGFRIVGF KHHADFDENR EHARIFNTDQ LRILLAERIV GRKRHIDRIA
201 GILTVQRLFH QRENAVVTAV QIRNRFFGFV QKLIVGIIHL IMQRNHGILH
251 DSHICPFRNS RLITGAF*

```

m241-1/a241-1 95.1% identity in 267 aa overlap

	10	20	30	40	50	60
m241-1.pep	MPTRPTRAANPPTPPTWLQTAYCPRPYPYRPSVQTRTPREPASSTCAAKSANRRENSHNA					
a241	MPTRPTRA AKHPTPPTWLQTAYCPRPYPYRPSVQTHTPHEPASSTCAAKSANRRENFHNA					
	10	20	30	40	50	60
m241-1.pep	QPTYLLHPSN KMPSETEQTLFRRHQIPPSCRQSVVVM TVRAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSN KMPSEMEQTLFRRHQIPPSCRQSVVVM TVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
m241-1.pep	QPTYLLHPSN KMPSETEQTLFRRHQIPPSCRQSVVVM TVRAVDMTVCDFLIGCIAHAFNC					
a241	QPTYLLHPSN KMPSEMEQTLFRRHQIPPSCRQSVVVM TVRTVDMTVCDFLIGCIAHTFNR					
	70	80	90	100	110	120
m241-1.pep	SLKADFHACQ RMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFD TDQ					
a241	SLKADFHACQ RMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	SLKADFHACQ RMVAVHHRLAVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFD TDQ					
a241	SLKADFHACQ RMVAVHHRLTVGNIGYTIDDNIAGFRIVGFKHHADFDENREHARIFNTDQ					
	130	140	150	160	170	180
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	LRILLAERIVGRQRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
a241	LRILLAERIVGRKRHIDRIAGILTVQRLFHQRENAVVTAVQIRNRFFGFVQKLIVGIIHL					
	190	200	210	220	230	240
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				
m241-1.pep	IMQRNHGIFHDSHICPFRNSRLITGAFX					
a241	IMQRNHGILHDSHICPFRNSRLITGAFX					
	250	260				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 917>:

g242.seq

```

1  atgatcggcg aacttggtgt tttgttcgtg atcgagcact tcaagcaacg
51  cgctggcggg atcgccccga aagtcgctgc ccaatttgcg gatttcgctg
101 agcaggaaca acgggtttct tacgcctgct tttgccatat tctgcaaaat
151 cttgccgggc atagagccga tataggtacg gcggtgcccg cggatttcgc
201 tttcgctcgc cacgccgccc aaggccatac ggacatat ttcgccccgtt
251 gctttggcga tggattcgcc caaagagggt ttgccacgcg ccggaggggcc
301 gaccaaacac agaatcggac ctttgagctt gtccatacgt ttttgacggg
351 cgaggtattc caaaatccgt tctttgactt tttccaggcc gtagtggtcg
401 gcatccagca ccagtcgggc tttggcgatg tctttgctga cgcgggattt
451 tttcttccac ggcagtcgga gcagggtgtc gatgtagttg cgtacgacgg

```

556

```

501 tggattcggc agacatcggc ggcattcatt tgagtttttt cagttcggac
551 aggcatTTTT cttccgcttc tttggtcata cccgcctttt tgatgcctgc
601 ctccaaggca tccagttcgc cgttttcgct ttcttcgccc aattctttgt
651 gtatcgcttt aatctgttcg ttcagataat attcgcgttg ggatttttcc
701 atttggcgtt tgacgcgtcc gcgtatgcgt ttttcggcct gcataatgtc
751 gagttcggat tccagctttg ccagcaggaa ttccatccgt ttgccgattt
801 cgggaatctc caaaatctgt tggcgttgcg ccagtttcaa ctgcaaattgc
851 gctgcgaccg tatcggttag

```

This corresponds to the amino acid sequence <SEQ ID 918; ORF 242.ng>:

g242.pep

```

1 MIGELVVLFV IEHFKQRAGG IAPKVAAQFV DFVEQEQRVS YACFCHILQN
51 LAGHRADIGT AVPADFAFVA HAAQGHDTIF PPRCFDGF A QRGFAHARRA
101 DQTQNRTEFEL VHTFLDGEVF QNPFFDFFQA VVVGIIHQSG FGDVFADAGF
151 FLPRQSEQGV DVVAYDGGFG RHRRHHFEFF QFGQAFFFRF FGHTRLFDAC
201 LQGIQFAFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNL QNLLALRQFO LQMRCDRIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 919>:

m242.seq

```

1 ATGATCGGCA AACTTGTTGT TTTGTTCCGG ATCGAGCACT TCGAGCAACG
51 CGCTGGCGGG ATCGCCTCGG AAGTCGTTAC CCAATTTGTC GATTTTCGTCG
101 AGCAGGAACA AGGGGTTTTT CACGCCGGCT TTTGCCATAT TCTGCAAAAT
151 CTTACCGGGC ATAGAGCCGA TATAGGTGCG GCGGTGTCCC CTGATTTTCGC
201 TTTCGTCGCG CACGCCGCC AAAGCCATGC GGACATATTT CCGCCCCGTT
251 GCTTTGGCGA TGGATTGCGC CAAAGAGGTT TTGCCACGC CCGGAGGGCC
301 GACCAGGCAC AGAATCGGGC CTTTGAGTTT GTCCATACGT TTTTGGACGG
351 CGAGGTATTC CAAAATCCGT TCTTGACTT TTTCCAGGCC GTAGTGGTCG
401 GCATCCAGCA CCAGTCCGGC TTTGGCGATG TCTTTGCTGA CGCGGGATT
451 TTTCTTCCAC GGCAGCTCGA GCAAAGTGTC GATGTAGTTG CGTACGACGG
501 TGGATTCCGC AGACATCGGT GGCATCATTT TGAGCTTTT CAGTTCGGAC
551 AGGCATTTTT CTTCCGCTTC TTTGGTCATA CCCGCCTTTT TGATATCTGC
601 TTCCAAGGCA TCCAGTTCGC CGTTTTCGTC TTCTTCGCCC AGTTCCTTGT
651 GTATCGCTTT AATCTGTTTCG TTCAGATAAT ATTCGCGCTG GGATTTTTC
701 ATTTGGCGTT TGACGCGTCC GCGTATGCGT TTTTCGGCCT GCATAATGTC
751 GAGTTCGGAT TCCAGCTGTG CCAGCAGGAA TTCCATCCGT TTGCCGATT
801 CGGAATTTT CAAAATCTGT TGGCGTTGCG CCAGTTTCAA CTGCAAATGC
851 GCTGCGACCG TATCGGTTAG

```

This corresponds to the amino acid sequence <SEQ ID 920; ORF 242>:

m242.pep

```

1 MIGKLVVLFV IEHFEQRAGG IASEVVTQFV DFVEQEQQVF HAGFCHILQN
51 LTGHRADIGA AVSPDFAFVA HAAQSHADIF PPRCFDGF A QRGFAHARRA
101 DQAQNRAFEF VHTFLDGEVF QNPFFDFFQA VVVGIIHQSG FGDVFADAGF
151 FLPRQLEQSV DVVAYDGGFR RHRWHHFELF QFGQAFFFRF FGHTRLFDIC
201 FQGIQFAFV FFAQFFVYRF NLFVQIIFAL GFFHLAFDAS AYAFFGLHNV
251 EFGFQLCQOE FHPFADFGNF QNLLALRQFO LQMRCDRIG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 242 shows 90.3% identity over a 289 aa overlap with a predicted ORF (ORF 242.ng) from *N. gonorrhoeae*:

m242/g24290.3% identity in 289 aa overlap

```

10 20 30 40 50 60
m242.pep MIGKLVVLFVIEHFEQRAGGIASEVVTQFVDFVEQEQQVFHAGFCHILQNLTHRADIGA
|||:||||| ||||:||||| :||:||||| |||:| |||||:|||||:
g242 MIGELVVLFVIEHFKQRAGGIAPKVAAQFVDFVEQEQRVS YACFCHILQNL LAGHRADIGT
10 20 30 40 50 60

70 80 90 100 110 120
m242.pep AVSPDFAFVAHAAQSHADIFPPRCFGDGF A QRGFAHARRADQAQNRAFEFVHTFLDGEVF
|| |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g242 AVPADFAFVAHAAQGHDTIFPPRCFGDGF A QRGFAHARRADQTQNRTEFELVHTFLDGEVF
70 80 90 100 110 120

```

	130	140	150	160	170	180
m242.pep	QNPFFDFFQAVVVGIIQHQS	GFSGFDVFADAGFFLPRQLE	QSVDDVVA	DGGFRRHRWHH	FELF	
g242	QNPFFDFFQAVVVGIIQHQS	GFSGFDVFADAGFFLPRQSE	QGVDDVVA	DGGFGRHRRHH	FEFF	
	130	140	150	160	170	180
	190	200	210	220	230	240
m242.pep	QFGQAFFFRFFGHTRLFDIC	FQGIQFAVVFVFFAQFFV	YRNL	FVQII	FALGFFHLAFDAS	
g242	QFGQAFFFRFFGHTRLFDAC	LQGIQFAVVFVFFAQFFV	YRNL	FVQII	FALGFFHLAFDAS	
	190	200	210	220	230	240
	250	260	270	280	290	
m242.pep	AYAFFGLHNVEFGFQLCQ	QEFHFPADFNGFNQNL	LALRQFQLQMR	CDRIGX		
g242	AYAFFGLHNVEFGFQLCQ	QEFHFPADFNGNLQNL	LALRQFQLQMR	CDRIGX		
	250	260	270	280		

a242.seq					
1	ATGATCGGCG	AAC TTGT TGT	TTTGCTCGGG	ATCAAGCACT	TCGAGCAAAG
51	CGCTGGCGGG	ATCGCCCCGG	AAGTGCCTAN	CCAATT TGTC	GATTTCGTCG
101	AGCAGGAACA	ATGGGTTTTT	TACGCCGGCT	TTTGCCATAT	TC TGCAAAAT
151	CTTACC GGCG	ATGGAGCCGA	TATAGGTGCG	CGCGTGTCCC	CGGATTT CGC
201	TTTCGTCGCG	CACGCCGCCC	AAAGCCATGC	GGACATATTT	CCGCCCCGTT
251	GCTTTGGCGA	TGGATTCGCC	CAAAGAGGTT	TTGCCCACGC	CTGGAGGGCC
301	GACCAGGCAC	AGAATCGGGC	CTTTGAGTTT	GTCCATAGCT	TTTTGGACGG
351	CGAGGTATTC	CAAAATCCGT	TCTTTGACTT	TTTCCAGGCT	GTAGTGGTCG
401	GTATCCAGCA	CCAATCCGGC	TTTGGCGATG	TCTTTGCTGA	CGCGGGATTT
451	TTTCTTCCAC	GGCAGTTCGA	GCAGGGTGTC	GATGTAGTTG	CGTACGACGG
501	TGGATTCGGC	AGACATCGGC	GGCATCATTT	TGAGCTTTTT	CAGTTCGGAC
551	AGGCATTTTT	CTTCCGCTTC	TTTGGTCATA	CCC GCCTTTT	TGATATCTGT
601	TTCCAAGGCA	TCCAGTTCGC	CGTTTTCGCT	TTCTTCGCCC	AGATCTTTGT
651	GTATCGCTTT	AATCTGTTTC	TTCAGATAAT	ATTTCGCGCT	GGATTTTTTC
701	ATTTGGCGTT	TGACGCGTCC	GCGTATGCGT	TTTTCGGCCT	GCATAATGTC
751	GAGTTCCGGAT	TCCAGCTGTG	CCAGCAGGAA	TTCCATCCGT	TTGCCGATTT
801	CGGGAATTTT	CAAAATCTGT	TGGCGTTGCG	CCAGTTTCAA	CTGCAAATGC
851	GCTGCGACCG	TATCGGTTAG			

a242.pep

1	MIGELVLLLG	IKHFEQRAGG	IAPEVAXQFV	DFVEQEQWVF	YAGFCHILQN
51	LTGHGADIGA	AVSPDFAFVA	HAAQSHADIF	PPRCFGDGFA	QRGFAHAWRA
101	DQARNRAFEF	VHTFLDGEVF	QNPFDFDFFQ	VVVGIIQHSG	FGDVFADAGF
151	FLPRQFEQGV	DVVAYDGGFG	RHRRHHFELE	QFGQAFFERF	FGHTRLFDIC
201	<u>FQGIQFAVFV</u>	<u>FFAQYFVYRF</u>	<u>NLFVQIIFAL</u>	<u>GGFHLAFDAS</u>	<u>AYAFFGLHNV</u>
251	EGFGLCOOE	FHPFADGNGF	ONLLALROFO	LOMRCDRIG*	

	10	20	30	40	50	60	
m242.pep	MIGKLVVLF	GLGIEHFE	QRAGGIA	SEVVTQ	FVDFVEQ	EQGVFHAGFCHILQNL	TGHRADIGA
a242	MIGELVVLL	GLGIKHFE	QRAGGIA	PEVAXQ	FVDFVEQ	EQQWVFYAGFCHILQNL	TGHGADIGA
	10	20	30	40	50	60	
	70	80	90	100	110	120	
m242.pep	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGFGAQR	GFAHARRADQAQNRA	FEFVHTFLDGEVF
a242	AVSPDFAF	VAHAAQ	SHADIF	PPRCFG	DGFGAQR	GFAHAWRADQAQNRA	FEFVHTFLDGEVF
	70	80	90	100	110	120	
	130	140	150	160	170	180	
m242.pep	QNPFFD	FFQAVV	VGIQH	QSGFGD	VFADAG	FFLPRQL	EQSVDVVAYDGGFRRHRWHHFELF

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```

a242      QNPFDFDFQAVVVGIIHQSGFGDVFADAGFFLPRQFEQGVDDVAYDGGFGRHRRHHFELF
           130      140      150      160      170      180
           190      200      210      220      230      240
m242.pep  QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIIFALGFFHLAFDAS
           |||||
a242      QFGQAFFFRFFGHTRLFDICFQGIQFAVFVFFAQFFVYRENLFVQIIIFALGFFHLAFDAS
           190      200      210      220      230      240
           250      260      270      280      290
m242.pep  AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           |||||
a242      AYAFFGLHNVEFGFQLCQQEFHFPADFNGFNQNLALRQFQLQMRCDRIGX
           250      260      270      280      290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 923>:

```

g243.seq
1  ATGGTaatcg tctGGTTGcC cgAGTTaaccg CCGATGCCGG CGACGATGGG
51  CATCAGCGCG GCGAGTGCGA CGATTTTTTC gataactgcCT TCAAACGCGC
101 CGATGACGCG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAACA GGTCTTCCTC
201 TTCCTGCAAA CCTGCCATGT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCc tgCCGATGAG CTTTTTGTTT
301 TCATCAACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 924; ORF 243.ng>:

```

g243.pep
1  MVIVWLPELP PMPATMGISA ASATIFSILP SNAPMTRLAR KAVQRLTASH
51  IQRFLTESKT GANRSSSSCK PAMFNISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 925>:

```

m243.seq
1  ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51  CATCAGCGCG GyGAGTGCGA CGATTTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GyTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCGAGCCAC
151 ATCCAGyGGT TTTTCACCGA ATCCCACACG GGGGCGAAyA GGTCTTCCTC
201 TTCCTGCAAA CCCGCCATAT TCAGCATATC CGCTTCCGAT TCTTCGCGGA
251 TCACGTCCAC CATCTCGTCG ATGGTAATCC TGCCGATGAG CTTTTTGTTT
301 TCATCGACGA CGGGCGCGGT AACCAAGTCG TAG

```

This corresponds to the amino acid sequence <SEQ ID 926; ORF 243>:

```

m243.pep
1  MVIVWLPELP PMPATMGISA XSATIFSMLP SNAPITRLAR KAVQRLTASH
51  IQXFFTESHT GANRSSSSCK PAIFSISASD SSRITSTISS MVILPMSFLF
101 SSTTGAVTKS *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 243 shows 92.7% identity over a 110 aa overlap with a predicted ORF (ORF 243.ng) from *N. gonorrhoeae*:

```

m243/g243
           10      20      30      40      50      60
m243.pep  MVIVWLPELPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT
           |||||
g243      MVIVWLPELPMPATMGISAASATIFSILPSNAPMTRLARKAVQRLTASHIQRFLTESKT
           10      20      30      40      50      60
           70      80      90      100     110
m243.pep  GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX
           |||||
g243      GANRSSSSCKPAMFNISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX

```


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70 80 90 100 110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 927>:

```
a243.seq
1 ATGGTAATCG TCTGGTTGCC CGAGTTACCG CCTATGCCGG CGACGATGGG
51 CATCAGCGCG GCGAGTGCGA CGATTTTTC GATGCTGCCT TCAAACGCGC
101 CGATAACACG GCTGGCGAGG AAGGCGGTGC AGAGGTTGAC GGCAGGCCAC
151 ATCCAGCGGT TTTTGACGGA ATCCAAGACG GGGGCGAATA AGTCTTCCTC
201 TTCTTGCAA CCCGCCATAT TCAACATATC CGCTTCGGAT TCTTCGCGGA
251 TCACGTCCAC CATTTCGTCA ACGGTCACCC TGCCGATGAG CTTTTTGT
301 TCATCGACGA CGGCGCGGT AACCAAGTCA TAG
```

This corresponds to the amino acid sequence <SEQ ID 928; ORF 243.a>:

```
a243.pep
1 MVIVWLPELP PMPATMGISA ASATIFSMLP SNAPITRLAR KAVQRLTASH
51 IQRFLTESKT GANKSSSSCK PAIFNISASD SSRITSTISS TVTLPMSELF
101 SSTTGAVTKS *
```

m243/a243 92.7% identity in 110 aa overlap

	10	20	30	40	50	60
m243.pep	MVIVWLPELPPMPATMGISAXSATIFSMLPSNAPITRLARKAVQRLTASHIQXFFTESHT					
a243	MVIVWLPELPPMPATMGISAASATIFSMLPSNAPITRLARKAVQRLTASHIQRFLTESKT					
	10	20	30	40	50	60
	70	80	90	100	110	
m243.pep	GANRSSSSCKPAIFSISASDSSRITSTISSMVILPMSFLFSSTTGAVTKSX					
	: :					
a243	GANKSSSSCKPAIFNISASDSSRITSTISSTVTLPMSELFSTTGAVTKSX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 929>:

```
g244.seq
1 atgccgcctg aagcccgccg ggcgggttca gacggcattg ccgctttact
51 tcgatcggtt tatacgcaaa acgcgcttca ggaaataaat cagattattc
101 cccagacgcc ttcaggcttc cttccgtgcc accgtaacca tagccgggcg
151 caacacacgg tcggacaggg tataaccctt cttcatcaca ccaaccacgg
201 tattgggttc ctgctcactg gccaccgcct gcacgcctg atggatatcc
251 ggatcgagct tatcgcccgc tttaggattg atttccttga tttgcgtggc
301 atcaaacgcc ttctgcaact cattcaaagt catctgcaca cccattttca
351 gcgcacgaa attaccgctc tgatccaaaa gcgccatttc cagataatcc
401 ttgaccggca acattttcac ggcaaaacttc tgtccggcga acttgtgcgt
451 atcggcaatt tcctgctggt ggccggcgcg caggttttgc tcgtttgcca
501 aagcgcgcag ttgttcgtct ttcaactgcg cttccagctc ggcaatccgc
551 gcctgcaaat cctcataagc cggctcggcg gcagcctggt cctgtacacc
601 gtccgcattt cctactgtct cgacgggttc caccgcctcc acattttcaa
651 ccgcttcttc actgttttgc tgctgtgtct gttcgtcat atcgatatcc
701 tcaaaacaaa ttggaaatca aaatccggtt attaccgag caagataagg
751 acattttcaa gaaacttcaa gcaaaggcag gaaatttcac atccgccgcc
801 gaatacccta ccgcaaaaac catataaacg gtaa
```

This corresponds to the amino acid sequence <SEQ ID 930; ORF 244.ng>:

```
g244.pep
1 MPPEARPAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LPCHRNHSRA
51 QHTVGQGITL LHHTNHGIGF LLTGHRLHRL MDIRIELIAR FRIDFLDLRG
101 IKRLQLIQS HLHTHFORIE ITALIQKRHF QIILDRQHFH GKLLSGELVR
151 IGNFLLVAAA QVLLVCQSAQ LFVFQLRFQL GNPRLQILIS RLGGSLFLYT
201 VRISYCLDGF HRLHIFNRFF TVLLLCLFAH IVSLKTNWKS KSGYYPKIR
251 TFSRNFQQRQ EISHPPNTL PQKPYKR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 931>:

```
m244.seq
```

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```

1  ATGCCGTCTG AAGCCCGACA GCGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGCGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTATCACA CCCACCACGG
201 TATTCGGCTC CTGTTGCTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTAGGGTTG ATTTCCCTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCCAC GGCAAATTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TyCTGCTGGT GCGGCGGCG CAGGTTTTC TCGTTTGCCA
501 AAGCGCGCTG CTCGTCTTTC AACTGCGTTT CCAGCTCGGC AATCCGCGCC
551 TGCAAATCCT CATAAGCCGG CTCTGCGGCA GCCTGTTCTT GCACACCGTC
601 CGCATTTTCT ACTGTTTCGA CGGTTTCCAC CGCTCCACA TTTTCAACCG
651 CTTCTTCACT GTTTTGCTGC TGTGTCTGTT CGCTCATATC GTATCCCTTA
701 AAACAAATTG GAAATCAAAA TCCAGTTATT ACCCGCGCAA GATAAGGACA
751 TTTTCAAGAA ACTTCAAKCA AAakCAGAGA ATTTCAAATT CATTTTCAAA
801 TCCCCTACCG AAAAAATAAT ATAGACGGTA A

```

This corresponds to the amino acid sequence <SEQ ID 932; ORF 244>:

m244 . pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEIN QIIPQTPSGF LLRHRNHSRA
51  QHAVGQRITL LHHTHHGIRL LFACHRLHRL MDIRIELIAR FRVDFDLRLS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLLVAAA QVLLVCQSAL LVFQLRFQLG NPLRLQILIS LCGSLFLHTV
201 RISYCFDGFH RLHIFNRFFT VLLLCLEFAH VSLKTNWKS SSYYPRKIRT
251 FSRNFXQXQR ISNSFSNPLP KKXYRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 244 shows 86.3% identity over a 277 aa overlap with a predicted ORF (ORF 244.ng) from *N. gonorrhoeae*:

M244/G244

	10	20	30	40	50	60
m244 . pep	MPSEARQAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
g244	MPPEARPAGSDGIAALLRSVYTONALQEINQIIPQTPSGFLPCHRNHSRAQHTVGGGITL					
	10	20	30	40	50	60
m244 . pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRLSIKCFQLVQSHLHAHFQRIE					
g244	LHHTNHGIGFLLTGHRLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120
m244 . pep	IAALIQKRHFQIILDRQHFHKGKLLSGELVRIRNFLLVAAAQVLLVCQSAALLVFQLRFQL					
g244	ITALIQKRHFQIILDRQHFHKGKLLSGELVRIGNFLLVAAAQVLLVCQSAQLFVQLRFQL					
	130	140	150	160	170	180
m244 . pep	GNPRLQILISRLCGSLFLHTVIRISYCFDGFHRLHIFNRFFT VLLLCLEFAHIVSLKTNWKS					
g244	GNPRLQILISRLGGSFLYTVIRISYCLDGFHRLHIFNRFFT VLLLCLEFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244 . pep	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
g244	KSGYYPSKIRTFSRNFKQRQEISHPPNTLPQKPYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 933>:

```
a244.seq
1   ATGCCGTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCCTT CTTTCATCAG CCCACCACGG
201 TATTGGGTTC CTGTTGCTTT GCCACCGCCT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTCAT
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTTCAC GGCAAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATTT CCTACTGTCT CGACGGTTTC CACCGCCTCC ACATTTTCAA
651 CCGCTTCTTC ACTGTTTTCG TGCTGTGTCT GTTCGTCAT ATCGTATCCC
701 TTAAAACAAA TTGGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAA ATTCATTTTC
801 AAATCCCCTA CCGAAAAAAT AATATAGACG GTAA
```

This corresponds to the amino acid sequence <SEQ ID 934; ORF 244.a>:

```
a244.pep
1   MPSEARQAGS DGIAALLRSV YTQNALQEIN QIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQKRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQLRFQL GNPRQLILIS RLCGSFLFHT
201 VRISYCLDGF HRLHIFNRFF TVLLLCFLFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFQRQ RISNSFSNPL PKK*YRR*
```

m244/a244 96.8% identity in 277 aa overlap

	10	20	30	40	50	60
m244.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
m244.pep	70	80	90	100	110	120
	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
m244.pep	130	140	150	160	170	179
	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSA-LLVFQLRFQL					
a244	IAALIQKRHFQIILDRQHFHGKLLSGELVRIRNFLVAAAQVLLVCQSAQLLVFQLRFQL					
	130	140	150	160	170	180
m244.pep	180	190	200	210	220	230
	GNPRQLILISRLCGSLFHTVRISYCFDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
a244	GNPRQLILISRLCGSLFHTVRISYCLDGFHRLHIFNRFFTVLLLCFLFAHIVSLKTNWKS					
	190	200	210	220	230	240
m244.pep	240	250	260	270		
	KSSYYPRKIRTFSRNFXQXQRISNSFSNPLPKKXYRRX					
a244	KSSYYPRKIRTFSRNFKQRQRISNSFSNPLPKKXYRRX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 935>:

```
g244-1.seq
1   atgccgcctg aagcccgggc ggcgggttca gacggcattg cgcgtttact
```

This corresponds to the amino acid sequence <SEQ ID 936; ORF 244-1.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 937>:

This corresponds to the amino acid sequence <SEQ ID 938; ORF 244-1>:

m244-1/G244-1 86.3% identity in 277 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLLRHNRHNSRAQHAVGQRITL					
g244-1	MPPEARPAGSDGIAALLRSVYTQNALQEINQIIPQTPSGFLPCHNRHNSRAQHTVQGGITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRLSIKCFQLQVQSHLHAHFQRIE					
			::			
g244-1	LHHTNHGIGFLLTGHRHLHRLMDIRIELIARFRIDFLDLRGIKRLLQLIQSHLHTHFQRIE					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m244-1.pep	IAALIQRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSAALLVFQ LRFQL					
g244-1	ITALIQRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSAQLFVFQ LRFQL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
g244-1	GNPRLQILISRLGGSFLYTVRISYCLDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
	190	200	210	220	230	240
	250	260	270			
m244-1.pep	KSSYYPRKIRTF SRNFXQQRISNSFSNPLPKXX					
g244-1	KSGYYPSKIRTF SRNFKQRQEISHPPNTLPQKPKYKRX					
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 939>:

a244-1.seq

```

1  ATGCCGCTCTG AAGCCCGACA GCGGGGTTCA GACGGCATTG CCGCTTTACT
51  TCGATCGGTT TATACGCAAA ACGCGCTTCA GGAAATAAAT CAGATTATTC
101 CCCAGACGCC TTCAGGCTTC CTTCTGTGCC ACCGTAACCA TAGCCGGGCG
151 CAACACGCGG TCGGACAGCG TATAACCTT CTTCATCACG CCCACCACGG
201 TATTGGGTTT CTGTTGCTT GCCACCGCTT GCATCGCCTG ATGGATATTC
251 GGATCGAGCT TATCGCCCGC TTTAGGATTG ATTTCTTGA TTTGCGTAGC
301 ATCAAAATGCT TTCTGCAACT CGTTCAAAGT CATCTGCACG CCCATTTTCA
351 GCGCATCGAA ATTGCCGCTC TGATCCAAAA GCGCCATTTC CAGATAATCC
401 TTGACCGGCA GCATTCCAC GGCAACTTC TGTCCGGCGA ACTTGTGCGT
451 ATCCGCAATT TCCTGCTGGT GGCGGCGGCG CAGGTTTTCG TCGTTTGCCA
501 AAGCGCGCAG CTGCTCGTCT TTCAACTGCG CTTCCAGCTC GGCAATCCGC
551 GCCTGCAAAAT CCTCATAAGC CGGCTCTGCG GCAGCCTGTT CCTGCACACC
601 GTCCGCATT CTACTGTCT CGACGGTTTC CACCGCTCC ACATTTTCAA
651 CCGTTCTTC ACTGTTTTC TGCTGTGTCT GTTCGCTCAT ATCGTATCCC
701 TTTAAACAAA TTGAAATCA AAATCCAGTT ATTACCCGCG CAAGATAAGG
751 ACATTTTCAA GAAACTTCAA GCAAAGGCAG AGAATTTCAT ATTCATTTTC
801 AAATCCCTA CCGAAAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 940; ORF 244-1.a>:

a244-1.pep

```

1  MPSEARQAGS DGIAALLRSV YTONALQEI NQIIPQTPSGF LLCHRNHSRA
51  QHAVGQRITL LHHAHHGIGF LFACHRLHRL MDIRIELIAR FRIDFLDLRS
101 IKCFLQLVQS HLHAHFQRIE IAALIQRHF QIILDRQHFH GKLLSGELVR
151 IRNFLVAAA QVLLVCQSAQ LLVFQ LRFQL GNPRLQILIS RLCGSLFLHT
201 VRISYCLDGF HRLHIFNRFF TVLLLC LFAH IVSLKTNWKS KSSYYPRKIR
251 TFSRNFKQRQ RISNSFSNPL PKK*

```

m244-1/a244-1 96.8% identity in 274 aa overlap

	10	20	30	40	50	60
m244-1.pep	MPSEARQAGSDGIAALLRSVYTONALQEI NQIIPQTPSGFLLRHRNHSRAQHAVGQRITL					
a244-1	MPSEARQAGSDGIAALLRSVYTONALQEI NQIIPQTPSGFLLCHRNHSRAQHAVGQRITL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m244-1.pep	LHHTHHGIRLLFACHRLHRLMDIRIELIARFRVDFDLRSIKCFLQLVQSHLHAHFQRIE					
a244-1	LHHAHHGIGFLFACHRLHRLMDIRIELIARFRIDFLDLRSIKCFLQLVQSHLHAHFQRIE					
	70	80	90	100	110	120
	130	140	150	160	170	179
m244-1.pep	IAALIQRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSA-LLVFQ LRFQL					
a244-1	IAALIQRHFQIILDRQHFH GKLLSGELVRIRN FLLVAAAQVLLVCQSAQLLVFQ LRFQL					
	130	140	150	160	170	180
	180	190	200	210	220	239
m244-1.pep	GNPRLQILISRLCGSLFLHTVRISYCFDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
a244-1	GNPRLQILISRLCGSLFLHTVRISYCLDGFHRLHIFNRFFTVLLLC LFAHIVSLKTNWKS					
	190	200	210	220	230	240

```
g246.seq
1  atgtacgggc ggaacggtag tactcaagcg gccgttgccct tcgttttcga
51  ccagacacag cgtgcccggt tcggcaacgg cgaagtttac gccgctcaag
101 ccgacatcgg cagtgcgtgta aatatcgcgc agggctttgc gggcgaatcc
151 ggtcagttgg tccacgtcgt ctgtaagcgc tgtgccgagg ttttcgtgga
201 acagttcgct gacctgttct ttggttttat ggtatgcggg catcacgata
251 tgggtcggtt tttcgccctgc catttggaag ataaactcgc ccaagtcgct
301 ttccaccgcc ttaatgcctt ttgcttcaag ataatggttc agctcgattt
351 cttcgctgac catggatttg cctttgacca tcagcttgcc gtttttggtt
401 gtgatgatgt cgtggataat ttggcaggct tcggcagggg tttccgccca
451 gtgtacttcc acgcccaact tagtcagggt ttcttccaac tgctccagca
501 gcgcgggttaa
```

g246.pep

1	MYGRNGSTQA	AVAFVFDQTO	RARFGNGEYV	AAQADIGSAV	NIAQGFAGES
51	GQLVHVVCCK	CAEVLVEQFA	DLFFGFMDCG	HHDMGRFFAC	HLDDKLAQVA
101	FHRLNAFCFK	IMVQLDDFAD	HGFAFDHQLA	VFGCDDVVDN	LAGFGRGRFP
151	VYFHAQLSQV	FFQLLQQRG*			

m246.seq (partial)

1	ATGCACGGGC	GGTACGGTGG	TACTCAAGCG	ACCGTTgCTT	CGTTTTCCAC
51	CAGACACAGC	GTACCTGTTT	CAGCAACGGC	AAAGTTTACG	CCACTCAAAC
101	CGACATCGGC	AGTGCTGTAA	ATATCGCGCA	GTGCTTTACG	GGCGAAGCCG
151	GTCAGTTGGT	CTACATCGTC	TGTCAGCGGC	GTACCGAGGT	TTTGGTGGAA
201	CAGTTCGCTA	ACCTGTTCTT	TGTTTTGTG	GATAGCAGGC	ATCACGATAT
251	GGGTCCGTTT	TTCGCTGCCC	ATTTGGACGA	TGAACTCGCC	CAAGTCGCTT
301	TCTACCGCTT	TAATGCTTTT	TGCTTCAAGA	TAATGrTTCA	GCTCGATTTC
351	CTCGTGACC	ATCGATTGCG	CTTGACCAT	CAGCTTGGCG	TTTTTGGCTG
401	TGATGATGTC	GTGGATAATT	TGGCAGGCTT	CGGTTCGGGGT	TTCTGCGCG.

m246.pep (partial)

1	MHGRYGGTQA	TVAFVFHQ	RTCF	SN	GVY	ATQ	TDIG	SAV	NIAQ	CFTGEA
51	GQLVYIVCQR	RTEVLVEQFA	NLFFG	FVDSR	HHDM	GRFFAC	HLDDE	LAQVA		
101	FYRFNAFCFK	IMXQLDFLAD	HRFAFDHQLA	VFGCD	DVVDN	LAGFGR	GFCP...			

ORF 246 shows 80.0% identity over a 150 aa overlap with a predicted ORF (ORF 246.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m246.pep	MHGRYGGTQATVAFVFHQ	TQRTCSFNGKVYATQ	TDIGSAVNIAQCFTGEAGQLVYIVCQR			
	:	: : : :	: : : : : :	: : : : : :	: : : : : :	: : : : : :
g246	MYGRNGSTQAAVAFVFDQ	TQRRARFNGEVYAAQADIGSAVNIAQGFAGESGQLVHVCKR				
	10	20	30	40	50	60
	70	80	90	100	110	120
m246.pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDDELAQVAFYRFNAFCFKIMXQLDFLAD					
	: : : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :	: : : : : : :
g246	CAEVLVEQFADLFFGFMDCGHHDMGRFFACHLDCLKLAQVAFHRLNAFCFKIMVOLDFEAD					

565

	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
g246	HGFADFHDQLAVFGCDDVVDNLAGFGRGFRPVYFHAQLSQVFFQLLQQRGX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 945>:

a246 . seq (partial)

1	ATGCACGGGC	GGAACGGTGG	TACTCAAGCG	ACCGTTGCCT	TCGTTTTCCA
51	CCAGACACAG	CGTACCTGTT	TCAGCAACGG	CGAAGTTCAC	GCCACTCAAA
101	CCGACATCGG	CAGTGCTGTA	AATATCGCGC	AGTGCTTTAC	GGCGGAAGCC
151	GGTCAGTTGG	TCTACGTCGT	CCGTAAACGG	TGTGCCGAGG	TTTTGGTGGA
201	ACAGTTCGCT	AACCTGTTCT	TTGGTTTTAT	GGATTGCGGG	CATCACGATA
251	TGGGTCGGTT	TTTCACCTGC	CATTTGGACG	ATGAACTCGC	CCAAGTCGCT
301	TTCCACCGCT	TTAATGCCTT	TTGCTTCAAG	ATAATGGTTC	AGCTCGATTT
351	CCTCGCTGAC	CATCGATTG	CCTTTGACCA	TCAGCTTGCC	GTTTTTGGCT
401	GTGATGATGT	CGTGGATGAT	TTCGAGGCT	TCGGCCGGTG	TTCCGCCCA
451	GTGTACTTTT	ACGCCCAACT	TGGTCAGGTT	TTCTTCCAGC	TGCTCCAGCA
501	G				

This corresponds to the amino acid sequence <SEQ ID 946; ORF 246.a>:

a246 . pep (partial)

1	MHGRNGGTQA	TVAFVFHQQT	RTCFNSGEVH	ATQTDIGSAV	NIAQCFTGEA
51	GQLVYVVR*R	CAEVLVEQFA	NLFFGFMDCG	HHDMGRFFTC	HLDELAQVA
101	FHRFNAFCFK	IMVQLDFLAD	HRFAFDHQLA	VFGCDDVDD	FAGFGRCFRP
151	VYFYAQLGQV	FFQLLQQ			

m246/a246 88.0% identity in 150 aa overlap

	10	20	30	40	50	60
m246 . pep	MHGRYGGTQATVAFVFHQQTQRTCFNSGKVYATQTDIGSAVNIAQCFTGEAGQLVYIVCQR					
a246	MHGRNGGTQATVAFVFHQQTQRTCFNSGEVHATQTDIGSAVNIAQCFTGEAGQLVYVVRXR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m246 . pep	RTEVLVEQFANLFFGFVDSRHHDMGRFFACHLDELAQVAFYRFNAFCFKIMXQLDFLAD					
	:					
a246	CAEVLVEQFANLFFGFMDCGHHDMGRFFTCHLDELAQVAFHRFNAFCFKIMVQLDFLAD					
	70	80	90	100	110	120
	130	140	150			
m246 . pep	HRFAFDHQLAVFGCDDVVDNLAGFGRGFCP					
a246	HRFAFDHQLAVFGCDDVVDVDFAGFGRCFRPVYFYAQLGQVFFQLLQQ					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 947>:

g247 . seq

1	atgaaacgta	aaatgctaaa	cgtaccaaag	ggcgggttatg	atggtatgaa
51	gggttttacc	attgttgaat	ttctggttgc	gggcctgctc	agtataattg
101	tcctgatagc	ggtcgtatcg	agttacttta	catcccgga	attaaatgat
151	gtggcaaacg	agcgtcttgc	cattcaacag	gatttgcgga	atgcggcaac
201	attaattgtc	cgcgatgcaa	gaatggcggg	gagcttcggt	tgtttcaata
251	tgtccgagca	tactaaagac	gatattgttg	attcaagtaa	tcaaaactcaa
301	tctaaacctg	caaaaaccgg	tgccaaacaa	gaaaatcccc	ttttttcctt
351	aaaaaggagc	ggcatggata	aacaactgat	tcccgttgct	gaatccatag
401	atattaaata	tccgggtttt	atccagcgcc	ttaacgcatt	ggttttccaa
451	tacggtatcg	atgatcttga	tgcgagtgtc	gagactgttg	tagtcagcag
501	ctgttccaaa	atagcaaaac	cgggtaagaa	aatatctacc	ttgcaagaag
551	caaagagtgc	attacagatt	actaatgatg	ataaacaaaa	tggaaatatc

568

	170	180	190	200	210	220
m247.pep	PGKQIPTLED	AKKELKIP	DQDKEQNG	NIARQRHV	VNAYAVG	GRIADEES
	:	:	:	:	:	:
a247	PGKKISTL	QEAQSAL	QITNDDK	-QNGNITR	QRHVVN	AYAVGRI
	190	200	210	220	230	

m247.pep	GNPQL
a247	GNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKYTGTFDSSTNAVTPAGVEVLLSXG
	240 250 260 270 280 290

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 953>:

g247-1.seq (partial) ..

```

1   CCCGGTGCCA AACAAGAAAA TCCCCTTTTT TCCTTAAAAA GGAGCGGCAT
51  GGATAAACAA CTGATTCCCG TTGCTGAATC CATAGATATT AAATATCCGG
101 GTTTTATCCA GCGCCTTAAC GCATTGGTTT TCCAATACGG TATCGATGAT
151 CTTGATGCGA GTGCTGAGAC TGTGTAGTTC AGCAGCTGTT CCAAAATAGC
201 AAAACCGGGT AAGAAAATAT CTACCTTGCA AGAAGCAAAG AGTGCATTAC
251 AGATTACTAA TGATGATAAA CAAAATGGAA ATATCACCCG TCAGAAACAT
301 GTGGTCAATG CCTATGCGGT CGGCAGGTTT GGCAATAATG AGGAAAGTTT
351 GTTCCGCTTC CAATTGGATG ATAAGGGCAA GTGGGGTAAT CCTCAGTTGC
401 TCGTGAAAAA GGTAAACGAT ATGGATGTGC GGTATATTTA TGTTTCCGGT
451 TGTCCTGAAG ATGAAGATGC CGGCAAAGAG GAAAAATTC AATATACGAA
501 TAAATTCGAC AAATCCAAAA ATGCTGTTCG GCCTGCCGGG GTGGAGGTTT
551 TATTGGATAG CGGCCTTAAT GCCAAGATTG CCGCTTCTTC AGACAATAGT
601 ATTTATGCTT ACCGTATCAA TGCGACAATA CGCGGGGGAA ATGTATGCGC
651 AAACAGAACA CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 954; ORF 247-1.ng>:

g247-1.pep (partial) ..

```

1   PGAKQENPLF SLKRSMDKQ LIPVAESIDI KYPGFIQRLN ALVFQYGIDD
51  LDASAEVTVV SCSKIAKPG KKISTLQEAQ SALQITNDDK QNGNITRQKH
101 VVNAYAVGRF GNNEESLFRF QLDDKGKWN PQLLVKKVKR MDVRYIYVSG
151 CPEDEDAGKE EKFRYTNKFD KSKNAVTPAG VEVLLDSGLN AKIAASSDMS
201 IYAYRINATI RGGNVCANRT L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 955>:

m247-1.seq

```

1   ATGAGACGTA AAATGCTAAA CGTACCAAAA GGCAGTTATG ATGGTATGAA
51  AGGTTTACC ATTATTGAAT TTTTGGTTGC GGGCCTGCTC AGTATGATTG
101 TCCTGATGGC GGTCCGATCG AGTTACTTCA CATCCCGGAA ATTAAATGAT
151 CGCGCAAACG AGCGTCTTGC CGCGCAACAG GATTTGCGGA ATGCGGCAAC
201 ATTGATTGTC CGCGATGCGA GAATGGCAGG CGGCTTCGGT TGTTTCAATA
251 TGTCGAGACA TCCTGCAACT GATGTTATTC CCGATACGAC GCAACAAAAT
301 TCTCCTTTTT CCTTAAAAAG GAACGGTATA GATAAATTTA TTCCCATAGC
351 GGAATCTTCA AATATCAATT ATCAGAATTT TTTCCAGGTT GGTAGCGCAT
401 TGATTTTTCA ATACGGAATC GATGATGTTA ATGCAAGCAC CGCGACTACC
451 GTCGTCAGCA GCTGTGCCGC AATATCGAAA CCGGGCAAGC AAATCCCTAC
501 TTTAGAAGAT GCAAAAAAAG AATTGAAGAT TCCGGATCAG GATAAGGAGC
551 AAAATGGCAA TATAGCGCGT CAAAGGCATG TGGTCAATGC CTATGCGGTC
601 GGCAGGATTG CCGATGAGGA AGGTTTGTTC CGCTTCCAAT TGGATGATAA
651 GGGCAAGTGG GGTAATCCTC AGTTGCTCGT GAAAAAGGTT AGACATATGA
701 AAGTGCGGTA TATCTATGTT TCCGGCTGTC CTGAAGATGA CGATGCCGGC
751 AAAGAGGAAA CATTCAAATA TACGGATAAA TTCGACAGCG CCCAAAATGC
801 TGTTACGCCC GCCGGGTGG AGGTTTATT GAGTAGCGGT ACTGATACCA
851 AGATTGCCGC TTCTTCAGAC AATCATATTT ATGCTTACCG TATCGATGCG
901 ACAATACGCG GGGGAAATGT ATGCGCAAAC AGAACACTTT GA

```

This corresponds to the amino acid sequence <SEQ ID 956; ORF 247-1>:

m247-1.pep

```

1   MRRKMLNVPK GSYDGMKGFT IIEFLVAGLL SMIVLMAVGS SYFTSRKLND
51  AANERLAAQQ DLRNAATLIV RDARMAGGFG CFNMSEHPAT DVIPDTTQQN
101 SPFSLKRNGI DKLPIAESS NINYQNFFQV GSALIFQYGI DDVNASATTT
151 VVSSCAAISK PGKQIPTLED AKKELKIPDQ DKEQNGNIAR QRHVVNAYAV
201 GRIADEEGLF RFQLDDKGKW GNPQLLVKKV RHMKVRYIYV SGCPEDDDAG
251 KEETFKYTDK FDSAQNAVTP AGVEVLLSSG TDTKIAASSD NHIYAYRIDA
301 TIRGGNVCAN RTL*

```

569

m247-1 / g247-1 72.1% identity in 222 aa overlap

```

      70      80      90      100      110      120
m247-1.pep  NAATLIVRDARMAGGFGCFNMSEHPATDVIPDTTQONSPFSLKRNGIDK-LIPIAESSNI
              | : | : | | | | : | | | | | : |
g247-1      PGAKQENPLFSLKRSMDKQLIPVAESIDI
              10      20      30

      130      140      150      160      170      180
m247-1.pep  NYQNFFQVGSALIFQYGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDK
              : | : | : | : | | | | : | : | : | : | : | : | : |
g247-1      KYPGFIQRLNALVFQYGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK
              40      50      60      70      80      90

      190      200      210      220      230      240
m247-1.pep  EQNGNIARQRHVVNAYAVGRIAD-EEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVS
              | | | | : | | | | | | | | | | | | | | | | | | | | |
g247-1      -QNGNITRQKHVVNAYAVGRFGNNEESLFRFQLDDKGKGNPQLLVKKVRMDVRYIYVS
              100      110      120      130      140

      250      260      270      280      290      300
m247-1.pep  GCPEDDDAGKEETFKYTDKFDQAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDAT
              | | | | : | | | : | | | | | | | | : | | | | | | | |
g247-1      GCPEDDAGKEEFKRYTNKFDKSKNAVTPAGVEVLLDSGLNAKIAASSDNSIYAYRINAT
              150      160      170      180      190      200

      310
m247-1.pep  IRGGNVCANRTLX
              | | | | | | | |
g247-1      IRGGNVCANRTLX
              210      220

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 957>:

a247-1.seq (partial)

```

1  AATAATACAG CTAAATTGAT TCCTATTGCT GAATCCACAG ATATTAAATA
51  TCCGGGTTTT GCCCAGGCTC GTCCGGCATT GATTTTCCAA TACGGCATCG
101 ATGATCTTGA TGCGAGTGCT GAGACTGTTG TAGTCAGCAG CTGTTCCAAA
151 ATAGCAAAAC CGGGTAAGAA AATATCTACC TTGCAAGAAG CAAAGAGTGC
201 ATTACAGATT ACTAATGATG ATAAACAAAA TGGAAATATC ACCCGTCAAA
251 GGCAATGTGGT CAATGCCTAT GCGGTCGGCA GGATTGCCGG TGAGGAAGGT
301 TTGTTCCGCT TCCAATTGGA TGATAAGGGC AAGTGGGGTA ATCCTCAGTT
351 GCTCGTGAAG AAGATTAGAC ATATGAAAGT GCGGTATATC TATGTTCCG
401 ACTGTCCCTGA AGATGACGAT GCCGGCAAAG AGGAAAAATT CAAATATACG
451 GGTACATTCG ACAGCTCCAC AAATGCTGTT ACGCCGCCCG GGGTGGAGGT
501 TTTATTGAGT AGCGGTACTG ATACCAAGAT TGCCGCTTCT TCAGACAATC
551 ATATTATGTC TTACCGTATC GATGCGACAA TACGCGGGGG AAATGTATGC
601 GCAAACAGAA CACTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 958; ORF 247-1.a>:

a247-1.pep (partial)...

```

1  NNTAKLIPIA ESTDIKYPGF AQARPALIFQ YGIDDLASA ETVVVSSCSK
51  IAKPGKKIST LQEAKSALQI TNDDKQNGNI TRQRHVVNAY AVGRIAGEEG
101 LFRFQLDDKG KWGNPQLLVK KIRHMKVRYI YVSDCPEDDD AGKEEFKYT
151 GTFDSSTNAV TPAGVEVLLS SGTDTKIAAS SDNHIYAYRI DATIRGGNVC
201 ANRTL*

```

m247-1 / a247-1 80.6% identity in 206 aa overlap

```

      10      20      30
a247-1.pep  NNTAKLIPIAESTDIKYPGFAQARPALIFQ
              | : | | | | | | : | : | : |
m247-1      GFGCFNMSEHPATDVIPDTTQONSPFSLKRNGIDKLIPIAESSNINYNQNFFQVGSALIFQ
              80      90      100      110      120      130

      40      50      60      70      80      89
a247-1.pep  YGIDDLASAETVVVSSCSKIAKPGKKISTLQEAKSALQITNDDK-QNGNITRQRHVVN
              | | | | : | : | : | : | : | : | : | : | : | : |
m247-1      YGIDDVNASTATTVVSSCAAISKPGKQIPTLEDAKKELKIPDQDKEQNGNIARQRHVVN
              140      150      160      170      180      190

      90      100      110      120      130      140      149
a247-1.pep  YAVGRIAGEEGLFRFQLDDKGKGNPQLLVKKIRHMKVRYIYVSDCPEDDDAGKEEFKY
              | | | | | | | | | | | | | | : | | | | | | | | | |

```

570

```

m247-1      YAVGRIADEEGLFRFQLDDKGKGNPQLLVKKVRHMKVRYIYVSGCPEDDDAGKEETFKY
            200      210      220      230      240      250

a247-1.pep  150      160      170      180      190      200
            TGTFDSSSTNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            |   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
m247-1      TDKFDSAQNAVTPAGVEVLLSSGTDTKIAASSDNHIYAYRIDATIRGGNVCANRTLX
            260      270      280      290      300      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 959>:

```

g248.seq
1   atgcgcaaac agaacacttt gacaggaatc ccgacttctg acggacagag
51  ggggtccgca ctgtttatcg tgctgatggt gatgatagtc gtggcctttt
101 tggttgtaac tgccgcccag tcctacaata ccgaacagag gatcagtgcc
151 aacgaatcag acaggaaatt ggctttgtct ttagccgagg cggctttgcg
201 ggagggcgaa ttccaggttt tggatttggg atatgctgag gacagtaagg
251 ttacgtttag cgaaaactgt gaaaaagggtc tgtgtaccgc agtgaatgtg
301 cggacaaata ataatggtag tgaagagggt tttggcaata tcgtggtgca
351 aggcaagccc gccgttgagg cggtgaaacg ttcttgccct gcaaatgctg
401 gcaaaaattc taccgacctg tgcattgaca ataaagggat ggaatataat
451 aaaggcgagg caggcgctcag caaatgccg cgctatatta tcgaatattt
501 aggcgtgaag aacggacaaa atgtttatcg gggtactgcc aaggcttggg
551 gtaagaatgc caataccgtg gtcgtccttc aatcttatgt aggcataaat
601 gatgagcaat aa

```

This corresponds to the amino acid sequence <SEQ ID 960; ORF 248.ng>:

```

g248.pep
1   MRKQNTLTGI PTSDGQRGSA LFIVLMVMIV VAFLLVTTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE FQVLDLEYAA DSKVTFSENC EKGLCTAVNV
101 RTNNNGSEEA FGNIVVQKPK AVEAVKRSCP AKSGKNSTD L CIDNKGMEYN
151 KGAAGVSKMP RYIEYLG VK NGQNVYRVTA KAWGKNANTV VVLQSYVGNN
201 DEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 961>:

```

m248.seq (partial)
1   ..GGGTTTGCAC TGTTAATCGT GCTGATGGTG ATrATCGTCG TGGCT.Tywt
51  gGwTGTAAct GCCGCGCAGT CTTACAATAC cGAGCAGCGk ATCAGTkCCA
101 ACGAATCAGA CAGGAAATTG GCTwTGCTT TGGCCGAGkC GkCTwTGCGG
151 GAAGGCGAAC TTCAGGTTTT GGATTTGGAA TATGATACGG ACAGTAAGGT
201 TACATTTAGC GAAAACTGTG GAAAAGGTCT GTsTGCCGCA GTGAATGTGC
251 GGACAAATAA TGATAATGAA GAGGCTTTTG ACAATATCGT GGTGCAAGGC
301 AAGCCCACCG TTGAGGCGGT GAAGCGTTCT TGCCCTGCAA ATTCTACCGA
351 CCTGTGCATT GACAAGAAAG GGwTGGAATA TAAGAAAGGC ACGAGAAGCG
401 TCAC.AAAAT GCCACGTTAT ATTATCGAAT ATTTGGGCGT GwAGAACGGA
451 GAAATGTTT ATCGGGTTAC TGCCAAGGCT TGGGGAAGA ATGCCAATAC
501 CGTGGTCGTC CTTCAATCTT ATGTAAGCAA TAATGATGAG TAA

```

This corresponds to the amino acid sequence <SEQ ID 962; ORF 248>:

```

m248.pep (partial)
1   ..GFALLIVLMV XIVVAFXXVT AAQSYNTEQR ISXNESDRKL AXSLAEXXXXR
51  EGELQVLDLE YTDTSKVTF S ENCGKGLXAA VNVRTNNDNE EAFDNIVVQG
101 KPTVEAVKRS CPANSTDLCI DKKGXKEYKKG TRSVTKMPRY IIEYLGXVNG
151 ENVYRVTA KA WGKNANTVVV LQSYVSNND E *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 248 shows 81.1% identity over a 185 aa overlap with a predicted ORF (ORF 248.ng) from *N. gonorrhoeae*:

m248/g248

```

m248.pep      10      20      30      40
              GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
              | | | | | | | | | | | | | | | | | | | | | | | |

```

571

```

g248      MRKQNTLTGIPTSDGQRGSAFLVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNND-NEEAFDNIVVQGKP
           |||  ||||:||||| :||||||| ||| :||||||| : |||| |||||
g248      LAEAAALREGEFQVLDLEYAADSKVTFSENCEKGLCTAVNVRTNNNGSEEAFGNIVVQGKP
           70      80      90      100      110      120

           110      120      130      140      150
m248.pep  TVEAVKRSCPA----NSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVTXNGENVYRVTA
           :||||||| |||||:| |||: |||: |||: |||: |||: |||: |||: |||
g248      AVEAVKRSCPAKSGKNSTDLCIDNKGMEYKNGAAGVSKMPRYII EYLGVTXNGQNVYRVTA
           130      140      150      160      170      180

           160      170      180
m248.pep  KAWGKNANTVVVLQSYVSNNDEX
           ||||| ||||| ||||| :|||
g248      KAWGKNANTVVVLQSYVGNNDQX
           190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 963>:

```

a248.seq
1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTTT
101 TGGTTGTAACT TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAAGGTC TGTGTACCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGCAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCACTGCA AAATCTACAG
401 GCCTGTGCAT TGACAATAAA GGGATGGAAT ATAAGAAAGG CACGCAAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 964; ORF 248.a>:

```

a248.pep
1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFVLTAAQ SYNTEQRISA
51  NESDRKLALS LAEAAALREGE LQVLDLEYDT DSKVTFSENC GKGLCTAVNV
101 RTNNDNEEAF DNIVVQGKPT VEAVKRSCTA KSTGLCIDNK GMEYKKGTS
151 VSKMPRYIIE YLGVTXNGENV YRVTAKAWGK NANTVVVLQS YVSNNDE*

```

m248/a248 89.4% identity in 180 aa overlap

```

           10      20      30      40
m248.pep  GFALLIVLMVXIVVAFXXVTAAQSYNTEQRISXNESDRKLAXS
           |||:||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFVLTAAQSYNTEQRISANESDRKLALS
           10      20      30      40      50      60

           50      60      70      80      90      100
m248.pep  LAEXXXREGELQVLDLEYDTSKVTFSENCGLXAAVNVRTNNDNEEAFDNIVVQGKPT
           |||  ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a248      LAEAAALREGEFQVLDLEYDTSKVTFSENCGLCTAVNVRTNNDNEEAFDNIVVQGKPT
           70      80      90      100      110      120

           110      120      130      140      150      160
m248.pep  VEAVKRSCPANSTDLCIDKKGXEYKKGTRSVTKMPRYII EYLGVTXNGENVYRVTAKAWGK
           ||||| |||: |||||: |||||: |||||: |||||: |||||: |||||: |||||
a248      VEAVKRSCTAKSTGLCIDNKGMEYKKGTSVSKMPRYII EYLGVTXNGENVYRVTAKAWGK
           130      140      150      160      170      180

           170      180
m248.pep  NANTVVVLQSYVSNNDEX

```

572

|||||
a248 NANTVVVLQSYVSNNDEX
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 965>:

m248-1.seq

```

1  ATGCGCAAAC AGAACACTTT GACGGGAATC CCGACTTCTG ACGGACAGAG
51  GGGGTTTGCA CTGTTTATCG TGCTGATGGT GATGATCGTC GTGGCTTTT
101 TGGTTGTAAC TGCCGCGCAG TCTTACAATA CCGAGCAGCG GATCAGTGCC
151 AACGAATCAG ACAGGAAATT GGCTTTGTCT TTGGCCGAGG CGGCTTTGCG
201 GGAAGGCGAA CTTCAGGTTT TGGATTGGA ATATGATACG GACAGTAAGG
251 TTACATTTAG CGAAACTGT GGAAAGGTC TGTGTGCCGC AGTGAATGTG
301 CGGACAAATA ATGATAATGA AGAGGCTTTT GACAATATCG TGGTGAAGG
351 CAAGCCCACC GTTGAGGCGG TGAAGCGTTC TTGCCCTGCA AATTCTACCG
401 ACCTGTGCAT TGACAAGAAA GGGATGGAAT ATAAGAAAGG CACGAGAAGC
451 GTCAGCAAAA TGCCACGTTA TATTATCGAA TATTGGGCG TGAAGAACGG
501 AGAAATGTT TATCGGGTTA CTGCCAAGGC TTGGGGTAAG AATGCCAATA
551 CCGTGGTCGT CCTTCAATCT TATGTAAGCA ATAATGATGA GTAA

```

This corresponds to the amino acid sequence <SEQ ID 966; ORF 248-1>:

m248-1.pep

```

1  MRKQNTLTGI PTSDGQRGFA LFIVLMVMIV VAFLVVTAAQ SYNTEQRISA
51  NESDRKLALS LAEALREGE LQVLDLEYDT DSKVTFSENC GKGLCAAVNV
101 RTNNDNEEAF DNIVVQKPT VEAVKRSCPA NSTDLCKDKK GMEYKKGTRS
151 VSKMPRYIIE YLGVKNGENV YRVTAKEWGK NANTVVVLQS YVSNNDE*

```

m248-1/g248 89.1% identity in 202 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
g248	MRKQNTLTGIPTSDGQRGSAFLFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	119
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNND-NEEAFDNIVVQKGP					
g248	LAEALREGE FQVLDLEYAADS KVTFSENC EKGLCTAVNVRTNNGSEEA FGNIVVQKGP					
	70	80	90	100	110	120
	120	130	140	150	160	170
m248-1.pep	TVEAVKRSCPA-----NSTDLCKDKK GMEYKKGTRSVSKMPRYIIEYLVKNGENVYRVTA					
g248	AVEAVKRSCPAKSGKNSTDLCIDNKGMEYNKGAAGVSKMPRYIIEYLVKNGQNVYRVTA					
	130	140	150	160	170	180
	180	190				
m248-1.pep	KAWGKNANTVVVLQSYVSNNDEX					
g248	KAWGKNANTVVVLQSYVGNNDQX					
	190	200				

m248-1/a248 97.0% identity in 197 aa overlap

	10	20	30	40	50	60
m248-1.pep	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
a248	MRKQNTLTGIPTSDGQRGFALFIVLMVMIVVAFLVVTAAQSYNTEQRISANESDRKLALS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m248-1.pep	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCAAVNVRTNNDNEEAFDNIVVQKGP					
a248	LAEALREGE LQVLDLEYDTDSKVTFSENC GKGLCTAVNVRTNNDNEEAFDNIVVQKGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m248-1.pep	VEAVKRSCPANSTDLCIDKKGMEYKKGTRSVSKMPRYIIEYLVKNGENVYRVTAKEWGK					
a248	VEAVKRSC TAKSTGLCIDNKGMEYKKGTSVSKMPRYIIEYLVKNGENVYRVTAKEWGK					
	130	140	150	160	170	180

```

                190
m248-1.pep  NANTVVVLQSYVSNINDEX
            | | | | | | | | | | | | | | | | | |
a248        NANTVVVLQSYVSNINDEX
                190

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 967>:

```

g249.seq
  1  atgaagaata atgattgctt gcgcctgaaa aatccccagt ccggtatggc
 51  gttgatagaa gtcttggtcg ctatgctcgt tctgaccatc ggtatatttg
101  cattgctgtc cgtacagttg cggacagtcg cttccgtcag ggaggcggaa
151  acgcaaacca tcgtcagcca aatcacgcaa aacctgatgg aaggaatggt
201  gatgaatccg accattgatt tggacagcaa caagaaaaac tatagtcttt
251  acatgggaaa acagacacta tcagctgtgg atgggtgagt tatgcttgat
301  gccgagaaaa gtaaggcgca gttggcagag gaacaattga agagatttag
351  tcatgagctg aaaaatgcct tgccggatgc ggtagctatt cattacgccg
401  tctgcaagga ttcgtcgggt gacgcgccga cattgtccga cagcgggtgt
451  ttttcttcaa attgcgacaa taaggcaaac ggggatactt tgattaaagt
501  attgtgggta aatgattcgg caggggattc ggatatttcc cgtacgaatc
551  ttgaagtgag cggcgacaat atcgtatata cctatcaggc aagggtcgga
601  ggtcgtgaat ga

```

This corresponds to the amino acid sequence <SEQ ID 968; ORF 249.ng>:

```

g249.pep
  1  MKNNDCLRKL NPQSGMALIE VLVAMLVLT I GILALLSVQL RTVASVREAE
 51  TQTIVSQITQ NLMEGMLMNP TIDLSDNKK YSLYMGKQTL SAVDGEFM LD
101  AEKSKAQLAE EQLKRFSHEL KNALPDAVAI HYAVCKDSSG DAPTLSDSGA
151  FSSNCDNKAN GDTLIKVLWV NDSAGDS DIS RTNLEVSGDN IVYTYQARVG
201  GRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 969>:

```

m249.seq
  1  ATGAAGAATA ATGATTGCTT CCGCCTGAAA GATTCCCAGT CCGGTATGGC
 51  GCTGATAGAA GTCTTGGTTG CTATGCTCGT TCTGACCATC GGTATTTTGG
101  CACTATTGTC TGTACAGTTG CGGACAGTCN NNNNNNNNNN NNNNNNNNNN
151  NNNNNNNNNN NNNNNNNNNN NNNNNNNNNN NNNTTGATGG AGGGAATGTT
201  GATGAATCCG ACCATTGATT CGGACAGCAA CAAGAAAAAC TATAATCTTT
251  ACATGGGAAA CCATACACTA TCAGCTGTGG ATGGCGATTT TGCGATTGAT
301  GCCATGAAAA CTAAGGGGCA ATTGGCAGAG GCACAATTGA AGAGATTTAG
351  TTATGAGCTG AAAAATGCCT TGCCGGATGC GGCAGCCATC CATTACGCCG
401  TCTGCAAGGA TTCGTCGGGT AACGCGCCGA CATTGTCCGG CAATGCTTTT
451  TCTTCAAATT GCGACAATAA GGCAAACGGG GATACTTTAA TTAAAGTATT
501  GTGGGTAAAT GATTCGGCAG GGGATTCGGA TATTCCCCTG ACGAATCTTG
551  AGGTGAGCGG CGACAATATC GTATATACTT ATCAGGCAAG GGTCGGAGGT
601  CGGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 970; ORF 249>:

```

m249.pep
  1  MKNNDCFRLK DSQSGMALIE VLVAMLVLT I GILALLSVQL RTVXXXXXXXX
 51  XXXXXXXXXXX XLMEGMLMNP TIDSDSNKK YNLYMGNHTL SAVDGDFAID
101  AMKTGQLAE AQLKRFSYEL KNALPDAAAI HYAVCKDSSG NAPTLSGNAF
151  SSNCDNKANG DTLIKVLWVN DSAGDS DISR TNLEVSGDNI VYTYQARVGG
201  RE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 249 shows 81.3% identity over a 203 aa overlap with a predicted ORF (ORF 249.ng) from *N. gonorrhoeae*:

m249/g249

```

                10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
            | | | | | : | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

574

```

g249      MKNNDCLRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     120
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYEL
           |||||:|||||:|||||:|||||:|:| |:| |||||:|
g249      NLMEGMLMNPTIDSDSNKKNYSLYMGKQ-TLSAVDGEFMLDAEKSQAQLAEELKRFSHEL
           70      80      90      100     110     120

           130     140     150     160     170     179
m249.pep  KNALPDAAAIHYAVCKDSSGNAPTLSGN-AFSSNCDNKANGDTLIKVLWVND-SAGDS-
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g249      KNALPDAAAIHYAVCKDSSGDAPTLSDSGAFSSNCDNKANGDTLIKVLWVND-SAGDS-
           130     140     150     160     170     180

           180     190     200
m249.pep  RTNLEVSGDNIVYTYQARVGGREX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g249      RTNLEVSGDNIVYTYQARVGGREX
           190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 971>:

```

a249.seq
1   ATGAAGAATA ATGATTGCTT CCGCCTGAAA AACCCCCAGT CCGGTATGGC
51  GCTGATAGAA GTCTTGCTCG CTATGCTCGT TCTGACCATC GGTATTTTGG
101 CACTATTGTC TGTTCACTTG CCGACAGTCG CTTCCGTCAG GGAGGCAGAG
151 ACGCAAACCA TCGTCAGTCA AATCACGCAA AACCTGATGG AAGGAATGTT
201 GATGAATCCG ACCATTGATT CCGACAGCAA CAAGAAAAAC TATAATCTTT
251 ACATGGGAAA CCATCATGCA CTATCAGTTG TGGATGGCGA TTTTCAGGTT
301 GATGCCATAA AAACATAAGAC GCAGTTGGCA GAGGCACAAAT TGAAGAGATT
351 TAGTTATGAG CTGAAAAATG CCTTGCCGGA TCGCGCAGCC ATCCATTACG
401 CCGTCTGCAA GGATTGCTCG GGTGTTGCGC CGACATTGTC CGCCGGCAGT
451 ACTTTTCTT CAAATTGCGA TGGTAGTGCA AATGGGGATA CTTTGATTAA
501 AGTATTGTGG GTAAATGATT CGGCAGGGGA TTCGGATATC GCCCGTACGA
551 ATCTTGAGAC GAACGGCAAC AATATCGTAT ATACCTATCA GGCAAGGGTC
601 GGAGGTCGGG AATGA

```

This corresponds to the amino acid sequence <SEQ ID 972; ORF 249.a>:

```

a249.pep
1   MKNNDCFRLK NPQSGMALIE VLVAMLVLTIGILALLSVQL RTVASVREAE
51  TQTIVSQITQ NLMEGMLMNP TIDSDSNKKN YNLYMGNHHA LSVVDGDFQV
101 DAIKTKTQLA EAQLKRFSYE LKNALPDAAA IHYAVCKDSS GVAPTLSAGS
151 TFSSNCDGSA NGDTLIKVLW VND-SAGDS- DI ARTNLETNGN NIVYTYQARV
201 GGRE*

```

m249/a249 81.9% identity in 204 aa overlap

```

           10      20      30      40      50      60
m249.pep  MKNNDCFRLKDSQSGMALIEVLVAMLVLTIGILALLSVQLRTVXXXXXXXXXXXXXXXXXXXX
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a249      MKNNDCFRLKNPQSGMALIEVLVAMLVLTIGILALLSVQLRTVASVREAETQTIVSQITQ
           10      20      30      40      50      60

           70      80      90      100     110     119
m249.pep  XLMEGMLMNPTIDSDSNKKNYNLYMGNH-TLSAVDGDFAIDAMKTGQLAEALKRFSYE
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a249      NLMEGMLMNPTIDSDSNKKNYNLYMGNH-HALSVVDGDFQVDAIKTKTQLAEALKRFSYE
           70      80      90      100     110     120

           120     130     140     150     160     170
m249.pep  LKNALPDAAAIHYAVCKDSSGNAPTLS-GNAFSSNCDNKANGDTLIKVLWVND-SAGDS-
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a249      LKNALPDAAAIHYAVCKDSSGVAPTLSAGSTFSSNCDGSANGDTLIKVLWVND-SAGDS-
           130     140     150     160     170     180

```


576

D + M G A + T L +A +L ++ ++KN LP A
 Sbjct: 72 LYDVKDQ-----MATQSDFFKAKGSAFPTAPSSCTPLPDAIKDRLGCWAEQVKNELPGAG 126
 Query: 130 AI---HYAVCKDSSGVAPTLSAGSTFSSNCDGSAANGDTL-IKVLWVNDSSAGDSDIARTNL 185
 + Y +C+ S +CDG G L I++ W + A ++
 Sbjct: 127 DLLKSDYYICRSSK-----PGDCDG--KGSMLERLAWRGKQGACVNAADSSA 172
 Query: 186 ETN 188
 +T+
 Sbjct: 173 DTS 175

m249-1/a249 90.7% identity in 204 aa overlap

	10	20	30	40	50	60
m249-1.pep	MKNND	CFRLK	DSSQSG	MALIE	VLVAM	LVLTIG
a249	MKNND	CFRLK	NPQSG	MALIE	VLVAM	LVLTIG
	70	80	90	100	110	119
m249-1.pep	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
a249	NLM	EGMLM	NPTID	SDSNK	KNYNL	YMGNH-
	70	80	90	100	110	120
	120	130	140	150	160	170
m249-1.pep	LKN	ALPD	AAAIH	YAVCK	DSSGN	APTLS-
a249	LKN	ALPD	AAAIH	YAVCK	DSSGV	APTLS-
	130	140	150	160	170	180
	180	190	200			
m249-1.pep	SRT	NLEV	SGDN	IVYTY	QARV	GGREX
a249	ART	NLET	NGNN	IVYTY	QARV	GGREX
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 975>:

g250.seq

```

1 atgacgcaca cagcctctcc acgtgatgaa ttcatacgcg gcataaaaga
51 aagttcgccc atgctgattg ggcttttgcc ttgggcattg atactcggtg
101 tgcagggcgg gcaaaaaggt atgggcccgc tggaaatgct gctgatgacg
151 gggatgaact ttgccggcgg ctccgaattt gccacggtca acctgtgggc
201 ggaacctctg ccgatactgc ttatcgccac cataaccttt atgattaatt
251 cgcgggcatat cctgatgggg ggcggcgctt gccacgcaca tgaaagaaat
301 accgctgaaa aaagccgcgc ccgcgctgtt ttttatgtgt ga
  
```

This corresponds to the amino acid sequence <SEQ ID 976; ORF 250.ng>:

g250.pep

```

1 MHTASPRDE FIRGIKESSP MLIGLLPWAL ILGMQGGQKG MGRLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATITF MINSRHILMG GGACHAHERN
101 TAEKSRARAV FYV*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 977>:

m250.seq

```

1 ATGCACACCT TCCCCGCATA ACGAATTTAT ACGCGGCATC AAAGAAAGTT
51 CGCCTATGCT GATTGGGCTG CTGCCTTGGG CATTAATACT CGGTATGCAG
101 GGCGGACAAA AAGGCATGAG CTGGCTGGAA ATGTTGTTGA TGACCAGTAT
151 GAACTTCGCC GCGGCTCCG AGTTTGCCAC GGTCAACCTG TGGGCSGAAC
201 CTCTGCCGAT ACTGCTTATC GCCACCGTAA CCTTTATGAT TAATTCTCGG
251 CATATCCTGA T.GGGGGCGG CGCTTGCCCC GCACCTGAAA GGAaTACCGC
301 TGAAAAAAGC CGTGCCCGCA CTGTTTTTTA TGTGTGA
  
```

This corresponds to the amino acid sequence <SEQ ID 978; ORF 250>:

m250.pep

```

1 MHTPSPHNEF IRGIKESSPM LIGLLPWALI LGMQGGQKGM SWLEMLLMTS
51 MNFAGGSEFA TVNLWAEPLP ILLIATVTFM INSRHILMGG GACPAPERNT
101 AEKSRARTVF YV*
  
```

ORF 250 shows 91.0% identity over a 111 aa overlap with a predicted ORF (ORF 250.ng) from *N. gonorrhoeae*:

```

      10      20      30      40      50      59
m250.pep  MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGQKGMSWLEMLLMTSMNFAGGSEF
      |||::|||
g250      MHTASPRDEFIRGIKESSPMLIGLLPWALILGMQGQKGMRLEMLLMTGMNFAGGSEF
      10      20      30      40      50      60

      60      70      80      90      100     110
m250.pep  ATVNLWAEPLPILLIATVTFMINSRHILMGGGACAPAPERNTAEKSRTAVFYVX
      |||
g250      ATVNLWAEPLPILLIATITFMINSRHILMGGGACHAHERNTAEKSRRARVFYV
      70      80      90      100     110

```

a250.seq

1	ATGACACACA	TAAGCTCGCC	CCGTAACGAA	TTTATACGCG	GCATCAAAGA
51	AAGTTCGCCC	ATGCTGATCG	GGCTTTTGCC	TTGGGCATTA	ATACTCGGTA
101	TGCAGGGTGG	ACAAAAAGGC	ATGAGCTGGC	TGGAAATGTT	GTTGATGACC
151	GGTATGAACT	TCGCCGCGCG	CTCCGAGTTT	GCCACGGTCA	ACCTGTGGGC
201	GGAACTCTCT	CCGATACTGC	TTATCGCCAC	CGTAACCTTT	ATGATTAATT
251	CTCGGCATAT	CCGTGATGGG	G. CGGCAC TT	GCCCCGCACC	TGAAAGAAAT
301	ACCGCTGAAA	AAAGCCGTGC	CCGCACTGTT	TTTTATGTGT	GA

a250 . pep

1 MTHISSPRNE FIRGIKESS MLIGLLPWAL ILGMOGGQKG MSWLEMLLMT
51 GMNFAGGSEF ATVNLWAEPL PILLIATVTF MINSRHILMG XGTCPAPER
101 TAEKSRARTV FYV*

```

59
m250.pep
MHTPSPHNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTSMNFAGGSEF
|
||:|||||||||||||||||||||||||||||||||:|||||||
a250
MTHISSPRNEFIRGIKESSPMLIGLLPWALILGMQGGQKGMWLEMLLMTGMNFAGGSEF
10 20 30 40 50

60
m250.pep
ATVNLWAEPLPILLIATVTFMINSRHILMGGGACPAAPERNTAEKSRARTVFYVX
|||||||||||||||||||||||||||||||||:|||||||||||||||||
a250
ATVNLWAEPLPILLIATVTFMINSRHILMGXGTCPAPERNTAEKSRARTVFYVX
70 80 90 100 110

```

g251.seq

seq					
1	atgcctgacc	caatagggat	tcttttcgct	gccgtcgggg	ttgatttttt
51	tgccgttggt	ttgagggggc	gttttcaacg	aataggcgcg	gttggcatgt
101	tqataataat	aatcctgatg	gcggaggtcg	gaaccaaaac	ggtcgtaacc

578

```

151 gaggttgacg ctcaggttgt ggcggatttt ggcggtatcg aaggattttt
201 tgaatgccgc ctgcaagagc ctgtggcttt ccccgtaa at cagcggtcg
251 gatttgtagt aggaagacgg cttgtcggca ctcgggcggc aatatttgc
301 cgaaccgtcg gcggaacagt gcgtctgctg aaaatgattg tccaaaccga
351 tgccctgccg gtcgtaagag aggcgggcat aatccgcca agtgtctta
401 tcggcattgg tatagacata ttccaaaccg tagcggcttt tgggtgtcgt
451 ctgctcgtaa aacacgcccg taccgtatcc cgcgcccacc tccgcaccgt
501 tttcaccgtt ggtaatcagc ccgctgtatt tgcggccgcc cgcgtatttg
551 ccgtagcctc ttatcgatcc gtatttttta ttttcatcaa aaaccgcctt
601 ggtagcgaat gccggaaccg tcatatcgcg cgtgtcgaaa gtttgcgtcg
651 tgcgttcgag tatgccgccg atgtagtgcc gtttgttttc aaaacgaaaa
701 cccgggcgga acagccacga ccggctttcg tatga

```

This corresponds to the amino acid sequence <SEQ ID 982; ORF 251.ng>:

g251.pep

```

1 MPDPGILFA AVGVDFFAVV LRGRFORIGA VGMLIIIIILM AEVGTKTVVT
51 EVDAQVVA DF GGIEGFFECR LQEPVAFPVN HAVGFVVGRR LVGTAAIFV
101 RTVGGTVRL KMI VQTDALP VVREAGIIRP SVFIGIGIDI FQTVAAFGVR
151 LVVKHARTVF RAHLRTVFTV GNQPAVFAAA RVFAVASYRS VFFIFIKNRL
201 GQECRNRHIA RVESLLRAFE YAADVVPFVF KTKTRAEQPR PAFV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 983>:

m251.seq

```

1 ATGCGTGCTG CGGTAGTCGT AGCGCAAGCC CGCGCCGACA TCCGCCCACC
51 TGCCCAAACG GACATTGTCC CGAACTGCCG CGTAATAGCT TTTACCGTTG
101 ATGCTGCGCG GCGTGCAGTC CGTATAAGTA TTGTTGCCCA AGCGGCAGAT
151 TTGCCCCGTA ACGACATTTT CCCTGCCTAT GGTGACCCAA TAGGGGCTGG
201 TTTCACTGCC GTTGGGGCTG ATTTTTTTCG CGTTGTTTTC AGGGGGCTGT
251 TTCGACGAAT AGGCGCGGTT GGCATGTTGA TAATAATAAT CCTGATGGCG
301 GAGATTAGAG CCAAAGCGGT CAAACCCGAG ATTCACGCTC AGGTTGTGGC
351 GGATTTTGGC GGTATCGAAG GATTTTTCGA ATGCCGCCTG CAAGAGCCTG
401 TGGCTTTCCC CGTAAATCAC GCGATCGGAT TTGTAATAGG AAAACGGCTT
451 GTCGGCACTC GGGCGGCAAT ATTTGTCCGA ACCGTCGGCA GAACAGTGCG
501 TCTGCTGAAA ATGATTATCC AAACCGATGC CCTGCCGCTC GTAAGAGAGG
551 CGGGCATAAT CCGCCCAAGT GTCTTTATCG GCATTGGTAT AGACATATTC
601 CAAACCGTAG CGGCTTTTGG TGTGCGTCTC GTCGTAAAC ACGCCCGTAC
651 CGTATTCGCG GCCACCGAGC GCACCGTTTT CGCCGTTGGT AAACAGTCCG
701 CCGTATTTGT GGTGCGCCGC GTATTTGCCG TTACCGGGCA AAGAACCCGC
751 CTGTTTTTTA TTTGCATCAA AAACCGCCTT GGTGAGGAAT GCCGGAACCG
801 TCATATCGCG CGTGTGCGAA GTTTGTTGCG TGTGTTGAG TATGCCGCCG
851 ATGTAGTGCC GCTTATTCTC AAAACGAAAA CCCGGGCGGA ACAGCCACGA
901 CCGGCTTTTC TATGA

```

This corresponds to the amino acid sequence <SEQ ID 984; ORF 251>:

m251.pep

```

1 MRAAVVQA RADIRPPAQT DIVPNCRVIA FTVDAARRAV RISIVAQAAD
51 LPRNDISPAY GDPIGAGFTA VGADFFAVVL RGRVRRIGAV GMLIIIIILMA
101 EIRAKAVKPE IHAQVVADFG GIEGFFECRL QEPVAFPVNH AIGFVIGKRL
151 VGTRAAIFVR TVGRTVRLK MIIQTDALPV VREAGIIRPS VFIGIGIDIF
201 QTVAAFGVRL VVKHARTVFR AHQRTVFAVG KQSAVFVVAR VFAVTGQRTR
251 LFFICIKNRL GQECRNRHIA RVESLLRVFE YAADVPLIL KTKTRAEQPR
301 PAFV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 251 shows 85.2% identity over a 243 aa overlap with a predicted ORF (ORF 251.ng) from *N. gonorrhoeae*:

m251/g251

```

          40          50          60          70          80          90
m251.pep   TVDAARRAVRISIVAQAADLPRNDISPAYGDPIGAGFTA VGADFFAVVL RGRVRRIGAVG
          ||| | :|||:||||| | :||| |
g251        MPDPGILFAAVGVDFFAVVLRGRFORIGAVG
          10          20          30

```


582

	190	200	210	220	230	240
m253 .pep	VIEGRNLNGNIADARAWSGLLVGSIACYGILPRLLAWVVKILLKTSENGLDLEKPYQAV					
	: : : :					
g253	VIEGRNLNGNIADARAWSGLLVGSIVCYGILPRLLAWVVKILLKTSENGLDLEKTYQAV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m253 .pep	IRRWQNKITDADTRRETVS AVSPKII LNDAPKWAVMLETEWQDGEWFEGRLAQEWLDKGV					
	: : : :					
g253	IRRWQNKITDADTRRETVS AVSPKIV LNDAPKWALMLETEWQDQGWFEGR LAQEWLDKGV					
	250	260	270	280	290	300
	310	320	330	340	350	360
m253 .pep	ATNREQVA ALET ELKQKPAQL LIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	: : : : :					
g253	AANREQVA ALET ELKQKPAQL LIGVRAQTV PDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
	370	380	390			
m253 .pep	SDDLSEKLEHWRNALAECGA AWLEPDRAAQEGRLKDQX					
	: :					
g253	SDDLSEKLEHWRNALTECGA AWLEPDRVAQEGRLKDQX					
	370	380	390			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 991>:

a253 .seq	1	ATGATCGACA	GGAACCGTAT	GCTGCGGGAG	ACGTTGGAAC	GTGTGCGTGC
	51	GGGGTCGTTT	TGGTTGTGGG	TGGCGGCGGC	GACGTTTGCG	TTTTTTACCG
	101	GTTTTTCAGT	TACTTATCTT	CTAATGGACA	ATCAGGGTCT	GAATTTCCTT
	151	TTGGTTTTGG	CGGCGGTGTT	GGGCATGAAT	ACGCTGATGC	TGGCAGTATG
	201	GTTGGCAATG	TTGTTCTCTG	GCGTGAAAGT	GGGGCGTTTT	TTCAGCAGTC
	251	CGGCGACGTG	GTTTCGGGGC	AAAGACCTTG	TCAATCAGGC	GGTGTTCGGG
	301	CTGTATGCGG	ACGAGTGGCG	GCAACCTTCG	GTACGTTGGA	AAATAGGCGC
	351	AACGTCGCAC	AGCCTGTGGC	TCTGCAGGCT	GCTCGGAATG	CTGGTGTCCG
	401	TATTGTTGCT	GCTTTTGGTG	CGGCAATATA	CGTTCAACTG	GGAAAGCACG
	451	CTGTTGGGCG	ATTCGTCTTC	GGTACGGCTG	GTGGAAATGT	TGGCATGGCT
	501	GCCTGCGAAA	CTGGGTTTTT	CCGTGCCTGA	TGCGCGGGCG	GTCATCGAAG
	551	GTCGTCTGAA	CGGCAATATT	GCCGATGCGC	GGGCTTGGTC	GGGGCTGCTG
	601	GTCGGCAGTA	TCGCTGCTA	CGGCATCCTG	CCGCGCTCT	TGGCTTGGGC
	651	GGTATGCAAA	ATCCTTTTGA	AAACAAGCGA	AAACGGCTTG	GATTTGGAAA
	701	AGCCCTATTA	TCAGGCGGTC	ATCCGCCGCT	GGCAGAACAA	AATCACCAGT
	751	CGGATACGC	GTCGGGAAAC	CGTGTCCGCC	GTTTCGCCGA	AAATCGTCTT
	801	GAACGATGCG	CCGAAATGGG	CGGTCATGCT	GGAGACCGAA	TGGCAGGACG
	851	GCGAATGGTT	CGAGGGCAGG	CTGGCGCAGG	AATGGCTGGA	TAAGGGCGTT
	901	GCCGCCAATC	GGGAACAGGT	TGCCGCGCTG	GAGACAGAGC	TGAAGCAGAA
	951	ACCGGCGCAA	CTGCTTATCG	GCGTGCGCGC	CCAACTGTG	CCCGACCGCG
	1001	GCGTGTTCG	GCAGATCGTC	CGACTTTCGG	AAGCGGCGCA	GGGCGGCGCG
	1051	GTGGTGCAGC	TTTGGGCGGA	ACAGGGGCTT	TCAGACGACC	TTTCGGAAAA
	1101	GCTGGAACAT	TGGCGTAACG	CGCTGACCGA	ATGCGGCGCG	GCGTGGCTGG
	1151	AACCCGACAG	AGCGGCGCAG	GAAGGCCGTC	TGAAAACCAA	CGACCGCACT
	1201	TGA				

This corresponds to the amino acid sequence <SEQ ID 992; ORF 253.a>:

a253 .pep	1	MIDRNRMLRE	TLERVAGSF	WLWVAAATFA	FFTGFSVTYL	LMDNQGLNFF
	51	LVLAVGLGMN	TLMLAVWLAM	LFLRVKVGRF	FSSPATWFRG	KDPVNQAVLR
	101	LYADEWRQPS	VRWKIGATSH	SLWLCTLLGM	LVSLLLLLLV	RQYTFNWEST
	151	LLGDSSSVRL	VEMLAWLPK	LGFPVPDARA	VIEGRNLNGNI	ADARAWSGLL
	201	VGSIACYGIL	PRLLAWAVCK	ILLKTSENGL	DLEKPYQAV	IRRWQNKITD
	251	ADTRRETVSA	VSPKIVLND	PKWAVMLETE	WQDGEWFEGR	LAQEWLDKGV
	301	AANREQVAAL	ETELKQKPAQ	LLIGVRAQTV	PDRGVLRQIV	RLSEAAQGGA
	351	VVQLLAEQGL	SDDLSEKLEH	WRNALTECGA	AWLEPDRAAQ	EGRLKTNDR
	401	*				

m253/a253 97.2% identity in 395 aa overlap

	10	20	30	40	50	60
m253.pep	MIDRNRMLRETLERVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVIGMN					
a253	MIDRNRMLRETLERVRAGSFWLWVVAATFAFFTGFSVTYLLMDNQGLNFFLVLAGVIGMN					
	10	20	30	40	50	60
m253.pep	TLMLAVWLAMLFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
a253	TLMLAVWLAMLFLRVKVGREFSSPATWFRGKDPVNQAVLRLYADEWRQPSVRWKIGATSH					
	70	80	90	100	110	120
m253.pep	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLSNAASVRAVEMLAWLP SKLGFPVPDARA					
a253	SLWLCTLLGMLVSVLLLLLVRQYTFNWESTLLGDSSSVRLVEMLAWLP AKLGFPVPDARA					
	130	140	150	160	170	180
m253.pep	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWV VCKILLKTS ENGLDLEKPYQAV					
a253	VIEGRNLNGNIADARAWSGLLVGSIA CYGILPRLLAWV VCKILLKTS ENGLDLEKPYQAV					
	190	200	210	220	230	240
m253.pep	IRRWQNKITDADTRRET VSAVSPKII LNDAPKWAV MLETEWQDGEWFEGR LAQE WLDKGV					
a253	IRRWQNKITDADTRRET VSAVSPKIV LNDAPKWAV MLETEWQDGEWFEGR LAQE WLDKGV					
	250	260	270	280	290	300
m253.pep	ATNREQVA ALET ELKQKPAQL LIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
a253	AANREQVA ALET ELKQKPAQL LIGVRAQTVPDRGVLRQIVRLSEAAQGGAVVQLLAEQGL					
	310	320	330	340	350	360
m253.pep	SDDLSEKLEHWRNALAECGAAWLEPDRAAQEGR LK DQX					
a253	SDDLSEKLEHWRNALTECGAAWLEPDRAAQEGR LK TNDRTX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 993>:

g254.seq

```

1  atgtatgcag gcgaacgctt caatacttac agccatttga gcggtttgat
51  tctggcggcg gcagggttga tgctgatgct gctgaaaacc ataggacacg
101 gggacggata ccgtatcttc agcgtatcgg ttacggcat cagccttctt
151 ctgctctatt tgagttcctc gctgtaccac ggaattgcag ccggaanaact
201 gaaaagcatt ttgaaaaaaa ccgaccactg catgatttat gtgctgattg
251 ccggaagcta cacaccgttt gcaactggtt ctttgagaaa cgggcccggc
301 tggacggtat ttccactgtc ctggctgctg gcggctgcag gaatcgaca
351 agaactcacc atcgacgga aaagcgaaaa acgtctgctg tctattgcga
401 tttatatcgt aatgggctgg atggtcttgg cggtaatgaa atccctgaca
451 gcctcactcc cgccggcagg actggcttgg ctggcggcag gcggtatgct
501 gtacagcgtc ggcatttact ggtttgtaaa cgatgaaaaa atccgacacg
551 ggcacggaat ctggcatctg ttcgtattgg gcggcagcat aacccaattt
601 gtcagcgtgt acggttatgt aatctga

```

This corresponds to the amino acid sequence <SEQ ID 994; ORF 254.ng>:

g254.pep

```

1  MYAGERFNTY SHLSGLILAA AGLMLMLLKT IGHGDGYRIF SVSVYGISLL

```

```

51  LLYLSSSLYH GIAAGKLKSI LKKTDHCMY VLIAGSYTPF ALVSLRNGPG
101 WTVFSLSWLL AAAGIAQELT IGRKSEKRLS SIAIYIVMGW MVLAVMKSLT
151 ASLPAGLAW LAAGGMLYSV GIYWFVNDEK IRHGHGIWHL FVLGGSITQF
201 VSVYGYVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 995>:

```

m254.seq (partial)
1  ..GTATCGGTTT ACGGCATCAG CCTTCTTCTG CTCTATTGTA GTTCCTGGCT
51  GTACCACGGA ATTGCAGCCG GAAAACTGAA AAGCATTGTTG AAAAAAACC
101 ACCACTGCAT GATTTATGTG CTGATTGCCG GAAGCTACAC ACCGTTTGCA
151 CTGGTTTCTT TGAGAAACGG GCCGGGCTGG ACGGTATTTT CACTGTCCTG
201 GCTGCTGGCG GCTGCAGGAA TCGCACAAGA ACTCACCATC GGACGGAAAA
251 GCGAAAAACG TCTGCTGTCT ATTGTGATTT ATGTCGTCAT GGGTTGGATG
301 GTCTTGGCGG TAATGAAATC CCTGACAGCC TCACTCCCGT CGGCAGGACT
351 GGCTTGGCTG GCGGCAGGCG GTATGCTGTA CAGTGTCCGC ATTTACTGGT
401 TTGTAAACGA TGAATAATC CGACACGGGC ACGGAATCTG GCATCTGTTT
451 GTATTGGGCG GCAGCATCAC CCAATTGTG AGCGTGTACG GTTACGTAAT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 996; ORF 254>:

```

m254.pep (partial)
1  ..VSVYGISLLL LYLSSWLYHG IAAGKLKSI LKKTDHCMYV LIAGSYTPFA
51  LVSLRNGPGW TVFSLSWLLA AAGIAQELTI GRKSEKRLS IYIYVVMGWM
101 VLAVMKSLTA SLPSAGLAWL AAGGMLYSVG IYWFVNDEKI RHGHGIWHLF
151 VLGGSITQFV SVYGYVI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 254 shows 97.6% identity over a 167 aa overlap with a predicted ORF (ORF 254.ng) from *N. gonorrhoeae*:

```

m254/g254

m254.pep                                10      20      30
                                VSVYGISLLL LYLSSWLYHGIAAGKLKSI
                                |||
g254      HLSGLILAAAGLMLMLLKTIGHG DGYRIFSVSVYGISLLL LYLSSSLYHGIAAGKLKSI
                                20      30      40      50      60      70

m254.pep                                40      50      60      70      80      90
                                KKTDHCMYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTI GRKSEKRLS
                                |||
g254      KKTDHCMYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTI GRKSEKRLS
                                80      90      100     110     120     130

m254.pep                                100     110     120     130     140     150
                                IVIYVVMGWMVLAVMKSLTASLPAGLAWLAAGGMLYSVG IYWFVNDEKIRHGHGIWHLF
                                |:|:|
g254      IAIYIVMGWMVLAVMKSLTASLPAGLAWLAAGGMLYSVG IYWFVNDEKIRHGHGIWHLF
                                140     150     160     170     180     190

m254.pep                                160
                                VLGGSITQFVSVYGYVIX
                                |||
g254      VLGGSITQFVSVYGYVIX
                                200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 997>:

```

a254.seq
1  ATGTATACAG GCGAACGCTT CAATACTTAC AGCCATTGTA GCGGTTTGTAT
51  TCTGGCGGCG GCAGGTTTGG CGCTGATGCT GCTGAAAACC ATAGGACACG
101 GGGACGGCTA CCGTATCTTC AGCGTATCGG TTTACGGCAT CAGCCTTCTT
151 CTGCTCTATT TGAGTTCCTC GCTGTACCAC GGAATTGCAG CCGGAAAAC
201 GAAAAGCATT TTGAAAAAAA CCGACCACTG CATGATTTAT GTGCTGATTG
251 CCGGAAGCTA CACACCGTTT GCACTGGTTT CTTTGAGAAA CGGGCCGGGG

```

301	TGGACGGTAT	TTTCACTGTC	CTGGCTGCTG	GCGGCTGCAG	GAATCGCACA
351	AGAACTCACC	ATTGGACGGA	AAAGCGAAAA	ACGACTGCTG	TCTATTGCGA
401	TTTATATCGT	AATGGGCTGG	ATGGTCTTGG	CGGTAATGAA	ATCCCTGACA
451	GCCTCACTCC	CGCCGGCAGG	ACTGGCTTGG	CTGGCGGCAG	GCGGTATGCT
501	GTACAGCGTC	GGCATTTACT	GGTTTGTAAA	CGATGAAAAA	ATCCGACACG
551	GGCAGCGAAT	CTGGCATCTG	TTCGTATTGG	GCGGCAGCAT	CACCCAATTT
601	GTCAGCGTGT	ACGGTTACGT	AATCTGA		

a254 . pep

1	MYTGERFNTY	SHLSGLILAA	AGLALMLLKT	IGHGDGYRIF	SVSVYGISLL
51	LLYLSSSLYH	GIAAGKLKSI	LKKTDHCMYI	VLIAGSYTPE	ALVSLRNGPG
101	WTVFSLSWLL	AAAGIAQELT	IGRKSEKRLL	SIATYIVMGW	MVLAVMKSLT
151	ASLPPAGLAW	LAAGGMLYSV	GIYWFVNDEK	IRHGHWIWHL	FVLGGSITQF
201	VSVYGYVI*				

```

30                                     10                                20
m254.pep
VSVYGISLLLLLYLSSWLYHGIAAGKLKSIL
|||||
a254
HLSGLILAAAGLALMLLKTIGHGDGYRIFSVSVYGISLLLLLYLSSSLYHGIAAGKLKSIL
20          30          40          50                                60
70
40          50          60          70                                80
90
m254.pep
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
|||||
a254
KKTDHCMIIYVLIAGSYTPFALVSLRNGPGWTVFSLSWLLAAAGIAQELTIGRKSEKRLLS
80          90          100         110                                120
130
100          110          120          130                                140
150
m254.pep
IVIIYVVMGWMVLAVMKSLTASLPSAGLAWLAAGGMLYSVGIYWVFVNDEKIRHGHGIWHLF
|:|:|
a254
IAIIYVVMGWMVLAVMKSLTASLPPAGLAWLAAGGMLYSVGIYWVFVNDEKIRHGHGIWHLF
140          150          160          170                                180
190
160
m254.pep
VLGGSITQFVSVYGYVIX
|
a254
VLGGSITQFVSVYGYVIX
200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 999>:

586

g255.seq
 1 atggttgac aggaagcctt gcgggggtcag ttcgtcgccg tgttcgctgc
 51 cgcgttgctg tacgctgtca aaacctgccc cgattttccac gcctttgacg
 101 gcgttgatgc ccatacatcg gtaggcgatt tcggcatcga ggcggtcgaa
 151 aacgggttcg cccaaccga cggggacgtt ggcggcttcg atatgcagtt
 201 tcgcgccgac ggaatccaag gatttgcgca caccgtccat atagtgttcc
 251 agttcggcga tttggctttg gttggcggca aaaaaaggat tttgggaaat
 301 gtgttcgctg ccttcaaacc ggattttttt ttcgccgact tgggtaacgt
 351 aggcggtgat ttccgtgccc aatttttctt tcagccattt tttggcaacg
 401 gctccggcgg caacgcgggc tgcggtttcg cgggcggaac tcctgccgcc
 451 gccccggtag tcgcgcgtac cgtattttgtg ccaataggta tagtcggcgt
 501 gtccggggcg gaaggcgtg gcgatgtcgc cgtagtcttc gctgcgctgg
 551 tcggtgttgc ggattag

This corresponds to the amino acid sequence <SEQ ID 1000; ORF 255.ng>:

g255.pep
 1 MVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAHHR VGDFGIEAVE
 51 NGFAQTDGDV GGFDMQFRAD GIQGFHATVH IVFQFGDLAL VGGKKRILGN
 101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG CGFAGGTPAA
 151 APVVARTVFV PIGIVGVSAG EGGDVAVVF AALVGVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1001>:

m255.seq
 1 GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTGCGCG TGTTCGCTGC
 51 CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCAC GCCTTTGACG
 101 GCGTTGATGC CCATCATCGC GTAGGCGATT TCGGCATCGA GCGGTCAAA
 151 AACAGGTTTCG CCAAGCCGA CAGGGACATT GGCTGCTTCG ATATGCAGCT
 201 TCGCGCCGAC GGAATCCAAG GATTGCGCA CGCTGTCCAT ATAGTTTTC
 251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
 301 GTGTTGCGAG CTTCAAACC GGATTTCCTT TTCGCCGACT TGGGTAACGT
 351 AGGCGGTGAT TTCCGTGCGC AATTTTCTT TCAACCATT TTTGGCAACG
 401 GCTCCGCGAG CAACGCGGGC GCGGTTTCA CCGGCGGAGC TCCTGCCGCC
 451 GCCCGGCTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
 501 GGCCGGGCG GAAGCTGTTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
 551 TCGGTATTGC GGATTAA

This corresponds to the amino acid sequence <SEQ ID 1002; ORF 255>:

m255.pep
 1 VVGQEALRGQ FVAVFAAALR YAVKTCADFH AFDGVDAHHR VGDFGIEAVK
 51 NRFAQADRI GCFDMQLRAD GIQGFHAVH IVFQLGNLAM VGGKKRILGN
 101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGSNAG GGFTGGAPAA
 151 AAVVARAVFV PIGIVGVAGA EAGDVAVVF AALVGIAD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 255 shows 88.8% identity over a 188 aa overlap with a predicted ORF (ORF 255.ng) from *N. gonorrhoeae*:

m255/g255

	10	20	30	40	50	60
m255.pep	VVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVKNRFAQADRI					
g255	MVGQEALRGQFVAVFAAALRYAVKTCADFHAFDGVDAHHRVGDFGIEAVENGFAQTDGDV					
	10	20	30	40	50	60
m255.pep	GCFDMQLRADGIQGFHAVHIVFQLGNLAMVGGKKRILGNVFAAFKPDFFADLGNVGGD					
g255	GGFDMQFRADGIQGFHATVHIVFQFGDLALVGGKKRILGNVFAAFKPDFFADLGNVGGD					
	70	80	90	100	110	120
m255.pep	FRAEFFFQPF FGNGSGSNAGGGFTGGAPAAA VVARAVFVPIGIVGVAGAEAGGDVAVVF					
g255	FRAEFFFQPF FGNGSGSNAGCGFAGGTPAAAPVVARTVFVPIGIVGVSGAEGGGDVAVVF					
	130	140	150	160	170	180

587

		130	140	150	160	170	180
	189						
m255.pep	AALVGIADX						
	:						
g255	AALVGVADX						

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1003>:

```

a255.seq
1   GTGGTTGGAC AGGAAGCCTT GCGGGGTGAG TTCGTCGCCG GTTTCGCTGC
51  CGCGTTGCGT TACGCTGTCA AAACCTGCGC CGATTTCCAC GCCTTTGACG
101 GCGTTGATGC CCATCATGGC GTAGGCGATT TCGGCATCGA GGCGGTGCAA
151 TACGGGTTCG CCCAAGCCGA CGGGGACGTT GGCGGCTTCA ATATGCAGCT
201 TCGCGCCGAC GGAATCCAAG GATTTGCGCA CGCTGTCCAT ATAGTTTTC
251 AGCTCGGCAA TTTGGCTATG GTTGGCGGCA AAAAAAGGAT TTTGGGAAAT
301 GTGTCGCAG CCTTCAAACC GGATTTCTTT TTCGCCGACT TGGGTAACGT
351 AGGCGGTGAT TTCCGTGCCG AATTTTCTTT TCAACCATT TTTGGCAACG
401 GCTCCGGCGG CAACGCGGGC GGCGGTTTCG CGGGCGGAAC TCCTGCCGCC
451 GCCCCGGTAG TCGCGCGTGC CGTATTTGTG CCAATAGGTA TAGTCGGCGT
501 GGCCGGGGCG GAAGCTGGTG GCGATGTTGC CGTAGTCTTT GCTGCGCTGG
551 TCGGTATTGC GGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1004; ORF 255.a>:

```

a255.pep
1   VVGQALRGE FVAVFAAALR YAVKTCADFH AFDGVDAHHG VGDFGIEAVE
51  YGFAQADGDV GGFNMQLRAD GIQGFAHAVH IVFQLGNLAM VGGKKRILGN
101 VFAAFKPDFF FADLGNVGGD FRAEFFFQPF FGNGSGGNAG GGFAGGTPAA
151 APVVARAVFV PIGIVGVAGA EAGGDVAVVF AALVGIAD*

```

m255/a255 93.1% identity in 188 aa overlap

	10	20	30	40	50	60
m255.pep	VVGQ ALRGE FVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	FDGIEAVKNRFAQAD	RDI			
	:					
a255	VVGQ ALRGE FVAVFAAALRYAVKTCADFHAFDGVDAHHRVGD	FDGIEAVEYGF	AQADGDV			
	10	20	30	40	50	60
	70	80	90	100	110	120
m255.pep	GCFDMQLRADGIQGF AHAVH IVFQLGNLAMVGGKKRILGNVFAAFKPDFF	FADLGNVGGD				
	:					
a255	GGFNMQLRADGIQGF AHAVH IVFQLGNLAMVGGKKRILGNVFAAFKPDFF	FADLGNVGGD				
	70	80	90	100	110	120
	130	140	150	160	170	180
m255.pep	FRAE FFFQPF FGNGSGGNAGGGFTGGAPAAA	AVVARAVFVPIGIVGVAGAEAGGDVAVVF				
	:					
a255	FRAE FFFQPF FGNGSGGNAGGGFTGGAPVVARAVFVPIGIVGVAGAEAGGDVAVVF					
	130	140	150	160	170	180
	189					
m255.pep	AALVGIADX					
a255	AALVGIADX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1005>:

```

g256.seq
1   atgctcgcgg tacgcaatcg gggttggcac ggcgagtcg tccatttcg
51  cagctgcggc ggcgtagcga acaccgcccc ggtgttctac cacttgggtg
101 ataccgccga aatcgctttt gctttggaca cgctcaccgc gcgttaccgt
151 gaaatatacg ccgtcggcgt atcgctgggc ggcaacgcgc cggcaaaata
201 tttgggcgaa cagggcaaaa aggcattgcc gcacgcctcg gccgccgtat
251 ccgccccgtg tgatgcagag gcggcaggca gccgcttcga cagcggcatc
301 acgcggtgc tctacacgcg ctacttcctc cgcacactga taccctaaagc

```

588

```

351  acgttcgctc caaggttttc agacggcatt tgccgcaggg tgcaaaacac
401  tgggcgagtt tgacgaccgt ttcaccgcac cgctgcacgg ctttgccgac
451  cggcacgact actaccgcca aacttcctgc aaaccgctgc tcaaacacgt
501  tgccaaaccg ctgctcctgc tcaatgccgc caacgacccc ttcctgccgc
551  ccgaagccct gccccgtgca gacgaagcgt ccgaagccgt taccctgttc
601  caacctgcac acggcgggca cgccggcttt gtcagcagca ccggcggcag
651  gctgcacctg caatggctgc cgcagaccgt cctgtcctat tttgacagct
701  tccgcacaaa caggcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1006; ORF 256.ng>:

```

g256.pep
  1  MLAVRNRGWH GAVVHFRSCG GVANTAPVIFY HLGDTAEIAF ALDTLTARYR
 51  EIYAVGVSLG GNAPAKYLGE QGKKALPHAS AAVSAPVDAE AAGSRFDSGI
101  TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151  RHDYYRQTSC KPLLKHVAKP LLLLNAANDP FLPPEALPRA DEASEAVTLF
201  QPAHGGHAGF VSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1007>:

```

m256.seq
  1  ATGCTTGCGG TACGCGATCG GGGTTGGCAC GCGTAGTCG TCCATTTCCG
 51  CAGCTGCGGC GGCATTGCCA ACACCGCTCC GGTGTTCTAC CA.CTtGGCG
101  ATACCGCCGA AATCGCCTTT ACTTTGGACA CGTTCGCCGC GCGTTACCGT
151  GAAAtATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201  TTTGGGCGAA CAGGGCAAAA AGGCATTGCC GCAAGCCGCT GCCGTCATCT
251  CCGCCCCCGT CGATGCAGAG GCGGCAGGCA GACGCTTCGA CAGCGGCATC
301  ACGCGGCTGC TCTACACGCG TACTTCTCTC CGCACCTGA TACCCAAAGC
351  AAAATCGCTC CAAGGTTTTC AGACGGCATT TGCCGCAGGG TGCAAAACAC
401  TGGGCGAGTT TGACGACCGC TTCACCGCAC CGCTGCACGG CTTTGCCGAC
451  CGGCACGACT ACTACGCCA AACTTCTCTG AAACCGCTGC TCAAACACGT
501  TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCTTGCCGC
551  CCGAAGCCCT GCCCGCGCA GACGAAGTAT CCGAAGCCGT TACCCTGTTT
601  CAGCCGGCAT ATGGTGGTCA TGTCGGCTTT GTCAGCAGCA CCGGCGGCAG
651  GCTGCACCTG CAATGGCTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701  TCCGCACAAA CAGGCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1008; ORF 256>:

```

m256.pep
  1  MLAVRDRGWH GVVVHFRSCG GIANTAPVIFY XLGDTAEIAF TLDTFAARYR
 51  EIYAVGVSLG GNALAKYLGE QGKKALPQAA AVISAPVDAE AAGRFRDSGI
101  TRLLYTRYFL RTLIPKAKSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFAD
151  RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201  QPAYGGHVG FVSSTGGRHLH QWLPQTVLSY FDSFRTNRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 256 shows 92.9% identity over a 239 aa overlap with a predicted ORF (ORF 256.ng) from *N. gonorrhoeae*:

```

m256/g256
      10      20      30      40      50      60
m256.pep  MLAVRDRGWHGVVHFRSCGGIANTAPVIFYHLGDTAEIAFTLDTFAARYREIYAVGVSLG
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256      MLAVRNRGWHGAVVHFRSCGGVANTAPVIFYHLGDTAEIAFALDTLTARYREIYAVGVSLG
          10      20      30      40      50      60

      70      80      90      100     110     120
m256.pep  GNALAKYLGEQGKKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL
          ||| |||||:|||||:|:|:| ||||| ||||| ||||| ||||| |||||:|
g256      GNAPAKYLGEQGKKALPHASAAVSAPVDAEAGSRFDSGITRLLYTRYFLRTLIPKARSL
          70      80      90      100     110     120

      130     140     150     160     170     180
m256.pep  QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g256      QGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYYRQTSCKPLLKHVAKPLLLLNAANDP

```

589

	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
g256	FLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1009>:

```

a256.seq
1  ATGCTCGCGG TACGCGATCG GGGTTGGAAC GCGTAGTCG TCCATTTCGG
51  CAGCTGCGGC GCGTAGCGA ACACGCCCC GGTGTTCTAC CACTTGGGCG
101 ATACGCCGA AATTGCCTTT ACTTTGGACA CGCTCGCCG GCGTTACCGT
151 GAAATATACG CCGTCGGCGT ATCGCTGGGC GGCAACGCGC TGGCAAAATA
201 TTTGGGCGAA CAGGGCGAAA ACGCGCTGCC GCAAGCCGCC GCCGTCATCT
251 CCGCACCCGT CGATGCAGAG GCGGCAGGCA ACCGCTTCGA CAGCGGCATC
301 ACACGGCTGC TCTACACGCG CTACTTCCTC CGCACACTGA TACCCAAAGC
351 ACGGTCGCTC CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC
401 TGGGCGAGTT TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAT
451 CGGCACGACT ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT
501 TGCCAAACCG CTGCTCCTGC TCAATGCCGT CAACGACCCC TTCCTGCCGC
551 CCGAAGCGCT GCCCGCGCA GACGAAGTGT CCGAAGCCGT TACCTGTTC
601 CAGCCGACAC ACGGTGGTCA TGTCCGCTTT GTCGGCAGCA CCGGCGGCG
651 GCTGCACCTG CAATGGTTGC CGCAGACCGT CCTGTCCTAT TTCGACAGCT
701 TCCGCACAAA CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1010; ORF 256.a>:

```

a256.pep
1  MLAVRDRGWN GVVVHFRSCG GVANTAPVFY HLGDTAEIAF TLDTLAARYR
51  EIIYAVGSLG GNALAKYLGE QGENALPQAA AVISAPVDAE AAGNRFDSCI
101 TRLLYTRYFL RTLIPKARSL QGFQTAFAAG CKTLGEFDDR FTAPLHGFD
151 RHDYYRQTSC KPLLKHVAKP LLLNNAVNDP FLPPEALPRA DEVSEAVTLF
201 QPTHGGHVG FVSTGGRLHL QWLPQTVLSY FDSFRTNRR*

```

m256/a256 95.4% identity in 239 aa overlap

	10	20	30	40	50	60
m256.pep	MLAVRDRGWHGVVVHFRSCGGIANTAPVFYXLGDTAEIAFTLDTFAARYREIYAVGVSLG					
	: : : : :					
a256	MLAVRDRGWNQVVVHFRSCGGVANTAPVFYHLGDTAEIAFTLDTLAARYREIYAVGVSLG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m256.pep	GNALAKYLGEQGKKALPQAAVISAPVDAEAGRRFDSGITRLLYTRYFLRTLIPKAKSL					
	: : : : :					
a256	GNALAKYLGEQGENALPQAAVISAPVDAEAGNRFDSGITRLLYTRYFLRTLIPKARSL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m256.pep	QGFQTAFAAGCKTLGEFDDRFTAPLHGFAADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	: : : : :					
a256	QGFQTAFAAGCKTLGEFDDRFTAPLHGFAADRHDYYRQTSCKPLLKHVAKPLLLLNAVNDP					
	130	140	150	160	170	180
	190	200	210	220	230	240
m256.pep	FLPPEALPRADEVSEAVTLFQPAYGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	: : : : :					
a256	FLPPEALPRADEVSEAVTLFQPTHGGHVGVSSTGGRLHLQWLPQTVLSYFDSFRTNRRX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1011>:

```

g256-1.seq
1  ATGATTTTGA CACCGCCGGA CACGCCCTT TTCCTCCGCA ACGGCAATGC
51  CGACACGATT GCCGCCAAAT TCCTGCAACA CCGCGACCC GCATACCGCC

```

590

```

101 GCGAGATGCT TCCCGACAGC ACGGGTAAAA CCAAACCCGC CTACGACTTT
151 TCAGCAGGCG GCATTTTCGCC CGATGCGCCG CTGGTCGTGC TGTTCACGG
201 TTTGGAAGGA AGCAGCCGCA GCCATTACGC GGTGCAACTG ATGCTCGCGG
251 TACGCAATCG GGGTTGGCAC GGCGCAGTCG TCCATTTCCG CAGCTGCGGC
301 GGCCTAGCGA ACACCGCCCC GGTGTTCTAC CACTTGGGTG ATACCGCCGA
351 AATCGCCTTT GCTTTGGACA CGCTCACCGC GCGTTACCGT GAAATATACG
401 CCGTCGGCGT ATCGCTGGGC GGCAACGCGC CGGCAAAATA TTTGGGCGAA
451 CAGGGCAAAA AGGCATTGCC GCACGCCTCG GCCGCCGTAT CCGCCCCCGT
501 TGATGCAGAG GCGGCAGGCA GCCGCTTCGA CAGCGGCATC ACGCGGCTGC
551 TCTACACGCG CTAATTCTCT CGCACACTGA TACCCAAAGC ACGTTCGCTC
601 CAAGGTTTTT AGACGGCATT TGCCGCAGGG TGCAAAACAC TGGGCGAGTT
651 TGACGACCGT TTCACCGCAC CGCTGCACGG CTTTGCCGAC CGGCACGACT
701 ACTACCGCCA AACTTCCTGC AAACCGCTGC TCAAACACGT TGCCAAACCG
751 CTGCTCCTGC TCAATGCCGC CAACGACCCC TTCCTGCCGC CCGAAGCCCT
801 GCCCCGTGCA GACGAAGCGT CCGAAGCCGT TACCCTGTTC CAACCTGCAC
851 ACGGCGGGCA CGCCGGCTTT GTCAGCAGCA CCGGCGGCAG GCTGCACCTG
901 CAATGGCTGC CGCAGACCGT CCTGTCTTAT TTTGACAGCT TCCGCACAAA
951 CAGGCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1012; ORF 256-1.ng>:

g256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQHPAP AYRREMLPDS TGKTKTAYDF
51 SAGGISPDAP LVLVLFHGLEG SSRSHYAVEL MLAVRNRGWH GAVVHFRSCG
101 GVANTAPVFY HLGDTAEIAF ALDTLTARYR EIYAVGVSLG GNAPAKYLGE
151 QGKKALPHAS AAVSAPVDAE AAGSRFDSGI TRLLYTRYFL RTLIPKARSL
201 QGFQTAFAAG CKTLGEFDDR FTAPLHGFAF RHDYRQTSC KPLLKHVAKP
251 LLLLNAANDP FLPEALPRA DEASEAVTLF QPAHGHHAGF VSSTGRLHL
301 QWLPQTVLSY FDSFRTNRR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1013>:

m256-1.seq

```

1 ATGATTTTAA CACCGCCGGA CACGCCCTTT TTCCTCCGCA ACGGCAATGC
51 GCACACGATT GCCGCCAAAT TCCTGCAACG CCCCAGCGCC GCATACCGCC
101 GAGAGCTGCT TCCCGACAGC ACGGGTAAAA CCAAGTCGC CTACGACTTT
151 TCAGACGGCA TTTCGCCCGA TGCGCCGCTG GTCGTGCTGT TTCACGGTTT
201 GGAAGGAAGC AGCCGCAGCC ATTACGCGGT CGAACTGATG CTTGCGGTAC
251 GCGATCGGGG TTGGCACGGC GTAGTCGTCC ATTTCCGCAG CTGCGGCGGC
301 ATTGCCAACA CCGCTCCGGT GTTCTACCAC TTGGGCGATA CCGCCGAAAT
351 CGCCTTTACT TTGGACACGT TCGCCGCGCG TTACCGTGAA ATATACGCCG
401 TCGGCGTATC GCTGGGCGGC AACCGCTGG CAAAATATTT GGGCGAACAG
451 GGCAAAAGG CATTGCCGCA AGCCGCTGCC GTCATCTCCG CCCCCTCGA
501 TGCAGAGGCG GCAGGCAGAC GCTTCGACAG CGGCATCAGC CGGCTGCTCT
551 ACACGCGCTA CTTCTCCGCG ACCCTGATAC CCAAAGCAAA ATCGCTCCAA
601 GGTTTTCAGA CGGCATTTGC CGCAGGGTGC AAAACACTGG GCGAGTTTGA
651 CGACCGCTTC ACCGCACCGC TGCACGGCTT TGCCGACCGG CACGACTACT
701 ACCGCCAAAC TTCCTGCAAA CCGTGCTCA AACACGTTGC CAAACCGCTG
751 CTCCTGTCTA ATGCCGTCAA CGACCCCTTC CTGCCGCCCC AAGCCCTGCC
801 CCGCGCAGAC GAAGTATCCG AAGCCGTAC CCTGTCCAG CCGGCATATG
851 GTGGTCATGT CGGCTTTGTC AGCAGCACCG GCGGCAAGGT GCACCTGCAA
901 TGGCTGCCCG AGACCGTCTT GTCCTATTTT GACAGCTTCC GCACAAACAG
951 GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1014; ORF 256-1>:

m256-1.pep

```

1 MILTPPDTPF FLRNGNADTI AAKFLQRPAP AYRRELLPDS TGKTKVAYDF
51 SDGISPDAPL VVLVLFHLEGS SRSHYAVELM LAVRDRGWHG VVVHFRSCGG
101 IANTAPVFYH LGDTAEIAFT LDTFAARYRE IYAVGVSLGG NALAKYLGEQ
151 GKKALPQAAA VISAPVDAEA AGRRFDSGIT RLLYTRYFLR TLIIPKAKSLQ
201 GFQTAFAAGC KTLGEFDDRF TAPLHGFAFR HDYRQTSCCK PLLKHVAKPL
251 LLLNAVNDPF LPPEALPRAD EVSEAVTLFQ PAYGGHVGFV SSTGRLHLQ
301 WLPQTVLSYF DSFRTNRR*

```

m256-1/g256-1 93.1% identity in 319 aa overlap

```

10 20 30 40 50 59
m256-1.pep MILTPPDTPFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFS-DGISPDAP
|||||:|||||:|||||:|||||:|||||
g256-1 MILTPPDTPFFLRNGNADTIAAKFLQHPAPAYRREMLPDSTGKTKTAYDFSAGGISPDAP
10 20 30 40 50 60
60 70 80 90 100 110 119
m256-1.pep LVLVLFHGLEGSSSRSHYAVELMLAVRDRGWHGVVVHFRSCGGIANTAPVFYHLGDTAEIAF

```


591

```

|||||:|||||:|||||:|||||
g256-1  LVVLFHGLEGSSRSYAVELMLAVNRGWHGAVVHFRSCGGVANTAPVFYHLGDTAEIAF
          70      80      90      100     110     120

          120     130     140     150     160     170     179
m256-1.pep  TLDTFARYREIYAVGVSLGGNALAKYLGEQKKALPQAAVISAPVDAEAAAGRRFDSGI
          |||||:|||||:|||||:|||||:|||||:|||||
g256-1  ALDTLTARYREIYAVGVSLGGNAPAKYLGEQKKALPHASAAVSAPVDAEAAAGSRFDSGI
          130     140     150     160     170     180

          180     190     200     210     220     230     239
m256-1.pep  TRLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYRQTSC
          |||||:|||||:|||||:|||||:|||||:|||||
g256-1  TRLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFTAPLHGFADRHDYRQTSC
          190     200     210     220     230     240

          240     250     260     270     280     290     299
m256-1.pep  KPLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHGVFVSSTGGRLHL
          |||||:|||||:|||||:|||||:|||||:|||||
g256-1  KPLLKHVAKPLLLNNAANDPFLPPEALPRADEASEAVTLFQPAHGGHAGFVSSTGGRLHL
          250     260     270     280     290     300

          300     310     319
m256-1.pep  QWLPQTVLSYFDSFRNRRX
          |||||:|||||
g256-1  QWLPQTVLSYFDSFRNRRX
          310     320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1015>:

```

a256-1.seq
1  ATGATTTTGA  CACCGCCGGA  CACACCCTTT  TTCCTCCGCA  ACGGCAATGC
51  CGACACGATT  GCCGCCAAAT  TCCTGCAACG  CTCCGCACCT  GCATACCGCC
101  GCGAGCTGCT  TCCCGACAGC  ACGGGTAAAA  CCAAAACCGC  CTACGACTTT
151  TCAGACGGCA  TTTCGCCCGA  TCGCCGCTG  GTCGTGCTGT  TTCACGGTTT
201  GGAGGGCGGC  AGTGGCAGCC  ATTACGCGGT  CGAACTGATG  CTCGCGGTAC
251  GCGATCGGGG  TTGGAACGGC  GTAGTCGTCC  ATTTCCGCAG  CTGCGGCGGC
301  GTAGCGAACA  CCGCCCGGTT  GTTCTACCAC  TTGGGCGATA  CCGCCGAAAT
351  TGCCTTTACT  TTGGACACGC  TCGCCGCGCG  TTACCGTGAA  ATATACGCCG
401  TCGGCGTATC  GCTGGGCGGC  AACGCGCTGG  CAAAATATTT  GGGCGAACAG
451  GCGGAAAACG  CGCTGCCGCA  AGCCGCGGCC  GTCATCTCCG  CACCCGTCGA
501  TGCAGAGGCG  GCAGGCAACC  GCTTCGACAG  CGGCATCACA  CGGCTGCTCT
551  ACACGCGCTA  CTTCTCCCGC  ACACTGATAC  CCAAAGCAGC  GTCGCTCCAA
601  GGTTTTCAGA  CGGCATTGTC  CGCAGGGTGC  AAAACACTGG  GCGAGTTTGA
651  CGACCGTTTC  ACCGCACCGC  TGCACGGCTT  TGCCGATCGG  CACGACTACT
701  ACCGCCAAAC  TTCCTGCAAA  CCGCTGCTCA  AACACGTTGC  CAAACCGCTG
751  CTCCTGCTCA  ATGCCGTCAA  CGACCCCTTC  CTGCCGCCCG  AAGCGCTGCC
801  CCGCGCAGAC  GAAGTGTCCG  AAGCCGTTAC  CCTGTTCCAG  CCGACACACG
851  GTGGTCATGT  CGGCTTTGTC  GGCAGCACCG  GCGGCAGGCT  GCACCTGCAA
901  TGGTTGCCCG  AGACCGTCCT  GTCCTATTTC  GACAGCTTCC  GCACAAACAG
951  GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1016; ORF 256-1.a>:

```

a256-1.pep
1  MILTPPDTPF  FLRNGNADTI  AAKFLQRSAP  AYRRELLPDS  TGKTKTAYDF
51  SDGISPDAPL  VVLFHGLEGG  SGSHYAVELM  LAVRDRGWNG  VVHFRSCGG
101  VANTAPVFYH  LGDTAEIAFT  LDTLAARYRE  IYAVGVSLGG  NALAKYLGEQ
151  GENALPQAAA  VISAPVDAEA  AGNRFDSDGI  RLLYTRYFLR  TLIPKARSLQ
201  GFQTAFAAGC  KTLGEFDDRF  TAPLHGFADR  HDYYRQTSC  PLLKHVAKPL
251  LLLNAVNDPF  LPPEALPRAD  EVSEAVTLFQ  PTHGGHGVFV  GSTGGRHLQ
301  WLPQTVLSYF  DSFRNRR*

```

a256-1/m256-1 95.6% identity in 318 aa overlap

```

          10      20      30      40      50      60
a256-1.pep  MILTPPDTPFFFLRNGNADTIAAKFLQRSAPAYRRELLPDSTGKTKTAYDFSDGISPDAPL
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1  MILTPPDTPFFFLRNGNADTIAAKFLQRPAPAYRRELLPDSTGKTKVAYDFSDGISPDAPL
          10      20      30      40      50      60

          70      80      90      100     110     120
a256-1.pep  VVLFHGLEGGSGSHYAVELMLAVRDRGWNGVVHFRSCGGVANTAPVFYHLGDTAEIAFT
          |||||:|||||:|||||:|||||:|||||:|||||
m256-1  VVLFHGLEGSSRSYAVELMLAVRDRGWNGVVHFRSCGGIANTAPVFYHLGDTAEIAFT

```

592

	70	80	90	100	110	120
a256-1.pep	130	140	150	160	170	180
	LDTLAARYREIYAVGVSLGGNALAKYLGEQGENALPQAAAVISAPVDAEAAGNRFD SGIT					
m256-1	LDTFAARYREIYAVGVSLGGNALAKYLGEQGKKALPQAAAVISAPVDAEAAGRRFD SGIT					
	130	140	150	160	170	180
a256-1.pep	190	200	210	220	230	240
	RLLYTRYFLRTLIPKARSLQGFQTAFAAGCKTLGEFDDRFAPLHGFADRHDYYRQTSCK					
m256-1	RLLYTRYFLRTLIPKAKSLQGFQTAFAAGCKTLGEFDDRFAPLHGFADRHDYYRQTSCK					
	190	200	210	220	230	240
a256-1.pep	250	260	270	280	290	300
	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPTHGGHVGVFVGSTGGRLHLQ					
m256-1	PLLKHVAKPLLLNNAVNDPFLPPEALPRADEVSEAVTLFQPAYGGHVGVFVSSTGGRLHLQ					
	250	260	270	280	290	300
a256-1.pep	310	319				
	WLPQTVLSYFDSFRTNRRX					
m256-1	WLPQTVLSYFDSFRTNRRX					
	310					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1017>:

g257.seq

```

1  atgggcaggc atttcgggcg cagacgtttt ctgacggctg ccgccgttgc
51  tgtggccggt gcggcggttt cttttttgcc gaatcctttt gccgccggcg
101 gcgaaaaacg caacatggat aaaaaacgag atgaaaatgt gtttttctgg
151 aaaggtgtcg cgctgggttc cggcgcgag ctgcgccgtg tcggcggtga
201 cgacagacag gcggcggtat tggtaataa ggttttggcg gaagtggcgc
251 gtttggaaaa aatgttcagc cttaccgtg aagacagcct gatcagccgt
301 ctgaaccgag acggttatct gacttcgcct ccggcggtat ttttggaaat
351 gttgagcctg gccgcgatat tcacgcgctg a

```

This corresponds to the amino acid sequence <SEQ ID 1018; ORF 257.ng>:

g257.pep

```

1  MGRHFGRRRF LTAAAVAVAG AAVSFLPNPF AAGGEKRNMD KKRDENVFFW
51  KGVALGSGAE LRLFGVDDRQ AADLVNKLVA EVARLEKMFS LYREDSLISR
101 LNRDGYLTSP PADFLELLSL AAIIFTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1019>:

m257.seq

```

1  ATGGGCAGGC ATTCGGGCG .CAGCGTTT CTGACGGTTG CCGCCGTTGC
51  GCGGGGgAc. GCGGcGGTTT CTTTCCTGCC GAATCCTTTT GCCGCCGATG
101 ATGAAAAACG CAACGGGGAT GAAAAACGCA ATGAAAATGT GTTTTCTGCG
151 AAAGGTGTCT CACTGGGTTC CGGTGCgGa. CTCCGTCTGT TCGGTGTGGA
201 CGACAGGCGT GCGGCGGATT TGGTCAACAA GGTTTTGGCG GAAGTGGCGC
251 GTTTGGAAAA ATTGTTCAGC CTTTACCGTG AAGACAGCCT GATCAGCCGC
301 CTGAACAGGG ACGGTTATCT GACTTCGCCG TCGGCGGATT TTTTGGAACT
351 GkTGAGCCTG GCCGCGATAT TCACGCKCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1020; ORF 257>:

m257.pep

```

1  MGRHFGXQRF LTVAAVAAGX AAVSFLPNPF AADDEKRNMD EKRDENVFFW
51  KGVALGSGAX LRLFGVDDR AADLVNKLVA EVARLEKLFS LYREDSLISR
101 LNRDGYLTSP SADFLELXSL AAIIFTX*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 257 shows 88.0% identity over a 125 aa overlap with a predicted ORF (ORF 257.ng) from *N. gonorrhoeae*:

m257/g257

10

20

30

40

50

60

593

```

m257.pep      MGRHFGRQRFLTVAAVAAGTAAVSFLPNPFAADDEKRNKGDEKRNENVFFWKGVGALGSGAD
               |||||:||||:||||: ||||| ||| |:|:|||||:|||||:
g257          MGRHFGRRRRFLTAAAVAVAGA AVSFLPNPFAAGGEKRNMDKKRDENVFFWKGVGALGSGAE
               10      20      30      40      50      60

               70      80      90      100     110     120
m257.pep      LRLFGVDDRRRAADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
               |||||:|||||:|||||: ||||| ||||| ||||| ||||| ||
g257          LRLFGVDDRQAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
               70      80      90      100     110     120

m257.pep      AAIFTXX
               |||||
g257          AAIFTRX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1021>:

```

a257.seq
1  ATGGGCAGGC  ATTTCTGGGCG  CAGGCGTTTT  TTGACAGTTG  CCGCCGTTGC
51 GGCGGCGGGC  GCGGCGGTTT  CTTTCCTGCC  GAATCCTTTT  GCCGCCGATG
101 ATGAAAACG  CAATAAAGAT  GAAAAACGCA  ATGAAAATGT  GTTTTCTGCG
151 AAAGGTGTCG  CACTGGGTTC  CGGTGCGGAG  CTCCGTCTGT  TCGGTGTGGA
201 CGACAGGCGT  GCGGCGGATT  TGGTCAACAA  GGTTTGGCG  GAAGTGGCGC
251 GTTTGGAAA  AATGTTTCAGC  CTTTACCGTG  AAGACAGCCT  GATCAGCCGT
301 CTGAACCGTG  ACGGTTATTT  GACTTCGCCG  CCGGCGGATT  TTTTGAAGT
351 GTTGAGCCTG  GCCGTGATAT  TCACGCGCTG  A

```

This corresponds to the amino acid sequence <SEQ ID 1022; ORF 257.a>:

```

a257.pep
1  MGRHFGRRRF  LTVAAVAAAG  AAVSFLPNPF  AADDEKRNKD  EKRNENVFFW
51  KGVALGSGAE  LRLFGVDDRR  AADLVNKKVLA  EVARLEKMFS  LYREDSLISR
101 LNRDGYLTSP  PADFLELLSL  AVIFTR*

```

m257/a257 92.0% identity in 125 aa overlap

```

               10      20      30      40      50
60
m257.pep      MGRHFGXQRFLTVAAVAAGXAAVSFLPNPFAADDEKRNKGDEKRNENVFFWKGVGALGSGAX
               ||||| :|||||: |||||
a257          MGRHFGRRRRFLTVAAVAAGAAVSFLPNPFAADDEKRNKDEKRNENVFFWKGVGALGSGAE
               10      20      30      40      50
60

               70      80      90      100     110
120
m257.pep      LRLFGVDDRRRAADLVNKKVLA EVARLEKLFSLYREDSLISRLNRDGYLTSPSADFLLELXSL
               |||||:|||||:|||||: ||||| ||||| ||||| |||||
a257          LRLFGVDDRRRAADLVNKKVLA EVARLEKMFSLYREDSLISRLNRDGYLTSPPADFLELLSL
               70      80      90      100     110
120

m257.pep      AAIFTXX
               |:|
a257          AVIFTRX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1023>:

```

g258.seq
1  atgcgccgct tcctaccgat cgcagccata tgcgcccgtcg tcctgctgta
51  cggattgacg gcgggcgaccg gcagcaccag ttcgctggcg gattatttct
101 ggtggatagt ctcgttcagc gcaatgctgc tgctggtgtt gtccgcccgtt
151 ttggcacgtt atgtcatatt gctgttgaaa gacaggcgca acggcgtgtt
201 cggttcgcag attgccaaac gcctttccgg gatgttcacg ctggtcgccg
251 tactgcccgg cttgttcctg ttcggcattt ccgcgcagtt tatcaacggc
301 acgattaatt cgtggttcgg caacgacacc cacgaagccc tcgaacgcag
351 ccttaatttg agcaagtccg cactggattt ggcggcagac aatgccgtca
401 gcaacgccgt tcccgtacag atagacctca tcggcaccgc ctccctgtcg
451 ggcaatatgg gcagtgtgct ggaacactac gccggcagcg gttttgccca
501 gcttgccctg tacaatgccg caagcgggaa aatcgaaaaa agcatcaatt
551 cgcaccaatt cgaccagccg cttcccgaca aagaacattg ggaacagatt
601 cagcagaccg gttcggttcg gagtttgtaa agcataggcg gcgtattgta
651 cgcgcagggg tggttgctcg caggtagcga caacgggccc gattacgcgc
701 tgttcttccg ccagccgatt cccgaaaatg tggcacagga tgccgttctg
751 attgaaaagg cgcgggcgaa atatgccgaa ttgagttaca gcaaaaaagg
801 tttgcagacc ttttttctgg taaccctgct gattgcctcg ctgctgtcga
851 ttttcttgc gctggtaatg gcactgtatt ttgcccggcg tttcgtcgaa
901 cccattctgt cgcttgccga gggcgcaaag gcggtggcgc aggggtgattt
951 cagccagacg cgcccgtat tgcgcaacga cgagttcggc cgtttgacca
1001 agctgttcaa ccatatgacc gagcagcttt ccatcgccaa agaagcagac
1051 gaacgcaacc gccggcgcgga ggaagccgcc cgctactacc tcgagtgcggt
1101 gttgatggg ttgactaccg gtgtggtggt ctctacccc ctctctgtt
1151 gccgtaccgc ggtgttttcc acttgtcatt cctccctct tcttatttc
1201 taa

```

This corresponds to the amino acid sequence <SEQ ID 1024; ORF 258.ng>:

```

g258.pep
1  MRRELPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVSFS AMLLLVLSAV
51  LARYVILLLK DRRNGVFGSQ IAKRLSGMFT LVAVLPGLFL FGISAQFING
101 TINSWFGNDT HEALERSLNL SKSALDLAAD NAVSNAVVPVQ IDLIGTASLS
151 GNMGSVLEHY AGSGFAQLAL YNAASGKIEK SINPHQFDQP LPDKEHWEQI
201 QQTGSVRSLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPI PENVAQDAVL
251 IEKARAKYAE LSYSKKGLOT FFLVTLIAS LLSIFLALVM ALYFARRFVE
301 PILSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLDG LTTGVVVSYP LSCCRTAVFS TCHSSPLSYF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1025>:

```

m258.seq
1  ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51  CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTCTT
101 GGTGGATTGT TGCCTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTGCGAG ATTGCCAAAC GCCTTTCTGG GATGTTTACG CTGGTTGCCG
251 TACTGCCCCG CGTGTTCCTG TTCGCGGTTT CCGCACAGTT CATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATTT GCGGCGAGAC AACGCCCTCG
401 GCAACGCCGT CCCCGTGCAG ATAGACCTCA TCGGCGCGGC TTCCCTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGCGAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAGCT CGATCAGCCG TTTCCAGGTA AGGCGGTTG GAAAAAATC
601 CAACGGGCGG GTTCGGTCAG GGATTGGAA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TGGCTGTCGG CGGGTACGCA CAACGGGCGC GATTACGCCT
701 TGTTTTTCGG TCAGCCGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTCTCTGG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTCTTGC ACTGGTCATG GCACTGTATT TCGCCCGCCG TTTCGTGCGA
901 CCCGTCCTAT CGCTTGCCGA GGGGGCGAAG GCGGTGGCGC AAGGCGATTT
951 CAGCCAGACG CGCCCCGTGT TGCGCAACGA CGAGTTCGGA CGCTTGACCA

```

595

```

1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCCGGCGCGA GGAAGCCGCC AGGCATTATC TTGAATGCGT
1101 GTTGGAGGGG CTGACCACGG GCGTGGTGGT GTTTGACGAA CAAGGCTGTC
1151 TGAAACsTT CAACAAAGCG GCGGAACAGA TTyTGGGGAT GCCGCTTACC
1201 CCCcTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAACCGGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCCT GCCCGAAGAC AACGGCAACg GCGTGGTAAT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCCGCGT
1451 GGGGCGAagT GGCgaAgCGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCCGCCGA ACgGsTGGCG TkGAAATTGG GCGGGAAGCT
1551 GGATGAGCAG GATGCGCAA TCCTGACGCG TTCGACCGAC ACCATCGTCA
1601 AACAGGTGGC GGCATTGAAG GAAATGGTCG AAGCATTCCG CAATTATGCG
1651 CGTTCCCTT CGCTCAAATT GGAAAATCAG GATTTGAACG CCTTAATCGG
1701 CGATGTGTTG GCATTGTATG AAGCCGGTCC GTGCCGGTTT GCGGCGGACT
1751 TGCCGGCGAA CCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1026; ORF 258>:

```

m258.pep
  1 MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
 51 LARYVILLLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNVAVPQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QRAGSVRDLE SIGGVLYAQG WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLQT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTGTVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQSSLL AEFVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERXA XKLGGKLD EQ DAQILTRSTD TIVKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCR F AADLPANR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 258 shows 90.9% identity over a 386 aa overlap with a predicted ORF (ORF 258.ng) from *N. gonorrhoeae*:

```

m258/g258

      10      20      30      40      50      60
m258.pep MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVAFS AMLLLVLSAVLARYVILLLK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      MRRFLPIAAICAVVLLYGLTAATGSTSSLA DYFWWIVSFS AMLLLVLSAVLARYVILLLK
          10      20      30      40      50      60

      70      80      90     100     110     120
m258.pep DRRDGVFGSQIAKRLSGMFTLVAVLPGVFLFGVSAQFINGTINSWFGNDTHEALERSLNL
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      DRRNGVFGSQIAKRLSGMFTLVAVLPGFLFLFGISAQFINGTINSWFGNDTHEALERSLNL
          70      80      90     100     110     120

      130     140     150     160     170     180
m258.pep SKSALNLAADNALGNVAVPQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SKSALDLAADNAVSNVAVPQIDLIGTASLSGNMGSVLEHYAGSGFAQLALYNAASGKIEK
          130     140     150     160     170     180

      190     200     210     220     230     240
m258.pep SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQGWLSAGTHNGRDYALFFRQPV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g258      SINPHQFDQPLPDKEHWEIQQTGSVRSLESIGGVLYAQGWLSAGTHNGRDYALFFRQPI
          190     200     210     220     230     240

```

	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAELSYSKKGLQTFFLATLLIASLLSIFLALVMALYFARRFVE					
	:: : :					
g258	PENVAQDAVLIEKARAKYAELSYSKKGLQTFVLVTLIASLLSIFLALVMALYFARRFVE					
	250	260	270	280	290	300
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLNRNDEFGRLLTKLFNHMTQELSIAKEADERNRRREEAA					
	:					
g258	PILSLAEGAKAVAQGDFSQTRPVLNRNDEFGRLLTKLFNHMTQELSIAKEADERNRRREEAA					
	310	320	330	340	350	360
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVVFDEQGCLKTFNKAAEQILGMPLTPLWGSSRRHGWHGVSAAQQSLL					
	: : :					
g258	RHYLECVLDGLTTGVVVSYPLSCCRTAVFSTCHSSPLSYFX					
	370	380	390	400		

```

a258.seq
1 ATGCGCCGTT TTCTACCGAT CGCAGCCATA TGCGCCGTCG TCCTGTTGTA
51 CGGACTGACG GCGGCAACCG GCAGCACCAG TTCGCTGGCG GATTATTTCT
101 GGTGGATTGT TGCGTTTCAGC GCAATGCTGC TGCTGGTGTT GTCCGCCGTT
151 TTGGCACGTT ATGTCTATATT GCTGTTGAAA GACAGGCGCG ACGGCGTATT
201 CGGTTTCGCAG ATTGCCAAAC GCCTTTCCGG GATGTTTACG CTGTTGCCG
251 TACTGCCCGG CGTGTTCCTG TTCGGCGTTT CCGCACAGTT TATCAACGGC
301 ACGATTAATT CGTGGTTCGG CAACGATACC CACGAGGCGC TTGAACGCAG
351 CCTCAATTG AGCAAGTCCG CATTGAATCT GCGGCGACAG AACGCCCTTG
401 GCAACGCCAT CCCCCTGCAG ATAGACCTCA TCGCGCGCGG TTCCTTGCCC
451 GGGGATATGG GCAGGGTGCT GGAACATTAC GCCGGCAGCG GTTTTGCCCA
501 GCTTGCCCTG TACAATGCCG CAAGCGGCAA AATCGAAAAA AGCATCAACC
551 CGCACAAAGT CGATCAGCCG TTTCCAGGTA AGGCGCGTTG GGAAAAAATC
601 CAACAGGCGG GTTCGGTCCG GGATTTGGA AGCATAGGCG GCGTATTGTA
651 CGCGCAGGGC TTGGCTGTCG CAGGTACGCA CAACGGGCGC GATTACGCCCT
701 TGTTTTTCCG TCAGCCGGTT CCCAAAGGCG TGGCAGAGGA TGCCGTCTTA
751 ATCGAAAAGG CAAGGGCGAA ATATGCTGAG TTGAGTTACA GCAAAAAGG
801 TTTGCAGACC TTTTTCCTG CAACCCTGCT GATTGCCTCG CTGCTGTCGA
851 TTTTTCCTGC ATGGTCTAG GCACGTGATT TCGCCCCCGG TTTTCGTCGAA
901 CCCGTCTAT CGTGTGCCGA GGGGGCGAAG CGGTTGGCG TCAAGCGATT
951 CAGCCAGACG CGCCCCGTGT TCGCAACGA CGAGTTCGGA CGTTGACCA
1001 AGTTGTTCAA CCACATGACC GAGCAGCTTT CCATCGCCAA AGAAGCAGAC
1051 GAGCGCAACC GCGGCGCGCA GGAAGCCGGT AGACATTATC TCGAATGCGT
1101 GTTGAGGGG GTGACCACGG GCGTGGTGTT GTTTGACGAA CAGGCTGTC
1151 TGAAAACTT CAACAAAGCG GCGGAACAGA TTTTGGGAT CCGGCTTACC
1201 CCCCTGTGGG GCAGCAGCCG GCACGGTTGG CACGGCGTTT CGGCGCAGCA
1251 GTCCTGCTT GCCGAAGTGT TTGCCGCCAT CGGCGCGGCG GCAGGTACGG
1301 ACAAAACCGT CCATGTGAAA TATGCCGCGC CGGACGATGC CAAAATCCTG
1351 CTGGGCAAGG CAACCGTCTT CCCCAGAGAC AACGGCAAC CGTGGTAACT
1401 GGTGATTGAC GACATCACCG TTTTGATACA CGCGCAAAAA GAAGCGCGT
1451 GGGCGAAGT GGCAAAACGG CTGGCACACG AAATCCGCAA TCCGCTCACG
1501 CCCATCCAGC TTTCTGCCGA ACGGCTGGCG TGGAAATTGG GCGGGAAGCT
1551 GGACGAGCAG GACGCGCAAA TCCTGACACG TTCGACCCAG ACCATCATCA
1601 AGACAAGTGG GGCATTAAAA GAAATGTCG AGGCATTCCG CAATTACCGC
1651 CGTTCCCCTT CGCTCAAATT GGAAATCAG GATTTGAACG CTTAATCCGG
1701 CGATGTGTTG GCATTGTACG AAGCTGGTCC GTGCCGTTT GCGGCGGAAC
1751 TTGCCGCGCA ACCGCTGATG ATGGCGGCGG ATACGACCGC CATGCGGCAG
1801 GTGCTGCACA ATATTTTCAA AAATCGCCGC GAAGCGGCGG AAGAAGCCGA
1851 TGTGCCCGAA GTCATGGTAA AATCGGAAG GGGGCAAGC GGACGGATTG
1901 TCCTGACAGT TTGCGACAAC GGCAAGGGGT TCGGCAGGGA AATGCTGCAC
1951 AATGCCTTCG AGCCGTATGT AACGGACAAA CCGGCTGGAA CGGGATTGGG
2001 ACTGCCCGTG GTGAAAAAAA TCATTGAAGA ACACGGCGGC CGCATCAGCC
2051 TAGAGATACA GGTATCGGGC GCGCGTGTG TCAGAATCAT CTTGCCAAAA
2101 ACGGTAGAAA CTTATGCGTA G

```

This corresponds to the amino acid sequence <SEQ ID 1028; ORF 258.a>:

```

a258.pep
1  MRRFLPIAAI CAVVLLYGLT AATGSTSSLA DYFWWIVAFS AMLLLVLSAV
51  LARYVILLK DRRDGVFGSQ IAKRLSGMFT LVAVLPGVFL FGVSAQFING
101 TINSWFGNDT HEALERSLNL SKSALNLAAD NALGNAIPVQ IDLIGAASLP
151 GDMGRVLEHY AGSGFAQLAL YNAASGKIEK SINPHKLDQP FPGKARWEKI
201 QQAGSVRDLE SIGGVLYAQQ WLSAGTHNGR DYALFFRQPV PKGVAEDAVL
251 IEKARAKYAE LSYSKKGLOT FFLATLLIAS LLSIFLALVM ALYFARRFVE
301 PVLSLAEGAK AVAQGDFSQT RPVLRNDEFG RLTKLFNHMT EQLSIAKEAD
351 ERNRRREEAA RHYLECVLEG LTTGVVVFDE QGCLKTFNKA AEQILGMPLT
401 PLWGSSRHGW HGVSAQQSLL AEFVFAAIGAA AGTDKPVHVK YAAPDDAKIL
451 LGKATVLPED NGNGVVMVID DITVLIHAQK EAAWGEVAKR LAHEIRNPLT
501 PIQLSAERLA WKLGGKLDEQ DAQILTRSTD TTIKQVAALK EMVEAFRNYA
551 RSPSLKLENQ DLNALIGDVL ALYEAGPCRF AAELAGEPLM MAADTTAMRQ
601 VLHNIKFNAE EAAEEADVPE VRVKSEAGQD GRIVLTVCDN GKGFGREMLH
651 NAFEPYVTDK PAGTGLGLPV VKKIIEEHGG RISLSNQDAG GACVRIILPK
701 TVETYA*

```

m258/a258 99.0% identity in 584 aa overlap

	10	20	30	40	50	60
m258.pep	MRRFLPIAAICAVVLLYGLTAAATGSTSSLAADYFWWIVAFSAML VLSAVLARYVILLK					
a258	MRRFLPIAAICAVVLLYGLTAAATGSTSSLAADYFWWIVAFSAML VLSAVLARYVILLK					
	10	20	30	40	50	60
m258.pep	70	80	90	100	110	120
a258	70	80	90	100	110	120
	130	140	150	160	170	180
m258.pep	SKSALNLAADNALGNAPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK					
a258	SKSALNLAADNALGNAPVQIDLIGAASLP GDMGRVLEHYAGSGFAQLALYNAASGKIEK					
	190	200	210	220	230	240
m258.pep	SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV					
a258	SINPHKLDQFPFGKARWEKIQRAGSVRDLESIGGVLYAQQWLSAGTHNGRDYALFFRQPV					
	250	260	270	280	290	300
m258.pep	PKGVAEDAVLIEKARAKYAE LSYSKKGLOTFFLATLLIASLLSIFLALVMALYFARRFVE					
a258	PKGVAEDAVLIEKARAKYAE LSYSKKGLOTFFLATLLIASLLSIFLALVMALYFARRFVE					
	310	320	330	340	350	360
m258.pep	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA					
a258	PVLSLAEGAKAVAQGDFSQTRPVLRNDEFGRLTKLFNHMT EQLSIAKEADERNRRREEAA					
	370	380	390	400	410	420
m258.pep	RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL					
a258	RHYLECVLEGLTTGVVVFDEQGCLKTFNKA AEQILGMPLTPLWGSSRHGW HGVSAQQSLL					
	430	440	450	460	470	480
m258.pep	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK					
a258	AEVFAAIGAAAGTDKPVHVKYAAPDDAKILLGKATVLPEDNGNGVVMVIDDITVLIHAQK					

598

	430	440	450	460	470	480
	490	500	510	520	530	540
m258.pep	EAAWGEVAKRLAHEIRNPLTPIQLSAERXAXKLGGKLDEQDAQILTRSTDTIVKQVAALK					
a258	EAAWGEVAKRLAHEIRNPLTPIQLSAERLAWKLGGKLDEQDAQILTRSTDTIIKQVAALK					
	490	500	510	520	530	540
	550	560	570	580	589	
m258.pep	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAADLPANRX					
a258	EMVEAFRNYARSPSLKLENQDLNALIGDVLALYEAGPCRFAELAGEPLMMAADTTAMRQ					
	550	560	570	580	590	600
a258	VLHNIFKNAAEAAEEADVPEVRVKSEAGQDGRIVLTVCDNGKGFGREMLHNAFEPYVTDK					
	610	620	630	640	650	660

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1029>:

g259.seq

```

1   atgatgatgc acgcttctgt ccaaagtcgt ttcgcaccga tacttttatgt
51  ttgatttttc tttgccggtt ttttgaccgc gcaaactctgg ttcaatcaga
101 aagcctatac tgaagagctg cctccgcttc tgtccgcatt gtccgccgctc
151 gcgctggtgt ggctggcgtg ggcgttcgtg tcggtgctgt caaaggctaa
201 ggagaaaaag ttctaccgcg aaaaaatgat acagaacgaa agcatatacc
251 ccgtcctgca cgcttctttg caacacttgg aacacaagcc gcaaattgctc
301 gccctgctgg tcaaaaacca cggcaaaggc atggcggaac aggtcaggtt
351 caaggcggaa gtgctgcccc acgacgaaga cgcgcgacg attgccgccg
401 agttggcaaa aatggatatg ttcgcattgg ggacggacgc ggtcgccctcg
451 ggcgaaacct atgggcgcgt gttcgccgat attttcgagt tgcggcgccg
501 tttggaaagg cgcgcggtca aagggatact gaaactgacg gcggaatata
551 aaaaacatct tcggcgatgc ctgccgttcg gaaacggcgt tggatttggg
601 cgcgctcaat caggcggtga gggaaatctc gaaaacgccg gaaaagccta
651 a

```

This corresponds to the amino acid sequence <SEQ ID 1030; ORF 259.ng>:

g259.pep

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALER RAFKGILKLT AEYKKHLRRC LPFGNGVGFG
201 RAQSGVEGNL ENAGKA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1031>:

m259.seq (partial)

```

1   ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GGC GTTCGTG TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCsTGCA CGCCTCTTGT CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCACG ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACkGACGC GGTGCCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTGCGmGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AA.AACATCT TCGGmGATGC CTGCCGTTTC GAAACGGCGT TGGAGTTGGG
601 CGCACTCAAT CAGCGTTTGC AGGAGATTTC AAAACATCC GG..

```

This corresponds to the amino acid sequence <SEQ ID 1032; ORF 259>:

m259.pep (partial)

```

1   MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVXHASL QHLEHKPQIL
101 ALLVKNHGKG MAEQVRFAE VLPDDEDART IAAELAKMDM FALGTDAVAS

```


599

151 GETYGRVFAD IFELSXALEG RAFKGMLKLT AEYKXHLRRC LPFGNGVGVG
201 RTQSGVAGDF KNIR..

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 259 shows 94.3% identity over a 212 aa overlap with a predicted ORF (ORF 259.ng) from *N. gonorrhoeae*:

m259/g259

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
g259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
	:					
g259	SVRSKAKAEKFYREKMIQNESIHPVLHASLQHLEHKPQMLALLVKNHKGKMAEQVRFKAE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSXALEGRAFKGMLKLT					
g259	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSAALERRAFKGILKLT					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKKHLRRLPFGNGVGVGRTQSGVAGDFKNIR					
g259	AEYKKHLRRLPFGNGVGFRAQSGVEGNLENAGKAX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1033>:

a259.seq (partial)

1	ATGATGATGC	ACGCTTCTGT	CCAAAGCCGT	TTCGCACCGA	TACTTTATGT
51	TTTGATTTTC	TTTGCCGGTT	TTTGACCGC	GCAAATCTGG	TTCAATCAGA
101	AAGCCTATAC	TGAAGAGCTG	CCTCCGCTTC	TGTCCGCATT	GTCCGCCGTC
151	GCGCTGGTGT	GGCTGGCGTG	GGCGTTCGTG	TCGGCGCGTT	CAAAGGCTAA
201	GGCGGAAAAG	TTCTACCGCG	AAAAAATGAT	ACAGAACGAA	AGCATACACC
251	CCGTCCTGCA	CGCTTCTTTG	CAACACTTGG	AACACAAGCC	GCAAATGCTC
301	GCCCTGCTGG	TCAAAAACCA	CGGCAAAGGG	ATGGCGGAAC	AGGTCAGGTT
351	CAAGGCGGAA	GTGCTGCCCG	ACGACGAAGA	CGCGCGCACG	ATTGCCGCCG
401	AGTTGGCAAA	AATGGATATG	TTTGCATTGG	GGACGGACGC	GGTCGCCTCG
451	GGCGAAACCT	ATGGACGCGT	GTTCCGCGAT	ATTTTCGAGT	TGTCGGCGGC
501	TTTGGAGGGG	CGCGCGTTCA	AAGGAATGTT	GAAACTGACG	GCGGAATATA
551	AAAA.CATCT	TCGGCGATGC	CTGCCGTTTC	GAAACGGCGT	TGGAGTTGGG
601	CGCGCTCAAT	CAGGCGTTGC	AGGAGATTTT	AAAAACATCG	GAAAAGTCCA
651	A				

This corresponds to the amino acid sequence <SEQ ID 1034; ORF 259.a>:

a259.pep (partial)

1	MMMHASVQSR	FAPILYVLIF	FAGFLTAQIW	FNQKAYTEEL	PPLLSALSAV
51	ALVWLAWAFV	SARSKAKAEK	FYREKMIQNE	SIHPVLHASL	QHLEHKPQML
101	ALLVKNHKGK	MAEQVRFKAE	VLPDDEDART	IAAELAKMDM	FALGTDAVAS
151	GETYGRVFAD	IFELSXALEG	RAFKGMLKLT	AEYKXHLRRC	LPFGNGVGVG
201	RAQSGVAGDF	KNIGKVQ			

m259/a259 98.1% identity in 213 aa overlap

	10	20	30	40	50	60
m259.pep	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					
a259	MMMHASVQSRFAPILYVLIFFAGFLTAQIWFNQKAYTEELPPLLSALSVALVWLAWAFV					

600

	10	20	30	40	50	60
	70	80	90	100	110	120
m259.pep	SARSKAKAEKFYREKMIQNESIHVPVXHASLQHLEHKPQILALLVKNHKGKMAEQVRFKAE					
a259	:					
	70	80	90	100	110	120
	130	140	150	160	170	180
m259.pep	VLPDDEDARTIAAELAKMDMFALGTDAVASGETYGRVFADIFELSALEGRAFKGMLKLT					
a259	:					
	130	140	150	160	170	180
	190	200	210			
m259.pep	AEYKXHLRRCCLPFGNGVGVGRTQSGVAGDFKNIR					
a259	:					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1035>:

g259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGTCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGTGCGTT CAAAGGCTAA
201 GGCAGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGC ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGGCGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAA

```

This corresponds to the amino acid sequence <SEQ ID 1036; ORF 259-1.ng>:

g259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SVRSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALE

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1037>:

m259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCCGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGGCGCGTT CAAAGGCCAA
201 GCGGAAAAG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATACTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTCGCATTGG GGACGGACGC GGTCCGCTCG
451 GGCGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCATGCC TGCCGTTCGG AAACGCGGTT GGAGTTGGGC
601 GCACTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1038; ORF 259-1>:

m259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQIL
101 ALLVKNHKGK MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDAVAS
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQLQEIS KTSEKSKRIF_Y*

```

g259-1/m259-1 98.8% identity in 169 aa overlap

601

	10	20	30	40	50	60
g259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
g259-1.pep	SVRSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGK	MAEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGK	MAEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	169	
g259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALE		
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALEGRAFGMLKLT		
	130	140	150	160	170	180

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1039>:

a259-1.seq

```

1  ATGATGATGC ACGCTTCTGT CCAAAGCCGT TTCGCACCGA TACTTTATGT
51  TTTGATTTTC TTTGCCGGTT TTTTGACCGC GCAAATCTGG TTCAATCAGA
101 AAGCCTATAC TGAAGAGCTG CCTCCGCTTC TGTCGGCATT GTCCGCCGTC
151 GCGCTGGTGT GGCTGGCGTG GCGGTTCTGT TCGCGCGGTT CAAAGGCTAA
201 GCGCGAAAGG TTCTACCGCG AAAAAATGAT ACAGAACGAA AGCATACACC
251 CCGTCTGCA CGCTTCTTTG CAACACTTGG AACACAAGCC GCAAATGCTC
301 GCCCTGCTGG TCAAAAACCA CGGCAAAGGG ATGGCGGAAC AGGTCAGGTT
351 CAAGGCGGAA GTGCTGCCCG ACGACGAAGA CGCGCGCAGC ATTGCCGCCG
401 AGTTGGCAAA AATGGATATG TTTGCATTGG GGACGGACGC GGTCGCCTCG
451 GCGGAAACCT ATGGACGCGT GTTCGCCGAT ATTTTCGAGT TGTCGGCGGC
501 TTTGGAAGGG CGCGCGTTCA AAGGAATGTT GAAACTGACG GCGGAATATA
551 AAAACATCTT CGGCGATGCC TGCCGTTCCG AAACGGCGTT GGAGTTGGGC
601 GCGCTCAATC AGGCGTTGCA GGAGATTTC AAAACATCGG AAAAGTCCAA
651 ACGGATATTT TATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1040; ORF 259-1.a>:

a259-1.pep

```

1  MMMHASVQSR FAPILYVLIF FAGFLTAQIW FNQKAYTEEL PPLLSALSAV
51  ALVWLAWAFV SARSKAKAEK FYREKMIQNE SIHPVLHASL QHLEHKPQML
101 ALLVKNHGKG MAEQVRFKAE VLPDDEDART IAAELAKMDM FALGTDASV
151 GETYGRVFAD IFELSAALEG RAFKGMLKLT AEYKNIFGDA CRSETALELG
201 ALNQALQEIS KTSEKSKRIF Y*

```

a259-1/m259-1 99.5% identity in 221 aa overlap

	10	20	30	40	50	60
a259-1.pep	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
m259-1	MMMHASVQSRFAPILYVLIF	FAGFLTAQIWFNQKAYTEEL	PPLLSALS	SAVALVWLAWAFV		
	10	20	30	40	50	60
	70	80	90	100	110	120
a259-1.pep	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQMLALLVKNHGK	MAEQVRFKAE		
m259-1	SARSKAKAEK	FYREKMIQNESIHPVLHASL	QHLEHKPQILALLVKNHGK	MAEQVRFKAE		
	70	80	90	100	110	120
	130	140	150	160	170	180
a259-1.pep	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALEGRAFGMLKLT		
m259-1	VLPDDEDARTIAAELAKMDM	FALGTD	DAVASGETYGRVFADIFEL	SAALEGRAFGMLKLT		
	130	140	150	160	170	180
	190	200	210	220		
a259-1.pep	AEYKNIFGDACRSETALEL	GALNQALQEISK	KTSEKSKRIFYX			
m259-1	AEYKNIFGDACRSETALEL	GALNQALQEISK	KTSEKSKRIFYX			
	190	200	210	220		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1041>:

g260.seq

602

```

1   atgggtgctg  gtgtagtatt  cgttgctctt  cagccgttct  tcagcctgtt
51  tcgagcggtt  ttcgagggcg  gtagtcggtat  agtcgagggg  gcgcacgatg
101 ccgctgaatg  cgacttcctt  tccgaggaat  ttacccgtat  ccggatcggt
151 gatgttttta  ttgattcggt  aggtcagata  acggcccggg  tctttcaggc
201 ctttggtgta  aaccctggcg  cctttggtgt  acagcagcct  gccttcggg
251 cccgagagca  ggcgcggcgc  ggcagcggtt  tctttgctgg  aaacgatttg
301 cgggtgctgc  ataaagacgc  ggtagaagtt  gacatcgatg  gcgggaatac
351 cgtatccgga  cacttcctta  tccggactga  ttttgacgac  ggggatgccg
401 tctgtctgtt  ccaagccgag  gcgcggttcg  ccgccaacgt  agcgcaacac
451 caatacctgg  cccggataaa  tcaggtcggt  attgtggatt  tgatcccggt
501 tcgcgcccc  caggggggga  ccattgccac  gggctgtaca  ggtatttgcc
551 cgaaataccc  cacaggggtg  cgccctgttt  ga

```

This corresponds to the amino acid sequence <SEQ ID 1042; ORF 260.ng>:

g260.pep

```

1   MGAGVVFVVF  QPFFSLFRAL  FEGGVGIVEG  AHDAAECDFL  SEEFTRIRIG
51  DVFIDSVGQI  TARFFQAFGV  NPGAQVQQP  AFRAREQARR  GSGFFAGNDL
101 RVLHKDAVEV  DIDGGNTVSG  HFLIRTDFFD  GDAVCLFQAE  ARFAANVAQH
151 QYLARINQVG  IVDLIPVRAP  QGGTIATGCT  GICPKYPTGC  RPV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1043>:

m260.seq

```

1   ATGGGTGCGG  GTATGGTATT  CGTTGTCTTT  CGGCCGTTCT  CCAGCCTGTT
51  TCGAGCGTTG  TTCGAGGACA  GAGTCGGTAT  AGTCGAGGGA  GCGCACGATG
101 CCGCTGAATG  CGACTTCCTG  CCCGAGGAAT  TTACCCGTAT  CCGGATCGGT
151 GATGTTTTTA  TTGATTCGGT  AGGTCAGGTA  GCGGCCCGGC  TCTTTCAGGC
201 CTTTGGTGTA  AACCTGGTG  CCTTGGTGT  ACAGCAGCCT  GCCTTCCGGG
251 CCCGAGwCA  sGCGCGGyGC  GGCAGCGGTT  TCTTTGCGGG  AAACGATTTG
301 CGGATGCCGC  ATAAAGATGC  GGTAGAAGTT  GACATCGATG  GCGGGAATAC
351 CGTATCCGGA  CACTTCCTTA  TCCGGACTCA  TTTTGACGAC  GGGGATGCCG
401 TCTGTCTGTT  CCAAGCCGAG  GCGCGGTTTC  CCGTCAACGT  GGCGCAACAC
451 CAATACCTGG  TCCGATAAAA  TCAGGTCGGG  ATTGTGGATT  TGATCCCGGT
501 TCGCGTyCCA  CAG

```

This corresponds to the amino acid sequence <SEQ ID 1044; ORF 260>:

m260.pep

```

1   MGAGMVVFVF  RPFSSLFRAL  FEDRVGIVEG  AHDAAECDFL  PEEFTRIRIG
51  DVFIDSVGQV  AARLFQAFGV  NPGAQVQQP  AFRARXXARX  GSGFFAGNDL
101 RMPHKDAVEV  DIDGGNTVSG  HFLIRTHFDD  GDAVCLFQAE  ARFAVNVAQH
151 QYLVIRINQVG  IVDLIPVRVP  Q

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 260 shows 89.5% identity over a 171 aa overlap with a predicted ORF (ORF 260.ng) from *N. gonorrhoeae*:

m260/g260

	10	20	30	40	50	60
m260 . pep	MGAGMVVFVFRPFFSSLFRALFEDRVGIVEGAHDAAECDFLPEEFTRIRIGDVFIDSVGQV					
g260	MGAGVVFVVFQPFSSLFRALFEGGVGIVEGAHDAAECDFLSEEFTRIRIGDVFIDSVGQI					
	10	20	30	40	50	60
m260 . pep	AARLFQAFGVNPGAQVQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
g260	TARFFQAFGVNPGAQVQPAFRAREQARRGSGFFAGNDLRVLHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
m260 . pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVIRINQVGIVDLIPVRVPQ					
g260	HFLIRTDFFDDGDAVCLFQAEARFAANVAQHQYLARINQVGIVDLIPVRAPQGGTIATGCT					
	130	140	150	160	170	180

603

g260 GICPKYPTGCRPV
190

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1045>:

a260.seq
1 ATGGGTGCGG GTATGGTATT CGTTGTCTTT CGGCCGTTCT CCAGCCTGTT
51 TCGAGCGTTG TTCGAGGACA GAGTCGGTAT AGTCGAGGGA GCGCACGATG
101 CCGCTGAATG CGACTTCCTG CCCGAGGAAT TTACCCGTAT CCGGATCGGT
151 GATGTTTTTA TTGATTCGGT AGGTCAGGTA GCGGCCCGGC TCTTTCAGGC
201 CTTTGGTGTA AACCTGGTG CCTTTGGTGT ACAGCAGCCT GCCTTCCGGG
251 CCCGAGAGCA GCGCGGCGC GGCAGCGGT TCTTTGCGGG AAACGATTTG
301 CGGGTGCCGC ATAAAGATGC GGTAGAAGTT GACATCGATG GCGGGAATAC
351 CGTATCCGGA CACTTCCTTA TCCGGA CTCA TTTTGACGAC GGGGATGCCG
401 TCTGTCTGTT CCAAGCCGAG GCGCGGTTTC CCGTCAACGT GGCGCAACAC
451 CAATACCTGG TCCAGATAAA TCAGGTCGGG ATTGTGGATT TGATCCCGGT
501 TCGCGTCCCA CAGGCGGCC CCATTGCCAC GGGCTGTACA GGTATTTGCC
551 CGAAATGCCC CACAGGGTGT CGCCCTGTTT GA

This corresponds to the amino acid sequence <SEQ ID 1046; ORF 260.a>:

a260.pep
1 MGAGMVVFVF RPFSSLFRAL FEDRVGIVEG AHDAECDFL PEEFTRIRIG
51 DVFIDSVGQV AARLFQAFGV NPGAAGVQQP AFRAREQARR GSGFAGNDL
101 RVPKDAVEV DIDGGNTVSG HFLIRTHFDD GDAVCLFQAE ARFAVNVAQH
151 QYLVQINQVG IVDLIPVRVP QAAXIATGCT GICPKCPTGC RPV*

m260/a260 97.1% identity in 171 aa overlap

	10	20	30	40	50	60
m260.pep	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGQV					
a260	MGAGMVVFVFRPFSSLFRALFEDRVGIVEGAHDAECDFLPEEFTRIRIGDVFIDSVGQV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m260.pep	AARLFQAFGVNPGAAGVQQPAFRARXXARXGSGFFAGNDLRMPHKDAVEVDIDGGNTVSG					
a260	AARLFQAFGVNPGAAGVQQPAFRAREQARRGSGFFAGNDLRVPHKDAVEVDIDGGNTVSG					
	70	80	90	100	110	120
	130	140	150	160	170	
m260.pep	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQRINQVGIVDLIPVRVPQ					
a260	HFLIRTHFDDGDAVCLFQAEARFAVNVAQHQYLVQINQVGIVDLIPVRVQAAXIATGCT					
	130	140	150	160	170	180
a260	GICPKCPTGCRPVX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1047>:

g261.seq
1 atggagcttg ggcatacgt attccttctg ctttgccgcg gttcagacgg
51 cctttttact ttccagacat tccgccagcc cgcgttcgcg caagatacacg
101 ctccggcatt cgcggcagcc gccgacgata cccttgtagc aggtgtgggt
151 ctgttcgcgg atgtagtcca acacgccccat ttcgtccgcc aacgcccacg
201 tttgcgcctt ggtcaggtac atcagcggcg tgtggatttg aaaatcgtag
251 tccatcgcca gattaagggt aacgttcatt gatttgacga acacgccgcg
301 gcagtcggga tagcccgaaa aatcgggttc gcacacgccc gcgatgatgt
351 gccggatacc ctgccctttg gcaaaaatgg cggcgtaaag caggaaaagc
401 gcgttacgcc cgtccacaaa ggtattggga acgccgttgt cggcggtttc
451 gatggcggcg gtttcgatgg cggcggtttc gtccatcagg gcgttggtgcg
501 taatctgccg catcaggctc aaatcgagta cggtttgact gacacccaaa
551 tcctgcgcga tccactctgc gcgttcacgc tcgacggcat ggcgttgccc
601 gtatcggaag gtgatggctt ggacgttttc gcgccgtag gtttggattg

651 cctgaatcag gcaggtggtc gaatcctgac cgcccagaaa gatgaccaag
701 gctttttggt ttga

This corresponds to the amino acid sequence <SEQ ID 1048; ORF 261.ng>:

g261.pep

1 MELGHIVFLV LCARSDGLFT FQTFRQPAFA QDTARAFAAA ADDTLVAGVG
51 LFADVQHAH FVRQRPRLRL GQVHQRRVDL KIVVHRQIKG NVHGFDEHAA
101 AVGIARKIGF AHARDDVPDT LPFGKNGGVK QEKRVTPVHK GIGNAVVGGF
151 DGGGFDGGGF VHQGVVRNLP HQAQIEYGLT DTQILRDPLC AFQLDGMALP
201 VSEGDLDFV APVGLDCLNQ AGGRILTARE DDQGLV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1049>:

m261.seq

1 ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51 CCTTTTACT TTCCAGATAT TCCGCCAGCC cGcGTTCCGC CAAGATACAG
101 CTCGGGCATT CGCGgCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCACGCCCAT TTCGTCCGCC AACGCCACG
201 TTTGCGCCTT GGTCAGATAC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA AATTAAGGGT AACGTTTCATC GATTGACAA ACACGTCGCG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 gCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGCATCA
501 GgCTcAAGTC GAGTACGGTT TGTTCGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTG TTGGTTTGA

This corresponds to the amino acid sequence <SEQ ID 1050; ORF 261>:

m261.pep

1 MELGHIVFLM VCACSDGLFT FQIFRQPAFA QDTARAFAAA ADDAVIAGVG
51 LLADIVQHAH FVRQRPRLRL GQIHQRRVDL KIIVHRQIKG NVHRFDKHVA
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFPVGL DCLNQAGGRI LTARKDDQGL LV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 261 shows 79.7% identity over a 237 aa overlap with a predicted ORF (ORF 261.ng) from *N. gonorrhoeae*:

m261/g261

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFQIFRQPAFAQDTARAFAAAADDAVIAGVGLLADIVQHAH					
	: :					
g261	MELGHIVFLVLCARSDGLFTFQTFRQPAFAQDTARAFAAAADDTLVAGVGLFADVQHAH					
	10	20	30	40	50	60
m261.pep	FVRQRPRLRLGQIHQRRVDLKIIVHRQIKGNVHRFDKHVA AVGIAGEVGF AHARDDVPYP					
	: : : :					
g261	FVRQRPRLRLGQVHQRRVDLKIVVHRQIKGNVHGFDEHAAAVGIARKIGFAHARDDVPDT					
	70	80	90	100	110	120
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGV-----VHQGIVRNLPHQAVEYGLF					
	: : : : :					
g261	LPFGKNGGVKQEKRVTPVHKGIGNAVVGGFDGGGFDGGGFVHQGVVRNLPHQAQIEYGLT					
	130	140	150	160	170	180
m261.pep	DAQILRNPAFTQLDGMALPVLESNGLDVFPVGLDCLNQAGGRILTARKDDQGLLVX					
	: : : : :					
g261	DTQILRDPLCAFQLDGMALPVSEGDLDFVFPVGLDCLNQAGGRILTAREDDQGLVX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1051>:

```
a261.seq
1   ATGGAGCTTG GGCATATCGT ATTCCTTATG GTTTGCGCGT GTTCAGACGG
51  CCTTTTTACT TTCCAGATAT TCCGCCAGCC CGCGTTCGCG CAAGATACAG
101 CTCGGGCATT CGCGGCAGCC GCCGACGATG CCGTTATAGC AGGTGTGGGT
151 TTGCTCGCGG ATATAGTCCA GCGCGCCCAT TTCGTCCGCC AACGCCAAG
201 TTTGCGCCTT GGTACAGATC ATCAGCGGCG TGTGGATTG AAAATCATAG
251 TCCATCGCCA GATTAAGGGT AACGTTTCATG GATTTGACAA ACACGTCACG
301 GCAGTCGGGA TAGCCGGAGA AGTCGGTTTC GCACACGCCC GCGATGATGT
351 GCCGTATCCC CTGCCCTTTG GCGTAAATCG CGGCATAGAG CAGGAAAAGC
401 GCGTTGCGGC CGTCTACAAA GGTATTCGGA ACGCCGTTTT CGGCAGTTTC
451 GATGGCGGCG GTGTCGTCCA TCAGGGCATT GTGCGTAATC TGCCGTCAC
501 GGCTCAAGTC GAGTACGGTT TGTGTTGACGC CCAAATCCTG CGCAATCCAG
551 CGGGCACGTT CCAGCTCGAC GGCATGGCGT TGCCCGTATT GGAAAGTAAT
601 GGCTTGGACG TTTTCGCGCC CGTAGGTTTG GATTGCCTGA ATCAGGCAGG
651 TGGTCGAATC CTGACCGCCC GAAAAGATGA CCAAGGCTTT TTGGTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1052; ORF 261.a>:

```
a261.pep
1   MELGHIVFLM VCACSDGLFT FOIFRQPAFA QDTARAFAAA ADDAVIAGVG
51  LLADIVQRAH FVRQRPSLRL GQIHQRRVDL KIIVHRQIKG NVHGFDPKHVT
101 AVGIAGEVGF AHARDDVPYP LPFGVNRGIE QEKRVAAVYK GIRNAVFGSF
151 DGGGVVHQGI VRNLPHQAV EYGLFDAQIL RNPAGTFQLD GMALPVLESN
201 GLDVFAFVGL DCLNQAGGRI LTARKDDQGF LV*
```

m261/a261 97.8% identity in 232 aa overlap

	10	20	30	40	50	60
m261.pep	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
a261	MELGHIVFLMVCACSDGLFTFOIFRQPAFAQDTARAFAAAADDAVIAGVG	LLADIVQRAH				
	70	80	90	100	110	120
m261.pep	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHREFDKHVA	AVGIAGEVGF	AHARDDVPYP			
a261	FVRQRPSLRLGQIHQRRVDLKIIVHRQIKGNVHREFDKHVT	AVGIAGEVGF	AHARDDVPYP			
	130	140	150	160	170	180
m261.pep	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
a261	LPFGVNRGIEQEKRVAAVYKGIRNAVFGSFDGGGVVHQGIVRNLPHQAV	EYGLFDAQIL				
	190	200	210	220	230	
m261.pep	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					
a261	RNPAGTFQLDGMALPVLESNGLDVFAFVGLDCLNQAGGRILTARKDDQGLLVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1053>:

```
g263.seq
1   atggcacgtt taaccgtaca caccctcgaa accgccccg aagccgccaa
51  accgcgcgta gaggccgtac ccaaaaacaa cggctttatc ccaacctca
101 tcggcgattt ggcaaacgcc cccgaagctt tggcgtttta ccaagaagtc
151 ggcaagctca acgcccgaac cagcctgacc gccggcgaag tcgaagtgat
201 ccgatcatc gccgtccgca ccaaccaatg cagctctctg gtggcagggc
251 acaccaaaact cgcaaccctg aaaaaactcc tgtccgagca atccctcaat
301 gccgcccgcg ctttgccggc aggtaaatct gacgatgcca aactcggcgc
351 gcttgccgcc ttcaccaag ccgtaatggc gaaaaaaggc gcagtatccg
401 acgacgaact caacgccttc ctccaagcgg gctacaaccg gcagcaggca
```

g263.pcp

```

1  MARLTVHTLE TAPEAAKPRV EAVPKNNGFI PNLIGVLANA PEALAFYQEV
51  GKLNAANSLT AGEVEVIRII AVRTNQCSFC VAGHTKLATL KKLLSEQSLN
101 AARALAAGKS DDAKLGALAA FTQAVMAKKG AVSDDELNAF LEAGYNRQQA
151 VEVVMGVALA TLCNYANNLA QTEINPKLQA YA*

```

m263.seq (partial)

```

1      . . GCAGCAGGCG AATTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51     CCAAGCCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCTA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151    GGCGT . AsyC TgCGAACCTT GTGCAACTAC GTCAACAACC TCGGACAAAC
201    CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

m263.pep (partial)

```

1      . . GCAGCAGGCG AATTGACGA TGCCAAACTC GGCGCGCTCG CCGCCTTCAC
51     CCAGGCGCGTA ATGGCGAAAA AAGGCGCGGT ATCCGACGAG GAACTCAAAG
101    CATTTTTCTA TGCGGGCTAC AACCAGCAGC AGGCAGTCGA AGTCGTGATG
151    GGCGT . AsyC TgGCAACCTC GTGCAACTAC GTCAACAACC TCGGACAAAC
201    CGAAATCAAC CCCGAATTGC AGGCTTACGC CTGA

```

ORF 263 shows 85.7% identity over a 77 aa overlap with a predicted ORF (ORF 263.ng) from *N. gonorrhoeae*:

m263/g263

```

                                10      20      30
m263.pep                      AAGEFDDAKLGALAAFTQAVMAKKGAVSDE
                                |||: ||||| ||||| ||||| ||||| |||||
g263      QCSFCVAGHTKLATLKKLLSEQSLNAARALAAAGKSDDAKLGALAAFTQAVMAKKGAVSDD
              80      90      100      110      120      130

              40      50      60      70
m263.pep      ELKAFFDAGYNQQQAVEVVMGVXLATLCNYVNNLQGTEINPELQAYAX
              ||: ||: |||: ||||| ||||| ||||| ||||| ||||| |||||
g263      ELNAFLEAGYNRQQAVEVVMGVVALATLCNYANNLAQTEINPKLQAYAX
              140      150      160      170      180

```

a263.seq

1	ATGGCACGTT	TAACCGTACA	CACCCTCGAA	ACCGCCCCCG	AAGCCGCCAA
51	AGCGCGCGTC	GAGGCGGTAC	TTCAAAACAA	CGGCTTTATC	CCCAACCTTA
101	TGGCGGTATT	ATCAAACGCG	CCCGAAGCCT	TGGCGTTTTA	CCAGAAGTTC
151	GCGAAGCTCA	ACGCGGCCAA	CAGCCTGACC	GCCGGCGAAG	TCGAAGTAAT
201	CCAGATTATT	GCCGCGCGCA	CCAACCAATG	CGGCTTCTGC	TGGCAGGGC
251	ACACCAAACCT	CGCAACCCCTG	AAAAAACTCC	TTCCGAACA	ATCCGTCAAA
301	GCCGCGCGCG	CTTTGGCGGC	AGGCGAATTT	GACGATGCTA	AACTCGGCGC
351	GCTCGCGCGC	TTTACCCAAG	CCGTAATGGC	AAAAAAAAGC	GCGGTATCCG
401	ACGAGGAACCT	CAAAGCATTT	TTTGATGCGG	GCTACAACCA	GCAGCAGGCA
451	GTCGAAGTCG	TGATGGGCGT	AGCTTGGA	ACTTTGTGCA	ACTACGTCAA
501	CAACCTCGGA	CAAACCGAAA	TCAACCCCGA	ATTGAGGCT	TACGCCTGA

a263.pep

```

1  MARLTVHTLE TAPEAAKARV EAVLQNNGFI PNLIGVLSNA PEALAFYQEV
51  GKLNAANSLT AGEVEVIQII AARTNQCGFC VAGHTKLATL KLLSEQSVK
101 AARALAAGEF DDAKLGALAA FTQAVMAKKG AVSDEELKAF FDAGYNQQQA
151 VEVVMGVALA TLCNYVNNLG QTEINPELOA YA*

```


The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1059>:

This corresponds to the amino acid sequence <SEQ ID 1060; ORF 264.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1061>:

This corresponds to the amino acid sequence <SEQ ID 1062; ORF 264>:

m264.pep

1	<u>LTLTRKTLFL</u>	<u>LTAAFGTHSL</u>	<u>QTASADAVVK</u>	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGF	FHGRKTSNGE	RYDMNAFTAA	HKTLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FSGNRIIDVS	KAAAQKLGFV	NQGTAVHKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFNGTEHAQ	AYLNQAAQNF	AVSSSGTNLS
201	VEKRRYEYVV	KMGPFSTQER	AAEAQAQARG	MVRAVLTAG*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 264 shows 91.6% identity over a 239 aa overlap with a predicted ORF (ORF 264.ng) from *N. gonorrhoeae*:

m264/g264

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
g264	LTLTRKTLFLLTAAFGTHSLQTASADAVVKPEKLHASANRSYKVA-----EFTQ					
	10	20	30	40		
	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHFGRKTS GGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
g264	TGNASWYGGRFHFGRKTS GGDRYDMNAFTA AHKTLPIPSHVRVTNTKNGKSVIVRVNDRGP					
	50	60	70	80	90	100
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAA AQLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
g264	FHGNRIIDVSKAA AQLG FVSQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFSGTEHEAQ					
	110	120	130	140	150	160
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVR AVLTAGX					
g264	AYLNQAAQNFAASSSPNLSVEKRRYEYVVKMGPF ASQERAAEAE AQARGMVR AVLTSGX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1063>:

a264 . seq

1	TTGACTTTAA	CCC GAAAAAC	CCTTTTCCTC	CTCACC GCGC	CATT CGGCAT
51	ACATTCCTTT	CAGACGGCAT	CCGCCGACGC	AGTGGTCAGG	GCAGAAAAAC
101	TGCACGCCTC	CGCCAACCGC	AGCTACAAAG	TCGCCGGA	ACGCTACACG
151	CCGAAAAACC	AAGTCGCCGA	ATTACGCAA	ACCGGCAACG	CCTCGTG GTA
201	CGGCGGCAGG	TTTCACGGGC	GCAAACTTC	CGGCGGAGAA	CGATACGATA
251	TGAACGCCTT	TACCGCCGCC	CACAAAACCC	TGCCCATCCC	CAGCTATGTG
301	CGCGTAACCA	ATACCAAAAA	CGGCAAAAGC	GTCATCGTCC	GCGTCAACGA
351	CCGCGGCCCC	TTCCACGGCA	ACCGCATCAT	CGACGTATCC	AAAGCCGCGG
401	CGCAAAATTT	GGGCTTTGTC	AACCAAGGGA	CGGCGCACGT	CAAAATCGAA
451	CAAATCGTCC	CGGCGCAATC	CGCACC GGTT	GCCGAAAACA	AAGACATCTT
501	CATCGACTTG	AAATCTTTTCG	GTACGGAACA	CGAAGCACAA	GCCTATCTGA
551	ACCAAGCCGC	CCAAAACCTG	GCTTCATCGG	CATCAAACCC	GAACCTCTCG
601	GTTGAAAAAC	GCCGTTACGA	ATACGTCGTC	AAAATGGGAC	CGTTTGCCCTC
651	GCAGGAACGC	GCCGCCGAGG	CCGAAGCTCA	GGCGCGCGGT	ATGGTTCGGG
701	CGGTATTAAC	CGCCGGTTGA			

This corresponds to the amino acid sequence <SEQ ID 1064; ORF 264.a>:

a264 . pep

1	LTLTRKTLFL	LTA AFGIHSF	QTASADAVVR	AEKLHASANR	SYKVAGKRYT
51	PKNQVAEFTQ	TGNASWYGGR	FHGRKTS GGE	RYDMNAFTA	AHKLPIPSYV
101	RVTNTKNGKS	VIVRVNDRGP	FHGNRIIDVS	KAAAQKLGFV	NQGT AHVKIE
151	QIVPGQSAPV	AENKDIFIDL	KSFGTEHEAQ	AYLNQAAQNL	ASSASNPNLS
201	VEKRRYEYV	KMGPFASQER	AAEAE AQARG	MVRAVLTAG*	

m264/a264 96.2% identity in 239 aa overlap

	10	20	30	40	50	60
m264 . pep	LTLTRKTLFLLTAAFGTHSLQTASADAVVKA EKLHASANRSYKVAGKRYTPKNQVAEFTQ					
a264	LTLTRKTLFLLTAAFGIHSFQTASADAVVRAEKLHASANRSYKVAGKRYTPKNQVAEFTQ					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m264 . pep	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
a264	TGNASWYGGRFHGRKTSGGERYDMNAFTA AHKTLPIPSYVRVTNTKNGKSVIVRVNDRGP					
	70	80	90	100	110	120
	130	140	150	160	170	180
m264 . pep	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFGEHEAQ					
a264	FHGNRIIDVSKAAQKLG FVNQGT AHVKIEQIVPGQSAPVAENK DIFIDLKSFGEHEAQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m264 . pep	AYLNQAAQNFAVSSSGTNLSVEKRRYEYVVKMGPF TSQERAAEAE AQARGMVRVLTAGX					
a264	AYLNQAAQN LASSASNPNLSVEKRRYEYVVKMGPFASQERAAEAE AQARGMVRVLTAGX					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1065>:

```

m265 . seq
  1  ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCCGCTTG
 51  GCGCGGGCTG ATGATTTTGT CTTGTTTGTG GTGTTGGTGT GCGGCGTGTC
101  CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGCGC GGGGGCGGAA
151  ATGCTCAGCA GTGCGGTTGC GCGGAGGTC AAGAGAAGGT GTTTGATGTT
201  CATAT .TTTT GCCTTTGTAA ATCGTGGGTT GGAAAATGTG GATATTAATA
251  AGGTATCAAA TAACCGTCAG CCGGCGGTCA ATACCGCCCG AACCATACCG
301  CGCGCCTGAG CTTCGGCTTC GCGGCGCGCT TCCTGCGAGG TAAACGGTCC
351  CATTTTGACG ACGTATTCGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1066; ORF 265>:

```

m265 . pep
  1  MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
 51  MLSSAVAAEV KRRCLMFI XF AFVNRGLENV DINKVSNRQ PAVNTARTIP
101  RAXASASAAR SCEVNGPILT TYS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 265 shows 88.6% identity over a 123 aa overlap with a predicted ORF (ORF 265.ng) from *N. gonorrhoeae*:

m265/g265	10	20	30	40	50	60
m265 . pep	MSVILPPTRANA AFSAWARLMILSCLLCWCAACPWSSSPCPSWWASAGAEMLSSAVAAEV					
g265	MSVILPPTRAQA AFSAWARLMILSCLPCWCAACPWSSSPCPSWWASAGAEMPNSAVAAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m265 . pep	KRRCLMFI XFAFVNRGLENV DINKVSNRQPAVNTARTIPRAXASASAARSCEVNGPILT					
g265	KRRCLMFI -FALVNQGLKNGDINKVSNRQPEVSTARTIPRACASASAARSCEANGPILT					
	70	80	90	100	110	
m265 . pep	TYSX					
g265	TYSX					
	120					

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1067>:

a265.seq

```

1   ATGTCGGTGA TTTTGCCGCC GACACGCGCC AACGCTGCTT TTTCGGCTTG
51  GCGCGGGCTG ATGATTTTGT CTTGTTTGCT GTGTTGGTGT GCGGCGTGTC
101 CGTGGTCGTC ATCGCCGTGT CCGTCGTGGT GGGCGAGTGC GGGGGCGGAA
151 ATGCCCATCA GTGCGGTTGC GCGGCGGGTC AAGAGAAGGC GTTTGAAGTT
201 CATTTTGTCT CCTGCGAAGT ATCTGGT... . . . . GGTGT TTGAAGGACG
251 TAAAGGCGGG ACATCAACCG GCGGTTAATA CCGCCCGAAC CATACCGCGC
301 GCCTGAGCTT CGGCCTCGGC GCGCGGTTCC TCGAGGCAA ACGGTCCCAT
351 TTTGACGACG TATTCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1068; ORF 265.a>:

a265.pep

```

1   MSVILPPTRA NAAFSAWARL MILSCLLCWC AACPWSSSPC PSWWASAGAE
51  MPISAVAAAV KRRRLKFIFA PAKYLX..XC LKDVKAGHQP AVNTARTIPR
101 A*ASASAARS CEANGPILTT YS*

```

m265/a265 79.7% identity in 123 aa overlap

	10	20	30	40	50	60
m265.pep	MSVILPPTRANA	AFSAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	LSSAVAAEV
a265	MSVILPPTRANA	AFSAWARLMIL	SCLLCWCAAC	PWSSSPCPS	WWASAGAEM	PISAVAAAV
	10	20	30	40	50	60
	70	80	90	100	110	120
m265.pep	KRRCLMFI	XFVNRGLEN	VDINKVSN	RQPAVNT	ARTIPRAX	ASASAARS
a265	KRRRLKFI	---FAPAK	YLXCLKDV	KAGHQPAV	NTARTIPR	AXASASAARS
	70	80	90	100	110	
m265.pep	TYSX					
a265	TYSX					
	120					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1069>:

g266.seq

```

1   agttcagacg gcatcgccgc cgacaatgcc caaacagaaa gcccatcatg
51  accgcatcca tgtacatcct tttggtcttg gcactcatct ttgccaacgc
101 ccccttcctc acgaccagac tgctcgccgt ggccgcgctc aagcgcaaac
151 atttcggaca ccacctgate gagctggcgg cagggtttcgc gctgaccgcc
201 tctcttgccct acatcctcga atcccgtagc ggagcggtag acaatcaggg
251 ttggggagttt tacgccaccg tcgtctgcct gtacctcatt ttcgccttc
301 cgtggttcgt gcggcggtat tttggcaca cgcgcaacag ggaataa

```

This corresponds to the amino acid sequence <SEQ ID 1070; ORF 266.ng>:

g266.pep

```

1   MQFRRHRRRQ CPNRKPIMTA SMYILLVLAL IFANAPFLT RTLVGVAALKR
51  KHFGHHLIEL AAGFALTASL AYILESRAGA VHNQGWEFYA TVVCLYLIFA
101 FPCFVRRYFW HTRNRE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1071>:

m266.seq

```

1   ATGCCGTTCC GCAACGCGtT cAGACGGCAT CGCCGCCGAC AACGCCTAAA
51  CAGAAAGCCC ACCATGACCG CATCCATGTA CATCCTTTTG GTCTTGGCAC
101 TCATCTTTGC CAACGCCCCC TTCCTCACGA CCAGACTGTT CGGCGTGGCC
151 rCACTCAAGC GCAAACATTT CGGACACCAC ATGATCGAGC TGGCGGCAGG
201 TTTGCGGCTG ACCGCCGTTT TTGCTACAT CCTsGAATCC CGTGACAGGAT
251 CCGTACACGA TCAGGGTTGG GAGTTTATG CCACAGTCGT CTGCTGTAC
301 CTGATTTTGT CGTTTCCATG TTTTGTGTGG CCGTATTTTT GGCACACGCG
351 CAACAGGGAA TAG

```

This corresponds to the amino acid sequence <SEQ ID 1072; ORF 266>:

```
m266.pep
  1  MPFRNAFRRH RRRQRLNRKP TMTASMYILL VLALIFANAP FLTTRLFGVA
 51  XLKRKHFGHH MIELAAGFAL TAVLAYILES RAGSVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 266 shows 92.1% identity over a 114 aa overlap with a predicted ORF (ORF 266.ng) from *N. gonorrhoeae*:

```
m266/g266

      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||
g266      MQFRRHRRRQCPNRPIMTASMYILLVLALIFANAPFLTTRLFGVAALKRKHFGHH
          10      20      30      40      50

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW E FYATVVCLY LIFAFPCFVW RYFWHTRNREX
          : |||||
g266      LIELAAGFALTASLAYILES RAGAVHNQGW E FYATVVCLY LIFAFPCFVW RYFWHTRNREX
          60      70      80      90     100     110
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1073>:

```
a266.seq
  1  ATGCCGTTCC GCAATGCGTT CAGACGGCAT CGCCGCCGAC AATGCCCAAA
 51  CAGAAAGCCC GCCATGACCG CATCCATGTA CATCCTTTTG CTGCTTGCCT
101  TGATTTTTCG CAACGCCCCC TTCCTCACGA CCAAGCTGTT CGGCATCGTA
151  CCGCTCAAGC GCAAACATTT CGGACACCAC CTGATCGAGC TGGCGGCAGG
201  TTTCGCGCTG ACCGCCGTTT TTGCCTACAT CCTCGAATCC CGTGCGGGAG
251  CGGTACACGA TCAGGGTTGG GAGTTTTACG CCACCGTCGT CTGCCTGTAC
301  CTGATTTTTC CGTTTCCCTG TTTCGTGTGG CGGTATTTT GGCACACGCG
351  CAACAGGGAA TAG
```

This corresponds to the amino acid sequence <SEQ ID 1074; ORF 266.a>:

```
a266.pep
  1  MPFRNAFRRH RRRQCPNRKP AMTASMYILL LLALIFANAP FLTTKLFGIV
 51  PLKRKHFGHH LIELAAGFAL TAVLAYILES RAGAVHDQGW EFYATVVCLY
101  LIFAFPCFVW RYFWHTRNRE *
```

m266/a266 91.7% identity in 120 aa overlap

```
      10      20      30      40      50      60
m266.pep  MPFRNAFRRHRRRQRLNRKPTMTASMYILLVLALIFANAPFLTTRLFGVAXLKRKHFGHH
          |||||
a266      MPFRNAFRRHRRRQCPNRPAMTASMYILLLLALIFANAPFLTTLKLFIVPLKRKHFGHH
          10      20      30      40      50      60

      70      80      90     100     110     120
m266.pep  MIELAAGFALTAVLAYILES RAGSVHDQGW E FYATVVCLY LIFAFPCFVW RYFWHTRNRE
          : |||||
a266      LIELAAGFALTAVLAYILES RAGAVHDQGW E FYATVVCLY LIFAFPCFVW RYFWHTRNRE
          70      80      90     100     110     120

m266.pep  X
          |
a266      X
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1075>:

```
g267.seq
```

g267 . pep

1 MQVAFFLAVV FKNMGFHNRI GRAGLFAETA EDALGQVDVV TLGAAGAVFA
51 FFRFDVDRHC RTHRLAQFTR DAAFLSVRKT ALRVQTAETH GLRRFLFGKI
101 NCVFAGKKVF ERYAHAFDQF AKQKGFY*

m267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGCATC	AGTCGGGCAT	GCCTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGGT	CGATGTCGTA	ACGCTTGGTG	CGGCGCGTAC	CGTCTTCACG
151	TTCTTCCGAT	TCGATGTTAA	TCGCCATTGC	CGGACACACT	GCCTCACACA
201	ACTTACACGC	GATACACCGC	TCTTCGCCGT	TCGGATACCG	CcGCTGCGCG
251	TGCAGACCGC	GGAAACGCAC	GGATTTCGGC	GTTTCTCTTT	CGGGGAAATA
301	AATTGTGTCT	TTGCGGGCGA	AAAAGTTTTT	GAGCCTTACG	CCCATACCTT
351	TTACCAATTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

m267.pcp

1 VQVAFFLAVV FKNMGFHNRI SRACLFAETA EDALGQVDVV TLGAARTVFT
51 FFRFDVNRHC RTHCLTQLTR DTPLFAVRIP PLRVQTAETH GLRRFLFGEI
101 NCVFAGEKVF ERYAHTFYQF AKQKGFY*

Homology with a predicted ORF from *N. gonorrhoeae*

m267/g267

		10	20	30	40	50	60
m267.pep		VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDV	VLTGAARTVFTFFRFDVNRHC			
		:					
g267		MQVAFFLAVVFKNMGFHNRI	GRAGLFAETAEDALGQVDV	VLTGAAGAVFAFFRFDVDRHC			
		:					
		10	20	30	40	50	60
		70	80	90	100	110	120
m267.pep		RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
			: : : :	: : :			
g267		RTHRLAQFTRDAAPLSVRK	TALRVQTAETHGLRRFLFGK	INCVFAGKKVFERIAHAFDQF			
			: : : :	: : :			
		70	80	90	100	110	120
m267.pep		AKQKGFYX					
g267		AKQKGFYX					

a267.seq

1	GTGCAAGTCG	CCTTTTTTCT	CGCCGTGGTA	TTCAAAAATA	TGGGTTTCCA
51	CAATCGACAT	GGTCGGGCAG	GCTTCTTCGC	AGAAACCGCA	GAAGATGCAC
101	TTGGTCAGCT	CGATGTCGTA	ACGCTTTGGT	CGGC CGCTGC	CGTCTTCGCG
151	TTCTTCGAT	TCGATGTTGA	TCGCCATTGC	GGGGCAACG	GCTTCACACA
201	ATTTACACGC	GATGCAGCGT	TCCTCGCCGT	TTGGATAACG	GGCTTGC GCG
251	TGCAGACCGC	GGAAACGCAC	GGATTTCGGC	GTTTCTCTTT	CGGGAAAATA
301	AATCGTGTCT	TTGCGGGCAA	AAAAGTTTTT	GAGCTGTTACG	CCCATACCTT
351	TTACCAATTTC	GCCAAGCAGA	AAGGTTTTTA	CTAA	

This corresponds to the amino acid sequence <SEQ ID 1080; ORF 267.a>:

```
a267.pep
  1  VQVAFFLAVV FKNMGFHNRI GRAGFFAETA EDALGQVDVV TLGAARAVFA
 51  FFRFDVDRHC GANGFTQFTR DAAFLAVWIT ALRVQTAETH GLRRFLFGKI
101  NRVFAGKKVF ERYAHTFYQF AKQKGFY*
```

m267/a267 82.7% identity in 127 aa overlap

	10	20	30	40	50	60
m267.pep	VQVAFFLAVVFKNMGFHNRI	SRACLFAETAEDALGQVDVV	TLGAARTVETFFRFDVNRHC			
a267	VQVAFFLAVVFKNMGFHNRI	GRAGFFAETAEDALGQVDVV	TLGAARAVFAFFRFDVDRHC			
	10	20	30	40	50	60
	70	80	90	100	110	120
m267.pep	RTHCLTQLTRDTPLFAVRIP	PLRVQTAETHGLRRFLFGE	INCVFAGEKVFERYAHTFYQF			
	:::	:::				
a267	GANGFTQFTRDAAFLAVWIT	ALRVQTAETHGLRRFLFGK	INRVFAGKKVFERYAHTFYQF			
	70	80	90	100	110	120
m267.pep	AKQKGFYX					
a267	AKQKGFYX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1081>:

```
G268.seq
  1  atgaaaaaaaa atttaccgc actggcattg gcaagtatgc tgattttgtc
 51  gggctgcgac cgtttgggaa taggcaacc gttttccgga aaggaaat
101  cctgcggaag cgaagagact aaagagattt tggcctaaact ggtccgcgac
151  aatgtcgaag gtgaaaccgt caaaactttt gacgacgacg cattcaaaga
201  ccaagcattt gccgatatcg gcatatcgca tatccgcaga atggtcgaac
251  gtttgggcat aaccgtcgat gaagtccgaa ctaccgagaa aaccgacacg
301  tccagcaaac tcaaatgtga agccgcgtta aaactggacg tgcccagcga
351  tgtgtcgat tatgccgtcg ccgccaacca atctataggc aacagccata
401  agaaaacgcc cgactttttt gaaccctact accgcaaaga aggcgcgtat
451  tatgtcaaaa ctattttcta cagcgtccag ccgacagacg acaaaagcaa
501  aatctttgcc gaactcagtc aggcacacga tatcatccat ccgctcagcg
551  agctggtgtc tatggcactg attaaagagc cgttggacaa agcgaaacaa
601  aggaacgaaa aacttgaagc ggcagaagcc accgcgcagg aagcgaggga
651  ggcagaagaa gcggcggcgc aggaggcatt gggtcgggag caggaagccg
701  cccgcgtatc cgaatgggaa gaacgctaca agctgtcgcg cagcgagttc
751  gagcagtttt ggaaaggatt gcctcaaact gtacagaata agctgcaagc
801  ctgcagaaaa acatggaaaa gcggtatgga caagatctgt gccaacaatg
851  cgaaagccga aggtgaaacg ccaaacggca taaaagtcag tgagttggcg
901  tgtaaaacgg cagaaaccga agcacgcttg gaagagctgc acaaccgtaa
951  aaaagccctt atcgacgaaa tggtcagggg agaggacaag aaagaactgc
1001 caaagcggct ctga
```

This corresponds to the amino acid sequence <SEQ ID 1082; ORF 268.ng>:

```
m268.pep
  1  MKKNLPALAL ASMLILSGCD RLGIGNPFSG KEISCGSEET KEILVKLVRD
 51  NVEGETVKTF DDDAFKDQAF ADIGISHIRR MVERLGITVD EVRTTEKTD
101  SSKLKCEAAL KLDVPDDVDV YAVAAQSIG NSHKKTPDFF EPYYRKEGAY
151  YVKTISYSVQ PTDDKSKIFA ELSQAHDIIH PLSELVSMAL IKEPLDKAKQ
201  RNEKLEAAEA TAQEAREAE AAQAEALGRE QEAARVSEWE ERYKLSRSEF
251  EQFWKGLPQT VQNKLQASQK TWKSGMDKIC ANNAKAEGET PNGIKVSELA
301  CKTAETEAREL EELHNRKKAL IDEMVREEDK KELPKRL*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1083>:

```
m268.seq (partial)
  1  ..ATGGCACTGA TTAAAGAGCC GTTGACAAA GTGAAACAAA GGAACGAAGA
```

614

```

51   ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101  AGGAAGCCGC CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151  AG.CAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201  GCTGCAACCn TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251  CCAACAATGC GAAAGCTGAA GGTAAAACGC CAAACGGCAT AAAATTCAGC
301  GAACTGGCAT GCAAAACGGC GAAAACCGAA GCACGCTTGG AAGAGCTGCA
351  CAACCGTAAA AAAGCCCTTA TCGACGAAAT GGyCAGGGAA GCGGACAmGA
401  AAGAACTGTC AAAGCGGCTs TGA

```

This corresponds to the amino acid sequence <SEQ ID 1084; ORF 268>:

```

m268.pep (partial)
1   .MALIKEPLDK VKQRNEELEA AEEAAAQEAL GREQEAAARVS EWEERYKLSR
51  XQFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GKTPNGIKFS
101 ELACKTAKTE ARLEELHNRK KALIDEMXRE ADXKELSKRL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 268 shows 86.0% identity over a 150 aa overlap with a predicted ORF (ORF 268.ng) from *N. gonorrhoeae*:

m268/g268

```

                                10      20
m268.pep                      MALIKEPLDKVKQRNEELEAAE-----
                                |||:|||:|||:|||:|||:|||:|||:|||
g268      SVQPTDDKSKIFAELSQAHDIIHPLSELVSMALIKEPLDKAKQRNEKLEAAEATAQEARE
          160      170      180      190      200      210

                                30      40      50      60      70      80
m268.pep  - -EAAAQEALGREQEAAARVSEWEERYKLSRSQFEQFWKGLPQTQVQNKLP SQKTWKSMD
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      AEEAAAQEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTQVQNKLPQASQKTWKSMD
          220      230      240      250      260      270

                                90      100     110     120     130     140
m268.pep  KICANNAKAE GKTPNGIKFSELACKTAKTEARLEELHNRKKALIDEMXREADXKELSKRLX
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g268      KICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDEMVREEDKKELPKRLX
          280      290      300      310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1085>:

```

a268.seq
1   ATGGCACTGA TTAAAGAGCC GTTGGACAAA GCGAAACAAA GGAACGAAGA
51  ACTTGAAGCG GCAGAAGAAG CGGCGGCGCA GGAGGCATTG GGTCGGGAGC
101 AGGAAGTCGA CCGCGTATCC GAATGGGAAG AACGCTACAA GCTGTCGCGC
151 AGCGAGTTCG AGCAGTTCTG GAAAGGATTG CCTCAAACCG TACAGAATAA
201 GCTGCAAGCC TCACAGAAAA CATGGAAAAG CGGGATGGAT AAAATCTGTG
251 CCAACAATGC GAAAGCTGAA GGTGAAACGC CAAACGGCAT AAAATTCAGC
301 GAACTGGCAT GCAAAACGGC GGAAACCGAA GCACGCTTGG AAGAGCTGCA
351 CAACCGTAAA AAAGCCCTTC TCGACGAAAT GGCCAGGGAA GCGGACAAGA
401 AAGAACTGCC AAAGCGGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1086; ORF 268.a>:

```

a268.pep
1   MALIKEPLDK AKQRNEELEA AEEAAAQEAL GREQEVDRVS EWEERYKLSR
51  SEFEQFWKGL PQTQVQNKLP SQKTWKSMD KICANNAKAE GETPNGIKFS
101 ELACKTAETE ARLEELHNRK KALLDEMARE ADKKELPKRL *

```

m268/a268 91.4% identity in 140 aa overlap

```

                                10      20      30      40      50      60
m268.pep  MALIKEPLDKVKQRNEELEAAEAAAQEALGREQEAAARVSEWEERYKLSRXQFEQFWKGL
          |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
a268      MALIKEPLDKAKQRNEELEAAEAAAQEALGREQEVDRVSEWEERYKLSRSEFEQFWKGL

```


615

	10	20	30	40	50	60
	70	80	90	100	110	120
m268 . pep	PQTVQNKLPQSQKTWKS	GMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRK				
a268	PQTVQNKLPQASQKTWKS	GMDKICANNAKAEGETPNGIKFSELACKTAETEARLEELHNRK				
	70	80	90	100	110	120
	130	140				
m268 . pep	KALIDEMXREADXKELSKRLX					
a268	KALLDEMAREADKKELPKRLX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1087>:

m268-1 . seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGTGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG CCGCCCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTAAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGAAAAC CGAAGCACGC TTGGAAGAGC
401 TGCACAACCG TAAAAAAGCC CTTATCGACG AAATGGCCAG GGAAGCGGAC
451 AAGAAAGAAC TGTCAAAGCG GCTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1088; ORF 268-1>:

m268-1 . pep

```

1  VQSRDGLHK FKHICSAAMA LIKEPLDKVK QRNEELEAAE EAAAEALGR
51  EQEAARVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLPQAS KTWKSGMDKI
101 CANNAKAEGK TPNGIKFSEL ACKTAKTEAR LEELHNRKKA LIDEMAREAD
151 KKELSKRL*

```

m268-1/g268 82.3% identity in 164 aa overlap

		10	20	30
m268-1 . pep		VQSRDGLHKFKHICSAAMALIKEPLDKVKQRNE		
g268	KEGAYYVKTISYSVQPTDDKSKIFAELSQAHDIIHPLSELVS--MALIKEPLDKAKQRNE			
	150	160	170	180
	190	200		
	40	50	60	70
m268-1 . pep	ELEAAE-----EAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
g268	KLEAAEATAQEAREAEAAAEALGREQEAAARVSEWEERYKLSRSEFEQFWKGLPQTVQN			
	210	220	230	240
	250	260		
	90	100	110	120
m268-1 . pep	KLQASQKTWKSMDKICANNAKAEGKTPNGIKFSELACKTAKTEARLEELHNRKKALIDE			
g268	KLQASQKTWKSMDKICANNAKAEGETPNGIKVSELACKTAETEARLEELHNRKKALIDE			
	270	280	290	300
	310	320		
	150	159		
m268-1 . pep	MAREADKKELSKRLX			
g268	MVREEDKKELPKRLX			
	330			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1089>:

a268-1 . seq

```

1  GTGCAATCCC GATATGATGG TTTGCATAAA TTAAACATA TATGTTCCGC
51  AGCTATGGCA CTGATTAAAG AGCCGTTGGA CAAAGCGAAA CAAAGGAACG
101 AAGAACTTGA AGCGGCAGAA GAAGCGGCGG CGCAGGAGGC ATTGGGTCGG
151 GAGCAGGAAG TCGACCGCGT ATCCGAATGG GAAGAACGCT ACAAGCTGTC
201 GCGCAGCGAG TTCGAGCAGT TCTGGAAAGG ATTGCCTCAA ACCGTACAGA
251 ATAAGCTGCA AGCCTCACAG AAAACATGGA AAAGCGGGAT GGATAAAATC
301 TGTGCCAACA ATGCGAAAGC TGAAGGTGAA ACGCCAAACG GCATAAAATT
351 CAGCGAACTG GCATGCAAAA CGGCGGAAAC CGAAGCACGC TTGGAAGAGC

```

616

401 TGCACAACCG TAAAAAGCC CTTCTCGACG AAATGGCCAG GGAAGCGGAC
 451 AAGAAAGAAC TGCCAAAGCG GCTCTGA

This corresponds to the amino acid sequence <SEQ ID 1090; ORF 268-1.a>:

a268-1.pep

1 VQSRDGLHK FKHICSAAMA LIKEPLDKAK ORNEELEAAE EAAAEALGR
 51 EQEVDVSEW EERYKLSRSE FEQFWKGLPQ TVQNKLASQ KTWKSGMDKI
 101 CANNAAEGE TPNGIKFSEL ACKTAETEAR LEELHNRKKA LDEMAREAD
 151 KKELPKRL*

a268-1/m268-1 95.6% identity in 158 aa overlap

	10	20	30	40	50	60
a268-1.pep	VQSRDGLHKFKHICSAAMALIKEPLDKAKORNEELEAAEAAAQALGREQEVDRVSEW					
m268-1	VQSRDGLHKFKHICSAAMALIKEPLDKVKORNEELEAAEAAAQALGREQEAARVSEW					
	10	20	30	40	50	60
	70	80	90	100	110	120
a268-1.pep	EERYKLSRSEFEQFWKGLPQTVQNKLASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
m268-1	EERYKLSRSEFEQFWKGLPQTVQNKLASQKTWKSMDKICANNAKAEGETPNGIKFSEL					
	70	80	90	100	110	120
	130	140	150	159		
a268-1.pep	ACKTAETEARLEELHNRKKALLDEMAREADKKELPKRLX					
m268-1	ACKTAKTEARLEELHNRKKALIDEMAREADKKELSKRLX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1091>:

g269.seq

1 atggtttggc gtgtgaattg cgcggcaacg gcggcgctga ttttttcgtc
 51 cagcccttgg atttgggcgg tgggtggtggt gtggtcgcgg tcggcttttt
 101 cctgcaaacc ttgcgccagc cttgacgcgt ccagtgcgcc gccgttggcg
 151 gtttcgccgt gggactttat ccggaacacg gcttcgccca aggtgtcggc
 201 ggctttgatg cacagtttta aaaccagggc tttggggcgg ttttctgcgc
 251 cgcccggtgc cattttgctg tccaatcgcg gggtaaaaa accgttgctg
 301 ttaagtcgc cgtccgtcca agtcgatacg agcgcgcttc tttgcctttc
 351 attgcggtct tcgtaa

This corresponds to the amino acid sequence <SEQ ID 1092; ORF 269.ng>:

g269.pep

1 MVWRVNCAAT AALIFSSSPW IWAVVWWSR SAFSCKPCAS LDASSAPALA
 51 VSPWDFIRNT ASPKVSALM HSFKTRALGR FSAPPVAILL SNRGVKKPLS
 101 FKSPSVQVDT SALLCLSLRS S*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1093>:

m269.seq

1 ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
 51 CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGCTCTCGG TCGGCTTTGT
 101 CTTGCAAACC TTGCGCCaCG TGCCGCGTC CAGCGCCTGC GTTGATGGTT
 151 TCGCCGTGGG ACTTTATCCA AAACACGGCT TCGCCCAAGG TGTCGGCGGC
 201 TTTGATGCAC AGTTTAAAA CCAGGGCTTT GGGGCGGTTT TCGTCGCCGC
 251 CTGTCGCCAT TTTGCTGTCC GAGCGCGGGG TAAAAAGCC GTTGTCGTTT
 301 AAATTTTCGT CCGTCCAAGT CGATACGAGC GCGCTTCTCT GCCTTTCGTT
 351 GCGGTCTTCG TAA

This corresponds to the amino acid sequence <SEQ ID 1094; ORF 269>:

m269.pep

1 MVWRVNCAAT AVLIFSSSPW IWAHVWWSR SALSCKPCAT CPRPAPALMV
 51 SPWDFIQNTA SPKVSALMH SFKTRALGRF SSPPVAILLS ERGVKKPLSF
 101 KFSSVQVDT SALLCLSLRS *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 269 shows 87.6% identity over a 121 aa overlap with a predicted ORF (ORF 269.ng) from *N. gonorrhoeae*:

```

m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT  59
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269      MVWRVNCAATAALIFSSSPWIWAAVWVWSRSASFCKPCASLDASSAPALAVSPWDFIRNT  60

m269.pep  ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS  119
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g269      ASPKVSAAALMHSFKTRALGRFSAPPVAILLSNRGVKKPLSFKSPSVQVDT SALLCLSLRS  120

m269.pep  SX  121
          ||
g269      SX  122

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1095>:

```

a269.seq
1  ATGGTTTGGC GTGTGAATTG CGCGGCAACG GCGGTGCTGA TTTTTCGTC
51  CAGCCCTTGG ATTTGGGCGG CGGTGTGGGT GTGGGCGCGG TCTGCTTTGT
101 CTTGGAGGTT TTGCGCCAGC GTGCCGCGT CCAGCGCGCC GCGTTGACG
151 GTTTCGCCGT GGGACTTTAT CTAGAACACG GCTTCGCCCA AGGTGTCGGC
201 GGCTTTGATG CACAGTTTAA AAACCAGGGC TTTGGGCGCG TTTTCGTCGC
251 CGCCTGTGCG CATTTTGCTG TCCGGGCGCG GGGTTAAAAA GCCGTTGTCG
301 TTAAATTTT CGTCCGTCCA AGTCGATACG AGCGCGCTTC TCTGCCTTTC
351 GTTGTGGTCT TCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1096; ORF 269.a>:

```

a269.pep
1  MVWRVNCAAT AVLIFSSSPW IWAAVWVWAR SALSWRFCAS VPASSAPALT
51  VSPWDFIQNT ASPKVSAAALM HSFKTRALGR FSSPPVAILL SGRGVKKPLS
101 FKFSSVQVDT SALLCLSLWS S*

```

m269/a269 90.1% identity in 121 aa overlap

```

          10      20      30      40      50      59
m269.pep  MVWRVNCAATAVLIFSSSPWIWAAVWVWSRSALSCKPCATCP-RPAPALMVSPWDFIQNT
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269      MVWRVNCAATAVLIFSSSPWIWAAVWVWARSALSWRFCASVPASSAPALTVSPWDFIQNT
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m269.pep  ASPKVSAAALMHSFKTRALGRFSSPPVAILLSERGVKKPLSFKFSSVQVDT SALLCLSLRS
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a269      ASPKVSAAALMHSFKTRALGRFSSPPVAILLSGRGVKKPLSFKFSSVQVDT SALLCLSLWS
          70      80      90      100     110     120

m269.pep  120
          SX
          ||
a269      SX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1097>:

```

g270.seq
1  atgaataaaa accgcaaatt actgcttgcc gcaactgctgc tgactgcctt
51  tgccgccttc aagctcgttt tgttgcaatg gtggcaggcg cagcagccgc
101 aagccgtggc ggcgcaatgc gatttgaccg aggggtgcac gctgccggac
151 ggaagccgtg tccgcgcgcg cgccgtttca accaaaaaac cgtttgatat
201 ttatatcgaa cacgcgcccg ccggcacgga acaggtcagc atcagcttca
251 gtatgaaaaa tatggatatg ggtttcaacc gctatatgtt cgagcggcaa
301 ccgtcgggga cttggcaggc agcacgcatc cgcctgcccg tctgtgtcga
351 aggcaggcgc gattttacgg cggacattac aatcggcagc cggacatttc
401 agacggcatt taccgccgaa taa

```

This corresponds to the amino acid sequence <SEQ ID 1098; ORF 270.ng>:

618

g270.pep
 1 MNKNRKLLLA ALLLTAFAAF KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
 101 PSGTWQAARI RLPVCVEGRR DFTADITIGS RTFQTAFTAE*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1099>:

m270.seq
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG Ca.CAGCCGC
 101 AAGCTGTGGC GCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGT CGGACATTTC
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1100; ORF 270>:

m270.pep
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA XQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ
 101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 270 shows 96.4% identity over a 140 aa overlap with a predicted ORF (ORF 270.ng) from *N. gonorrhoeae*:

m270/g270

	10	20	30	40	50	60
m270.pep	MNKNRKLLLAALLLIAFAAVKLVLLQWWQAXQPQAVAAQCDL	TEGCTLPD	GSRVRAAAVS			
g270	MNKNRKLLLAALLLTAFAAF	KLVLLQWWQAQQPQAVAAQCDL	TEGCTLPD	GSRVRAAAVS		
	10	20	30	40	50	60
m270.pep	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQ	PSGTWQAVRIRLPICVEGRR				
g270	TKKPFDIYIEHAPAGTEQVSISFSMKNMDMGFNRYMFERQ	PSGTWQAARIRLPVCVEGRR				
	70	80	90	100	110	120
m270.pep	DFTADITIGSRTFQTAFTAEX					
g270	DFTADITIGSRTFQTAFTAEX					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1101>:

a270.seq
 1 ATGAATAAAA ACCGTAAATT ACTGCTTGCC GCACTGCTGC TGATTGCCTT
 51 TGCCGCCGTC AAGCTCGTTT TGTGCAATG GTGGCAGGCG CAGCAGCCGC
 101 AAGCTGTGGC GCGCAATGC GATTTGACCG AGGGTTGCAC GCTGCCGGAC
 151 GGAAGCCGCG TCCGCGCCGC CGCCGTTTCA ACCAAAAAAC CGTTTGATAT
 201 TTATATCGAA CACGCGCCCG CCGGCACGGA ACAGGTCAGC ATCAGCTTCA
 251 GTATGAAAAA TATGGATATG GGTTCaACC GCTATATGTT CGAGCGGCAA
 301 CCGTCGGGGA CTTGGCAGGC AGTACGCATC CGCCTGCCCA TCTGTGTCGA
 351 AGGCAGGCGC GATTTTACGG CGGACATTAC AATCGGCAGC CGGACATTTC
 401 AGACGGCATT TACCGCCGAA TAA

This corresponds to the amino acid sequence <SEQ ID 1102; ORF 270.a>:

a270.pep
 1 MNKNRKLLLA ALLLIAFAAV KLVLLQWWQA QQPQAVAAQC DLTEGCTLPD
 51 GSRVRAAAVS TKKPFDIYIE HAPAGTEQVS ISFSMKNMDM GFNRYMFERQ

101 PSGTWQAVRI RLPICVEGRR DFTADITIGS RTFQTAFTAE *

m270/a270 99.3% identity in 140 aa overlap

	10	20	30	40	50	60
m270.pep	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
a270	MNKNRKL	LLAALL	IAFAAV	KLVL	LQWQ	AXQPQ
	10	20	30	40	50	60
	70	80	90	100	110	120
m270.pep	TKKPF	DIYIE	HAPAG	TEQVS	SISFS	MKNMD
a270	TKKPF	DIYIE	HAPAG	TEQVS	SISFS	MKNMD
	70	80	90	100	110	120
	130	140				
m270.pep	DFTAD	ITIGS	RTFQ	TAFT	AEX	
a270	DFTAD	ITIGS	RTFQ	TAFT	AEX	
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1103>:

g271.seq

```

1   atgttcagtt cgcggatggc gaggatttgg gcgacggggg taacgttgtg
51  tatggtcagt ccgtgtccgg cgttgacgac caagcccaaa tcgccggcga
101 aatgcgcgcc gttttggatg cgctcgaact gcctgatttg ttcggcgtgg
151 ctttgtgcgt cggcatatgc gccggtgtgc agctcgacaa cgggcgcgcc
201 gacatcacgg gcggcttga tttgcctgtc gtcggcatcg ataaacaagg
251 acacgcgtat gcccgctcg gtcaggattt tggcgaattc ggcgattttt
301 tcctgttgcg ccaatacgtc caaacgcct tcggtcgtga tttcctgccg
351 tttttcaggc acgatgcaca cgtcttcgg catcacttta agcgcgtttt
401 cgagcatttc ttccgtcaac gccatttcaa gggtcaggcg cgtgcggatg
451 gcgtttttga cggcaaatac atccgcgtct ttgatgtggc ggcggtcttc
501 gcgcaggtgc atggtaatca ggtctgcacc gtgcgtttcg gcaaccagtg
551 ccgcctccac ggggctggga taa

```

This corresponds to the amino acid sequence <SEQ ID 1104; ORF 271.ng>:

g271.pep

```

1   MFSSRMARIW ATGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LCASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILANSIAIF
101 SCCANTSKPP SVVISCRFSG TMHTSSGITL SAFSSISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIRAPCVS ATSAASTGLG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1105>:

m271.seq

```

1   AwGTTcagTT CGCGGATGGC GAGGATTtGG GCGATGGGGG TAACGTTGTG
51  TATGGTCAGT CCGTGTCGGG CGTTGACGAC CAAGCCCAA TCGCCGGCGA
101 AATGCGCGCC GTTTTGGATG CGCTCGAACT GCCTGATTtG TTCGGCGTGG
151 CTGCGCGCGT CGGCATACGC GCCTGTGTGC AGCTCGACAA CGGGCGCGCC
201 GACATCACGG GCGGCTTGA TTTGCCTGTC GTCGGCATCG ATAAACAAAG
251 ACACGCGTAT GCCTGCGTCG GTCAGGATT TGGTGAACCC GCGGATTtTT
301 TCCTGTtGCG CCAATACGTC CAAACCGCCT TCGGTCTGTA TTTCTGACG
351 TTTTTCAGGC ACGATGCACA CGTCTTCCGG CATCACTtTC AAAGCGTTtT
401 CCAACATtTC TTCCGTCAAC GCCATTtCAA GGTTcAGGCG CGTGCGGATG
451 GCGTtTTTGA CGGCAACAC GTCCCGTCT TTGATGTGGC GCGGTCTTc
501 GCGCAGGTGC ATGGTAATCA AATCCGCACC GTGCGTTTCG GCAACCAGTG
551 CCGCTCCAC GGGGCTGGGA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1106; ORF 271>:

m271.pep

```

1   XFSSRMARIW AMGVTLCMVS PCPALTTKPK SPAKCAPFWM RSNCLICSAW
51  LRASAYAPVC SSTTGAPTSR AAWICLSSAS INKDTRMPAS VRILVNPAIF
101 SCCANTSKPP SVVISXRFSG TMHTSSGITF KAFSNISSVN AISRFRVRM
151 AFLTANTSAS LMWRRSSRRC MVIKAPCVS ATSAASTGLG *

```

Computer analysis of this amino acid sequence gave the following results:

620

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 271 shows 95.2% identity over a 189 aa overlap with a predicted ORF (ORF 271.ng) from *N. gonorrhoeae*:

m271/g271

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
g271	MFSSRMARIWATGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLCASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
g271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILANSALFSCCANTSKPPSVVISCRFSG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m271.pep	TMHTSSGITLFAKSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAAPCVS					
g271	TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAAPCVS					
	130	140	150	160	170	180
	190					
m271.pep	ATSAASTGLGX					
g271	ATSAASTGLGX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1107>:

a271.seq

```

1  ATGTTTCAGTT  CGCGGATGGC  GAGGATTGG  GCGATGGGGG  TAACGTTGTG
51  TATGGTCAGT   CCGTGTCGG  CGTTGACGAC  CAAGCCCAAA  TCGCTGGCAA
101 AATGCGCGCC   GTTTTGGATG  CGCTCGAACT  GCCTGATTGG  TTCGGCGTGG
151 CTGCGCGCGT   CGGCATACGC  GCCTGTGTGC  AGCTCGACAA  CGGGCGCGCC
201 GACATCACGG   GCGGCTTGGA  TTTGCCTGTC  GTCGGCATCG  ATAAACAAGG
251 ACACGCGTAT   GCGGCGGTCG  GTCAGGATTT  TGGTGAATTC  GGCAATTTTG
301 TCTTGTTGCG   CCAATACGTC  CAAGCCGCCT  TCGGTCGTGA  TTTCCTGACG
351 TTTTCCGGC    ACGATGCACA  CGTCTTCCGG  CATCACTTTA  AGCGCGTTTT
401 CGAGCATTTT   TTCCGTCAAC  GCCATTTCAA  GGTTCAGGCG  CGTGCGGATG
451 GCGTTTTTTGA  CAGCAAACAC  GTCCGCGTCT  TTGATGTGGC  GGCGGTCTTC
501 GCGCAGGTGC   ATGGTAATCA  GGTCCGCACC  GTGCGTTTCG  GCAACCAGTG
551 CCGCCTCCAC   GGGGCTGGGA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1108; ORF 271.a>:

a271.pep

```

1  MFSSRMARIW  AMGVTLCMVS  PCPALTTKPK  SLAKCAPFWM  RSNCLICSAW
51  LRASAYAPVC  SSTTGAPTSR  AAWICLSSAS  INKDTRMPAS  VRILVNSAIL
101 SCCANTSKPP  SVVIS*RFSG  TMHTSSGITL  SAFSSISSVN  AISRFRVRM
151 AFLTANTSAS  LMWRRSSRRC  MVIRSAPCVS  ATSAASTGLG  *

```

m271/a271 96.3% identity in 189 aa overlap

	10	20	30	40	50	60
m271.pep	XFSSRMARIWAMGVTLCMVSPCPALTTKPKSPAKCAPFWMRSNCLICSAWLRASAYAPVC					
a271	MFSSRMARIWAMGVTLCMVSPCPALTTKPKSLAKCAPFWMRSNCLICSAWLRASAYAPVC					
	10	20	30	40	50	60
	70	80	90	100	110	120
m271.pep	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNPAIFSCCANTSKPPSVVISXRFSG					
a271	SSTTGAPTSRAAWICLSSASINKDTRMPASVRILVNSAILSCCANTSKPPSVVISXRFSG					

		70	80	90	100	110	120
		130	140	150	160	170	180
m271.pep		TMHTSSGITFKAFSNISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIKSAPCVS					
		: : : : : : : : : :					
a271		TMHTSSGITLSAFSSISSVNAISRFRVRMAFLTANTSASLMWRRSSRRRCMVIRSAPCVS					
		130	140	150	160	170	180
		190					
m271.pep		ATSAASTGLGX					
a271		ATSAASTGLGX					
		190					

q272.seq

1	atgactgcaa	aggaagaact	gttcgcatgg	ctgcgccata	tgaacaaaaa
51	caaaggttcc	gacctgtttg	tgacgacca	ttccccgcc	gctatgaagc
101	tggacggcaa	aatcacccgc	atcacggacg	aaccgctgac	ggcggaaaaa
151	tgtatggaaa	tcgccttttc	gattatgagt	gcgaagcagg	cggagaagaat
201	ttcatcgacc	aacgagtgtca	attatgccat	cagctgcgcg	gacacagcgc
251	gcttcgcgct	caatgcgatg	atacagcgcg	gtgcgacggc	gttggtattc
301	gcgcgcgatta	ccagcaagat	tcccaagttt	gaaagcctga	acctgccgcc
351	ggccttgaag	gatgttgcg	tgaaaaaacg	cgggctggtt	atttttgctg
401	gcggcaccgg	ctcggggcaa	tcgacttcgc	tcgcctcgct	tatcgactac
451	cgcaatgaaa	attcgtttcg	acacatcat	accatcgaag	atccgatcga
501	gtttgtccac	gaacacaaaa	actgcctcat	taccacgcgc	gaggtcggcg
551	tggacacgga	aaactggatg	gcggcggttg	aaaatacgct	gcgtcaggcg
601	ccggatgtga	tccttatcgg	cgaaatccgc	gaccgtgaaa	caatggacta
651	cgccatcgcc	tttgccgaaa	cggggcattt	gtgtatggcg	acgctgcacg
701	ccaacagcac	caatcaggcg	ctgcaccgca	tcatcaactt	cttccccgag
751	gagcggcgcg	aacaattgtc	gacgagtttg	tcgctcaacc	ttcaggcggt
801	tatttcgcaa	cgcttcggtt	cgcgagacgg	cggcaagggc	agggtggcg
851	cagtcgaggt	gctgctcaat	tcgccctga	tttcggagtt	gattcacaa
901	ggcaacatcc	atgaaatcaa	agaagtgatg	aaaaaatcca	ctaccctggg
951	tatgcagacc	ttcgaccaac	acctttacca	attgtatgaa	aaagcgcaga
1001	tttccttgca	ggatgccttg	aaaaatgccg	attccgcaca	tgatttgctg
1051	ttggcggtac	agttgcgcag	cgcgagggca	caaagttccg	accccgattt
1101	qqaactgctc	tga			

g272.pcp

1	MTAKEELFAW	LRHMNKNKGS	DLFVTTTHFP	AMKLDGKITR	ITDEPLTAEK
51	CMEIAFSIMS	AKQAEESST	NECNFAISLP	DTSRFRVNAM	IQRGATALVF
101	RAITSKIPKF	ESLNLPPALK	DVALKKRGLV	IFVGGTGSGK	STSLASLIDY
151	RNENSFGHII	TIEDPIEFVH	EKNCIITQR	EVGVDTENWM	AALKNTLRQA
201	PDVILIGEIR	DRETM DYAIA	FAETGHL CMA	TLHANSTNQA	LDRIINFFPE
251	ERREQILLTDL	SLNLQAFISQ	RLVPRDGGKG	RVAAVEVLLN	SPLISELIHN
301	GNTHIIEKVM	KKSTTLGMO T	FDQHL YQLYE	KGEISLQDAL	KNADSAHDLR
351	LAVQLRSRRA	QSSDPDLELL*			

m272.seq

1	ATGACCGCAA	AGGAAGAAGT	GTTTCGCATGG	CTGCGCCATA	TGAwCCCCAA
51	CAAAGGTTCC	GACCTGTTCC	TGACAACCCA	TTTCCCGCCC	GCAATGAAGC
101	TGACGCGCAA	AATCACCCTG	ATCAGCGGAC	AACCGCTGAC	GGCGGAAAAA
151	TGTATGGAAA	TCCGCTTTTC	GATTATGAGT	GCGAAGCAGG	CGGAAGAATT
201	TTCATCGAAC	AACCAAGTGA	ACTTCGCCAT	CAGCCTGCCG	GACACGAGCC
251	GCTTCCGCGT	CAATGCGATG	ATACAGCGCG	GCGCGACGGC	GTTGGTATTC
301	CGTACGATTA	CCAGCAAGAT	TCCCAAGTTT	GAAAGCCTGA	ACCTGCCGCC
351	AGTCTTGAAG	GATGTCGCGC	TGAAAAAACG	CGGGCTGGTT	ATTTTGTTCG
401	GCGCAACCGG	CTCGGGTAAA	TGCACTTCGC	TTGCCTTCGT	TATCGACTAC
451	CGCAATGAAA	ATTCTGTTCCG	ACACATCATC	ACCATCGAAG	ACCCGATCGA
501	GTTTGTCCAC	GAACACAAAA	ACTGCATCAT	CACCCAGCGC	GAGGTCCGGC

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```

551 TGGATACGGA AAACCTGGATG GcGGCGTTGA AAAACACGCT GCGTCAGGCG
601 CCTGATGTCA TCCTTATCGG CGAAATCCGT GACCGCGAAA CAATGGACTA
651 CGCCATTGCC TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCCGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTG TCGCTCAACC TTCAGGCGTT
801 TATTTTCGCA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCCtGA TTTCGGAGTT GATTACAAAC
901 GGCAACATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACC TTCGATCAAC ACCTTTTACCA ATTGTATGAA AAAGGCGATA
1001 TTTCCCTGCA AGAAGCATTG AAAAATGCCG ATTCCGCACA CGATTTCGCT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCGCGCG CAaAGTTyCA GCCCCGATTT
1101 GGNACTGCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1112; ORF 272>:

m272.pep

```

1  MTAKEELFAW LRHMXQNKGS DLFVTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNAM IQRGATALVF
101 RTITSKIPKF ESLNLPVVK DVALKKRGLV IFVGGTGS GK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAIA FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLTDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLQLYE KGDISLQEAL KNADSAHDLR
351 LAVQLRSRRA QXSPDLXLL *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 272 shows 97.6% identity over a 370 aa overlap with a predicted ORF (ORF 272.ng) from *N. gonorrhoeae*:

m272/g272

m272.pep	10	20	30	40	50	60
	MTAKEELFAWLRHMXQNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
g272	MTAKEELFAWLRHMXQNKGS DLFVTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS					
	10	20	30	40	50	60
m272.pep	70	80	90	100	110	120
	AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPVVK					
g272	AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPVVK					
	70	80	90	100	110	120
m272.pep	130	140	150	160	170	180
	DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR					
g272	DVALKKRGLVIFVGGTGS GKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR					
	130	140	150	160	170	180
m272.pep	190	200	210	220	230	240
	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLCA TLHANSTNQA					
g272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYAIAFAETGHLCA TLHANSTNQA					
	190	200	210	220	230	240
m272.pep	250	260	270	280	290	300
	LDRIINFFPEERREQLLTDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
g272	LDRIINFFPEERREQLLTDLSLNLQAFISQRLVPRDGGKGRVAAVEVLLN SPLISELIHN					
	250	260	270	280	290	300
m272.pep	310	320	330	340	350	360
	GNIHEIKEVMKKSTTLGMQTFDQHLQLYE KGDISLQEALKNADSAHDLRLAVQLRSRRA					
g272	GNIHEIKEVMKKSTTLGMQTFDQHLQLYE KGEISLQDALKNADSAHDLRLAVQLRSRRA					
	310	320	330	340	350	360

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```

                370
m272.pep      QSXSPDLXLLX
                || :||| |||
g272          QSSDPDLELLX
                370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1113>:

```

a272.seq
1   ATGACCGCAA AGGAAGAACT GTTCGCATGG CTGCGCCATA TGAACAAAAA
51  CAAAGGTTCC GACCTGTTCC TGACGACCCA TTTCCCGCCC GCAATGAAGC
101 TGGACGGCAA AATCACCCGC ATCACGGACG AACCGCTGAC GGCGGAAAAA
151 TGTATGGAAG TCGCCTTTTC GATTATGAGT GCGAAGCAGG CGGAAGAATT
201 TTCATCGACC AACGAGTGCA ACTTCGCCAT CAGTCTGCCG GACACCAGCC
251 GCTTCCGCGT CAATGCGATG ATACAGCGCG GTGCGACGGC GTTGGTATTC
301 CGTGCGATTA CCAGCAAGAT TCCCAAGTTT GAAAGCCTGA ACCTGCCGCC
351 GGTCTTGAAG GATGTCGCGC TGAAAAAACG CGGGCTGGTT ATTTTGTGCG
401 CGGGCACCAG CTCGGGCAAA TCGACTTCGC TTGCCTCGT TATCGACTAC
451 CGCAATGAAA ATTCGTTCCG ACACATCATC ACCATCGAAG ACCCGATCGA
501 GTTTGTCCAC GAACACAAAA ACTGCATCAT CACCCAGCGC GAGGTCGGCG
551 TGGATACGGA AAACGGATG GCGGCGTTGA AAAACACGCT GCGTCAGGCA
601 CCGGATGTGA TTCTGATCGG CGAAATCCGC GACCGCGAAA CAATGGACTA
651 CGCCATTGCT TTTGCCGAAA CGGGGCATTT GTGTATGGCG ACGCTGCACG
701 CCAACAGCAC CAATCAGGCA CTCGACCGCA TCATCAACTT TTTCCCGGAG
751 GAGCGGCGCG AACAATTGCT GACGGATTTC TCGCTCAACC TTCAGGCATT
801 TATTTGCGAA CGCCTCGTTC CGCGAGACGG CGGCAAGGGC AGGGTGGCGG
851 CAGTCGAGGT GCTGCTCAAT TCGCCCTGA TTTCGGAGT GATTCACAAC
901 GGCAATATCC ATGAAATCAA AGAAGTGATG AAAAAATCCA CTACCCTGGG
951 TATGCAGACT TTCGACCAAC ACCTTTACCA ATTGTATGAA AAAGGCGAGA
1001 TTTCTTGA GATGCCTTG AAAAATGCCG ATTCCGCACA CGATTGCGT
1051 TTGGCGGTAC AGTTGCGCAG CCGCCAGGCG CAAAGTCCG GTCCCGATTT
1101 GGAAGTCTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1114; ORF 272.a>:

```

a272.pep
1   MTAKEELFAW LRHMNKNKGS DLFVTTTHFPP AMKLDGKITR ITDEPLTAEK
51  CMEIAFSIMS AKQAEFFSST NECNFAISLP DTSRFRVNM IQRGATALVF
101 RAITSKIPKF ESLNLPVVLK DVALKKRGLV IFVGGTSGSK STSLASLIDY
151 RNENSFGHII TIEDPIEFVH EHKNCIITQR EVGVDTENWM AALKNTLRQA
201 PDVILIGEIR DRETMDYAI FAETGHLCA TLHANSTNQA LDRIINFFPE
251 ERREQLLDL SLNLQAFISQ RLVPRDGGKG RVAAVEVLLN SPLISELIHN
301 GNIHEIKEVM KKSTTLGMQT FDQHLYQLYE KGEISLQDAL KNADSAHDLR
351 LAVQLRSRQA QSSGPDLELL *

```

m272/a272 97.6% identity in 370 aa overlap

```

                10      20      30      40      50      60
m272.pep      MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
                ||||| :|||||
a272           MTAKEELFAWLRHMNKNKGS DLFVTTTHFPPAMKLDGKITRITDEPLTAEK CMEIAFSIMS
                10      20      30      40      50      60

                70      80      90      100     110     120
m272.pep      AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRTITSKIPKFESLNLPVVLK
                ||||| :|||||
a272           AKQAEFFSSTNECNFAISLPDTSRFRVNAMIQRGATALVFRAITSKIPKFESLNLPVVLK
                70      80      90      100     110     120

                130     140     150     160     170     180
m272.pep      DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
                ||||| :|||||
a272           DVALKKRGLVIFVGGTSGSKSTSLASLIDYRNENSFGHII TIEDPIEFVHEHKNCIITQR
                130     140     150     160     170     180

```

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	190	200	210	220	230	240
m272 . pep	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCMATLHANSTNQA					
a272	EVGVDTENWMAALKNTLRQAPDVILIGEIRDRETMDYIAFAETGHLCMATLHANSTNQA					
	190	200	210	220	230	240
m272 . pep	LDRIINFFPEERREQLLTDLSLNLOAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLTDLSLNLOAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272 . pep	LDRIINFFPEERREQLLTDLSLNLOAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
a272	LDRIINFFPEERREQLLTDLSLNLOAFISQRLVPRDGGKGRVAAVEVLLNSPLISELIHN					
	250	260	270	280	290	300
m272 . pep	GNIHEIKEVMKKSTTLGMQTFDQHLQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKKSTTLGMQTFDQHLQLYEKGEISLQDALKNADSAHDLRLAVQLRSRQA					
	310	320	330	340	350	360
m272 . pep	GNIHEIKEVMKKSTTLGMQTFDQHLQLYEKGDISLQEALKNADSAHDLRLAVQLRSRRA					
a272	GNIHEIKEVMKKSTTLGMQTFDQHLQLYEKGEISLQDALKNADSAHDLRLAVQLRSRQA					
	310	320	330	340	350	360
m272 . pep	QSXSFDLXLLX					
a272	QSSGPDLELLX					
	370					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1115>:

g273 . seq

```

1  atgagtcttc aggcggtatt tatatacccc ccaagccgta ccgcacaata
51  caacgaaat caggaaaacg gcggtaaagc tcataaacag ggacaaagcg
101 gcaaacacac cgaccgccgt caggatatag gcgtattcga ggccggaact
151 ccattcacccg ttttcctgcc gtttcttgtc gcttttgaaa taaaggatga
201 tgccggcaag cagcgcggca gccgcgcccg acattggcat tgtgttcatt
251 gttgttcctt aacggttaaa aaccgcgccg gccgtgcaac cgttttaagg
301 cgggaaattg caaaatttgt ttgcgggccc gtgcgctga aatcaaggcg
351 gtttgagaag tgtttcnacc gcgcccgcct tatgtgccga aatattattt
401 gtcgctcacc tgcaaatcgc ccaagaacgc gctttgcgga atttccacgt
451 tgcccacttg tttcatacgg cgtttgccgt ctttttggtt ttcaagcagt
501 tttttcttac gcgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1116; ORF 273.ng>:

g273 . pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGKAHKQ QSGKHTDRR QDIGVFEAGT
51  PFTVFLPFLV AFEIKDDAGK QRGSRARHWH CVHCCSLTVK NPPGRATVLR
101 REIAKFVCGR VPLKSRRFEK CFXRARPMCR NIICRSPAKS PRTRFAEFPR
151 CPLVSYGVCL LFVFQAVFSY A*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1117>:

m273 . seq

```

1  ATGAGTCTTC AGGCGGTATT TATATACCCm CCAAGCCGTA CCGCACAATA
51  CAACGAAAAT CAGGAAAACG GCGGTAAAGC TCAYAAACAG GGACAAAGCG
101 GCAAACACGC CGACCGCTGT CAGGATATAG GCGTATTCAA GGCCGGAAC
151 CCATTCCCCG TTTTCCTGCC GCTTCTTGTC GCTTTTGAAA TAAAGGATGA
201 TGCCGGCAAG CAGCGCGGCA GCCGCGCCCG ACATTAGCAT TGTGTTCATT
251 GTTGTTCCTT AATGCTTAAA AACCCGCCTG TCCGTGCAAC CGTTTAAAG
301 CGGCAAATTG CAAAATTGTG TTGCGGGCGC GTGCCCTGA AATCAGGGCG
351 GTTTGAGGGG TGTTCCCGAC GCGCCGCCCT GTGTGCCGGA GTTATTTGTC
401 GCTCACCTGC AAAATCGCCA AGAACGCGCT TTGCGGAATT TCCACATTGC
451 CCACTTGTTT CACACGCGT TTACCTGCCT TTGTkTWTC AAGCAGTTT
501 TTCTTACGCG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1118; ORF 273>:

m273 . pep

```

1  MSLQAVFIYP PSRTAQYNEN QENGGKAHKQ QSGKHADRC QDIGVFKAGT
51  PFPVFLPLL V AFEIKDDAGK QRGSRARH*H CVHCCSLMLK NPPVRATVLR
101 RQIAKFVCGR VPLKSGRFEG CSRRAALCAG VICRSPAKSP RTRFAEFPHC
151 PLVSYGVYLP FVXQAVFSY A*

```

Computer analysis of this amino acid sequence gave the following results:

m273/g273

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1119>:

This corresponds to the amino acid sequence <SEQ ID 1120; ORF 273.a>:

m273/a273 80.1% identity in 171 aa overlap

	10	20	30	40	50	60
m273.pep	MSLQAVFIYPPSRTAQYNENQENGGAHKQGQSGKHADRCQDIGVFKAGTFPPVFLPLLV					
a273	MSLQAVFIYPPSRTAQYNENQENGGAHKQGQSGKHADRRQDIGVFTGTPTTFLPLFV					
	10	20	30	40	50	60
m273.pep	AFEIKDDAGKQGRSRAHXXHCVHCCSLMLKNPPVRATVL-RRQIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRAHXXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRRLLQSGRFK					
	70	80	90	100	110	119
m273.pep	AFEIKDDAGKQGRSRAHXXHCVHCCSLMLKNPPVRATVL-RRQIAKFVCGRVPLKSGRFE					
a273	AFEIKDDAGKQGRSRAHXXHNVHCCSLTVKNPPVRATVFKRRXITKFVGGRRLLQSGRFK					
	70	80	90	100	110	120
m273.pep	GCSRRALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPRTRFAGFPHCPLVSYGVCLLFVQAVFSYAX					
	130	140	150	160	170	
m273.pep	GCSRRALCAGVICRSPAKSPRTRFAEFPHCPLVSYGVYLPFVXQAVFSYAX					
a273	GHDALPRV-PDIICRSPAKLPRTRFAGFPHCPLVSYGVCLLFVQAVFSYAX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1121>:

g274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCatCGCC AgcgTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAGGATG
101 GCAAGCATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTCCT CATTTCTCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC ggCgagtTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GGCGGAATAT GAGGCGGTgt tcaaAACCCCT
351 TCCGCCGGCC AACCCTGGT ATGTGCGCGT GGAggacgCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AGGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAACTTTT CAATAATGCA GGAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1122; ORF 274.ng>:

g274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLPPA NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNA GSK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1123>:

m274.seq

```

1  ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGTTTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAACATAT CGACATCCAG CTTATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCCCC GATATGAATG CGGCAAAAGT
201 GTTTGTCGGC GCGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GGCGGAATAT GAGGCGGTGT TCAAACCCT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGC GCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTGATTG
451 ACCCCGATGG ACAAGCTTTT CAATAATACT GAAAGCAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1124; ORF 274>:

m274.pep

```

1  MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFGV GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 274 shows 97.5% identity over a 163 aa overlap with a predicted ORF (ORF 274.ng) from *N. gonorrhoeae*:

g274/m274

	10	20	30	40	50	60
g274.pep	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
m274	MAGPIFVVIASVAMFFVAQQHATDLVTDDYYKDGKHIDIQLHRDEEAVRRHIGVQVLISP					
	10	20	30	40	50	60
	70	80	90	100	110	120
g274.pep	DMNAAKVFGVGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLPPA					
m274	DMNAAKVFGVGGEFDGKQPLNLLLMHPTRKADDQTVALKPVGSAQNGRAEYEAVFKTLSPT					
	70	80	90	100	110	120
	130	140	150	160		
g274.pep	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNAGSKX					
m274	NHWYVRVEDAAGVWRVENKWITSQNAVDLTPMDKLFNNNTESKX					
	130	140	150	160		

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1125>:

```
a274.seq
1   ATGGCGGGGC CGATTTTGT CGTCATCGCC AGCGTCGCTA TGT TTTTGT
51  CGCGCAGCAG CACGCGACAG ATTTGGTTAC GGACGATTAT TATAAAGACG
101 GCAAGCATAT CGACATCCAG CTTTCATCGGG ATGAAGAAGC CGTCAGACGG
151 CATATCGGGG TGCAGGTTCT CATTTCCTCCC GATATGAATG CGGCAAAAGT
201 GTTGTGTCGGC GGCAGAGTTTG ACGGCAAACA GCCTTTGAAC CTGCTGCTGA
251 TGCACCCGAC CCGCAAGGCG GACGATCAAA CCGTCGCCCT CAAGCCCGTC
301 GGCAGCGCGC AGAACGGCAG GGCGGAATAT GAGGCGGTGT TCAAAACCTT
351 TTCGCCGACC AACCCTGGT ATGTGCGCGT GGAGGACGCG GCAGGCGTGT
401 GGCGCGTCGA GAACAAATGG ATTACCAGCC AAGGCAATGC GGTCGATTGT
451 ACCCCGATGG ACAAACCTTT CAATAATACT GAAAGCAAAT AA
```

This corresponds to the amino acid sequence <SEQ ID 1126; ORF 274.a>:

```
a274.pep
1   MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR
51  HIGVQVLISP DMNAAKVFVG GEFDGKQPLN LLLMHPTRKA DDQTVALKPV
101 GSAQNGRAEY EAVFKTLSPT NHWYVRVEDA AGVWRVENKW ITSQNAVDL
151 TPMDKLFNNT ESK*
```

m274/a274 100.0% identity in 163 aa overlap

	10	20	30	40	50	60
m274.pep	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
a274	MAGPIFVVIA SVAMFFVAQQ HATDLVTDDY YKDGKHIDIQ LHRDEEAVRR HIGVQVLISP					
	10	20	30	40	50	60
m274.pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
a274	DMNAAKVFVG GEFDGKQPLN LLLMHPTRK ADDQTVALKPV GSAQNGRAEY EAVFKTLSPT					
	70	80	90	100	110	120
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESKX					
	130	140	150	160		
m274.pep	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESKX					
a274	NHWYVRVEDA AGVWRVENKW ITSQNAVDL TPMDKLFNNTESKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1127>:

```
g276.seq
1   atgattttgc cgccatccat gacgatgatg cggtcggcgg attcgacggt
51  ggtcaggcgg tgggcgacga tgatgccggt gcggttttcc atcaggcgtt
101 cgagcgcttg ttggacgagg cgttcggatt cgttgtccaa tgcgctggtg
151 gcttcgtcca ataataatat cggcgcgtct ttcaaatgg cgcgggcgat
201 ggcgacgctg tgccgctgtc cgccgataa gttgctgccg ttcgatccga
251 tgggctggtg cagtcaggc ggggatgcgt cgatcaggct ttgcaggttg
301 gcggcttgga gggcggacag gacttcggct tcgcccgcgt cgggacggct
351 gtatcggacg ttttcaaca ggggtgcgtc aaacaggaa acgtcttggtg
401 agacgagggc gaattgggcg cgcaggcagt cgagtttgat gtcggcgatg
451 tcgataccgt ctatgcagat gttgccggca gacggttcga caaagcgggg
501 cagaaggttg acgacggttg atttgccgct gccggaacgt ccgaccaggg
551 cgacgcgttc gccttgctg atgtcgaggt tgaagttgtc gagggcttg
601 atgccgtctg aacgggtatc gacatcgacg ttgcggaagc tgatgcgcc
651 ttcgacacgc tcgggcgcga gcgtgccttt gtcctgttcg ggcggggtgt
701 cgagaaatgc acatacgccg tcggcggcga ggaacatcgt ctgcataggg
751 atgctgatgt tggcaaggct tttgatgggg gcgtacattt gcagcatcgc
801 gacgatgaat gccataaatt cgccgatggt ggtgtag
```

This corresponds to the amino acid sequence <SEQ ID 1128; ORF 276.ng>:

g276.pep

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```

1  MILPPSMTMM RSADSTVVRR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDCLKLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKRGRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1129>:

m276.seq

```

1  ATGATTTTGC CGTCGTCCAT CACGATGATG CGGTCGGCCC CTTCGATGGT
51  GGTACAGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCTAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCACGCGT TGCCCGTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGGGAGCTGT CAATCAGGCT TTGCAGGTTG
301 GCGGTTTGGA GGGCGAACAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 GTATCGGACG TTTTCAAACA GGGTGTCGTC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC GAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGTTGTC GAGGGCTTTG
601 ATGCCGCTCT AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TCGGTGCGA GCGTGCCCTT GTCCTGTTTC GCGGGGGTGT
701 CGAGAAATGC ACATACACCG TCGGCGGCGA GGAACATCGT CTGCATAGGG
751 ATGCTGATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1130; ORF 276>:

m276.pep

```

1  MILPSSITMM RSAPSMVVRR WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDCLKLP FDPMGWCSPS GELSIRLCRL
101 AVWRANRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKLSRAL
201 MPSERYSTST LRKLMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 276 shows 96.8% identity over a 278 aa overlap with a predicted ORF (ORF 276.ng) from *N. gonorrhoeae*:

m276/g276

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	:					
g276	MILPPSMTMMRSADSTVVRRWATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDCLKLPFDPMGWCSPSGELSIRLCRLAVWRANRTSASPASGRLYRT					
g276	FKMARAMATRCRCPDCLKLPFDPMGWCSPSGDASIRLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
g276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
g276	PTRATRSPCLMSRLKLSRALMPSERYSTSTLRKLMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240

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	250	260	270	279
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
g276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX			
	250	260	270	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1131>:

```
a276.seq
1  ATGATTTTGC CGTCGTCCAT TACGATGATG CGGTCGGCCC CTTGCATGGT
51  GGT CAGGCGG TGGGCGACGA TGATGCCGGT GCGGTTTTCC ATCAGGCGTT
101 CGAGCGCCTG TTGGACGAGG CGTTCGGATT CGTTGTCCAA TGCGCTGGTG
151 GCTTCGTCCA ATAATAATAT CGGCGCGTCT TTCAAATGG CGCGGGCAAT
201 GGCAACGCGT TGCCGCTGTC CGCCGGATAA GTTGCTGCCG TTCGATCCGA
251 TGGGCTGGTG CAGTCCGAGC GGTGATGCGT CGATCAGGCT TTGCAGGTTA
301 GCGGCTTGGA GGGCGGATAG GACTTCGGCT TCGCCCGCGT CGGGACGGCT
351 ATATCGGACG TTTTCAAACA GGGTGTCTGC AAACAGGAAT ACGTCTTGGG
401 AGACGAGGGC AAATTGGGCG CGCAGGCAGT CGAGTTTGAT GTCGGCGATG
451 TCGATACCGT CTATGCAGAT GTTGCCGGCA GACGGTTCGA CAAAGCGGGG
501 CAGCAGGTTG ACGACGGTGG ATTTGCCGCT GCCGGAACGT CCGACCAGGG
551 CGACGCGTTC GCCTTGCTCTG ATGTCGAGGT TGAAGCCGTC GAGGGCTTTG
601 ATGCCGTCCG AACGGTATTC GACATCGACG TTGCGGAAGC TGATGCGCCC
651 TTCGACACGC TGGCGTGCGA GCGTGCCTTT GTCCTGTTCG GGCGGGGTGT
701 CGAGAAATGC ACATACGCCG TCGGCGGCCG GGAACATCGT CTGCATAGGG
751 ATGCTAATGT TGGCAAGGCT TTTGATGGGG GCGTACATT GCAGCATCGC
801 GACGATGAAT GCCATAAATT CGCCGATGGT GGTGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1132; ORF 276.a>:

```
a276.pep
1  MILPSSITMM RSAPSMVVRW WATMMPVRFS IRRSSACWTR RSDSLSNALV
51  ASSNNNIGAS FKMARAMATR CRCPDKLLP FDPMGWCSPS GDASIRLCRL
101 AAWRADRTSA SPASGRLYRT FSNRVSSNRN TSWETRANWA RRQSSLMSAM
151 SIPSMQMLPA DGSTKGRSRL TTVDLPLPER PTRATRSPCL MSRLKPSRAL
201 MPSEYSTST LRLKMRPSTR CGASVPLSCS GGVSRNAHTP SAARNIVCIG
251 MLMLARLLMG AYICSIATMN AINSPMVV*
```

m276/a276 98.2% identity in 278 aa overlap

	10	20	30	40	50	60
m276.pep	MILPSSITMMRSAPSMVVRW WATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
a276	MILPSSITMMRSAPSMVVRW WATMMPVRFSIRRSSACWTRRSDSLSNALVASSNNNIGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m276.pep	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSI RLCRLAVWRANRTSASPASGRLYRT					
a276	FKMARAMATRCRCPDKLLPFDPMGWCSPSGELSI RLCRLAAWRADRTSASPASGRLYRT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m276.pep	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
a276	FSNRVSSNRNTSWETRANWARRQSSLMSAMSIPSMQMLPADGSTKGRSRLTTVDLPLPER					
	130	140	150	160	170	180
	190	200	210	220	230	240
m276.pep	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRLKMRPSTRCGASVPLSCSGGVSRNAHTP					
a276	PTRATRSPCLMSRLKPSRALMPSEYSTSTLRLKMRPSTRCGASVPLSCSGGVSRNAHTP					
	190	200	210	220	230	240
	250	260	270	279		
m276.pep	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					
a276	SAARNIVCIGMLMLARLLMGAYICSIATMNAINSPMVVX					

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250 260 270

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1133>:

```
g277.seq (partial)
  1 ..atggtacacg tcgccgtagc ttacgggtatt gccgtccggc gtttttgccc
  51 aaacgaggtc atagacgttt tccacgcctt gcagggtacat cgccaagcgt
 101 tcgatgccgt aggtaatctt gccgagtagc ggcgtgcaat cgataccgcc
 151 gacttggttg aaataggtaa actgggttac ttccatgccg ttgagccaga
 201 cttcccagcc caaacccac gcaccgaggg tgggggtttc ccagtcgtct
 251 tcgacaaagc ggatgtcgtg gactttggga tcgatgcca attcgcgcag
 301 ggagtcgaga tagaggtctt ggatattggc gggggcgggt ttgagggcga
 351 cttggaattg gtaatagtgt tgcaggcggg tgggggtgtc gccgtagcgg
 401 ccgtctttgg ggcggcggct ggggttgacg taggcggcaa accaaggctc
 451 ggggcccagc gcgcgcaggc aggtggcggg atgggatgtg ccggcaccga
 501 cttccatgtc gaagggttg atgacggtgc agcctttgtc tgcccagaag
 551 gtttgcatgt tgaagatgat ttggtggaag gtaagcatgg cttattgttc
 601 gataaaataa aggtttttatt ttactgtttc catagccgct tgaatagatt
 651 tatctcgaag acagcctga
```

This corresponds to the amino acid sequence <SEQ ID 1134; ORF 277.ng>:

```
g277.pep (partial)
  1 ..MVHVAVAYGI AVRRFCPNEV IDVFHALQVH RQAFDAVGNF AEYGRAIDTA
  51 DLLEIGKLG Y FHAVEPDFPA QTPRTEGGVF PVVFDKADV DFGIDAQFAQ
 101 GVEIEVL D I GGGFEGDLEL VIVLQAVGVV AVAAVFGAAA GLDVGGKPRL
 151 GAERAQAGG MGCAGTDFHV EGLDDGAAPV CPEGLQFEDD LLEGKHGLLF
 201 DKIKVLFYCF HSRLNRFISK TA*
```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1135>:

```
m277.seq
  1 ATGCCCGCT TTAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
  51 TTTCTTCGGC AAGCAGGCGT TTGGCTTTCG CTTCTAGTTC GTTGAAGTGG
 101 CGCAGCAGCC AGTCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGCTC
 151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA GGTGACGGTG TTGCCGTCGA
 201 GCGTTTTTGC CCAAACGAGG TCGTAGACGT TTTCTACACC TTGCAAGTAC
 251 ATCGCCAAGC GTTCGATGCC GTAGGTGATT TCGCCGAGTA CGGGCGTGCA
 301 GTCGATGCCG CCGACTTGTT GGAATAGGT AAAGTGGGT ACTTCCATGC
 351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
 401 TCCAGTCGT CTTGACAAA GCGGATGTCG TGGACTTTGG GATCGATGCC
 451 CAATTCGCGC AGAGAGTCGA GATAGAGGTC TTGGATATTG GCGGAGCGG
 501 GCTTGAGGGC GACTTGAAT TGGTAATAGT GTTGACGGCG GTTGGGGTTG
 551 TCGCCGTAGC GGCCGTCTTT GGGGCGGCGG CTGGGTGGA CGTAGGCGGC
 601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG GCAGGTGGCG GGATGGGATG
 651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
 701 TCTGCCCAGA ATGTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
 751 GGCTTATGA
```

This corresponds to the amino acid sequence <SEQ ID 1136; ORF 277>:

```
m277.pep
  1 MPRFEDKLVG RQEGGVFFG KQAFGLRFV VELAQQPVG AVFEVVGGLL
  51 DFVLVVHVAV GDGVAVERFC PNEVVDVFT LQVHRQAFDA VGDFAEYGRA
 101 VDAADLLEIG KLG Y FHAVEP DFPAQTPRAE GGVFPVVDK ADVVDFGIDA
 151 QFAQRVEIEV LDIGSGLEG DLELVIVLQA VGVVAVAVF GAAAGLDVGG
 201 KPRLGAECAQ AGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
 251 GL*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 277 shows 90.0% identity over a 221 aa overlap with a predicted ORF (ORF 277.ng) from *N. gonorrhoeae*:

g277/m277

g277.pep

10 20 30
MVHVAVAYGIAVRRFCPNEVIDVFHALQVH

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```

                                :|||||: |:|:|||||:|:|:|
m277      GLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAVGDGVAVERFCPNEVVDVFTLQVH
              30      40      50      60      70      80

              40      50      60      70      80      90
g277.pep   RQAFDAVGNFAEYGRAIDTADLLEIGKLGYPHAVEPDFPAQTPTREGGVFPVVFDDKADV
              |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      RQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAVEPDFPAQTPRAEGGVFPVVFDDKADV
              90      100     110     120     130     140

              100     110     120     130     140     150
g277.pep   DFGIDAQFAQGVIEVLDIGGGFEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
              |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      DFGIDAQFAQGVIEVLDIGGSGLEGDLELVIVLQAVGVVAVAAVFGAAAGLDVGGKPR
              150     160     170     180     190     200

              160     170     180     190     200
g277.pep   GAERAQAGGGMGCAGTDFHVEGLDDGAAFVCPEGLQFEDDLLEGKHGLL
              ||| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
m277      GAECAQAGGGMGCAGTDFHVEGLDDGAAFVCPECLQFEDDLLEGKHGLX
              210     220     230     240     250

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1137>:

```

a277.seq
1   ATGCCCCGCT TTGAGGACAA GCTCGTAGGC AGGCAGGGCG AGGGCGGCGT
51  TTTCTTCGGC AAGCAGGCGT TTGGCTTGCG CTTCGTAGTC GTTGAAGTGG
101 CGCAGCAGCC AATCGGCATC GCTGTATTCG AAGTTGTAGG TGGATTGTTT
151 GACTTCGTTT TGGTGGTACA CGTCGCCGTA AGTTACTGTA TTACCGTCCA
201 GCGTTTTTGC CCAAACGAGG TCATAGACGT TTTCCACGCC TTGCAGGTAC
251 ATCGCCAAGC GTTCGATGCC TAGGTGATT TCGCCGAGTA CGGGGGTGCA
301 TCGATGCCG CCGACTTGTT GGAAATAGGT GAAC TGGGTT ACTTCCATAC
351 CGTTGAGCCA GACTTCCCAG CCCAAACCCC ACGCGCCGAG GGTGGGGTTT
401 TCCCAGTCGT CTTGACAAA GCGGATGTCG TGCAC TTTGG GGTGATGCC
451 CAATTCGCGC AGGGAGTCGA GATAGAGGTC TTGGATATTG GCGGGAGCGG
501 GCTTGAGGGC GACTTGGAAT TGGTAATAGT GTTGCAGGCG GTTGGGGTTG
551 TCGCCGTAGC GACCGTCTTT GGGGCGGCGG CTGGGTTGGA CGTAGGCGGC
601 AAACCAAGGC TCGGGGCCGA GTGCGCGCAG ACAGGTGGCG GGATGGGATG
651 TGCCGGCACC GACTTCCATG TCGAAGGGT GGATGACGGT GCAGCCTTTG
701 TCTGCCAGA ATGTTTGCAG TTTGAAGATG ATTTGTTGGA AGGTAAGCAT
751 GGCTTATGA

```

This corresponds to the amino acid sequence <SEQ ID 1138; ORF 277.a>:

```

a277.pep
1   MPRFEDKLVG RQEGGVFFG KQAFGLRFVV VELAQQPIGI AVFEVVGGLF
51  DFVLVVHVAV SYCITVQRFC PNEVIDVFHA LQVHRQAFDA VGDFAEYGGA
101 VDAADLLEIG ELGYFHTVEP DFPAQTPRAE GGVFPVVFDD ADVVHFGVDA
151 QFAQGVIEV LDIGGSGLEG DLELVIVLQA VGVVAVATVF GAAAGLDVGG
201 KPRLGAECAQ TGGGMGCAGT DFHVEGLDDG AAFVCPECLQ FEDDLLEGKH
251 GL*

```

m277/a277 92.5% identity in 252 aa overlap

```

              10      20      30      40      50      60
m277.pep     MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLLDFVLVVHVAV
              |||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a277         MPRFEDKLVGRQEGGVFFGKQAFGLRFVVVELAQQPVGIAVFEVVGGLDFVLVVHVAV
              10      20      30      40      50      60

              70      80      90      100     110     120
m277.pep     GDGVAVERFCPNEVVDVFTLQVHRQAFDAVGDFAEYGRAVDAADLLEIGKLGYPHAVEP
              :  :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
a277         SYCITVQRFCPNEVIDVFHALQVHRQAFDAVGDFAEYGGAVDAADLLEIGELGYFHTVEP
              70      80      90      100     110     120

              130     140     150     160     170     180

```

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```

m277.pep      DFPAQTPRAEGGVFPVVFDDKADVDFGIDAQFAQRVEIEVLDIGGSGLEGDLVLVQLQA
a277          |||||:|||||
              130      140      150      160      170      180

              190      200      210      220      230      240
m277.pep      VGVVAVAAVFGAAAGLDVGGKPRLLGAECAQAGGGMGCAGTDFHVEGLDDGAAAFVCPCECLQ
a277          |||||:|||||
              190      200      210      220      230      240

              250
m277.pep      FEDDLLEGKHGLX
a277          |||||
              250

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1139>:

```

g278.seq (partial)
1   ttgcgtgcaa tcacgcccgg tgcgattttt tcgacagggg cgggtcaaagt
51  tgtattaatc ggacctttgc cgtcgatagg ccgacccaat gcatcgacga
101 cgcgtccgac caattcgcgt ccgaccggca cttctaaat acggccggta
151 caggtaaccg tgcgccttc tttaatatgt tcgtactcgc ccaacactac
201 ggcaccgacg gagtcgcgct ccagggttcat cgccaagcct aaagtgttac
251 ccgggaattc gagcatctca ccttgcatg catctgacaa accatggatg
301 cgaacgatac cgtcagttac cgaaatcacc gtaccacggg tactcacttc
351 ggcattttaca gacagatttt cgatcttggc tttaatcaga tcgctaattt
401 cagcaggatt aagctgcatg aaaactctcc taattcgtca tagtcgtgta
451 caaagcactc agtttgcctt gtacagacaa atccaaaacc tgatcaccca
501 cttcaacttt ta...

```

This corresponds to the amino acid sequence <SEQ ID 1140; ORF 278.ng>:

```

g278.pep (partial)
1   LRAITPGAIF STGAVKVVL I GPLPSIGRPN ASTTRPTNSR PTGTSKIRPV
51  QVTVSPSLIC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPRVLTSFT DRFSILALIR SLISAGLSCM KTLIRHSRV
151 QSTQFALYRQ IQNLITHFN...

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1141>:

```

m278.seq..
1   TTGCGCGCAA TCACGCCCCG TGCGATTTT TCGATAGGGG CGGTCAAAGT
51  TGTATTAATC GGGCCTTTGC CGTCGATAGG CCGACCCAAT GCATCAACGA
101 CGCGTCCGAC CAGTTCGCGT CCGACCGGCA CTTCCAAGAT ACGACCGGTA
151 CAGGTAACCG TGTCGCCTTC TTTAATGTGT TCGTACTCGC CCAACACTAC
201 GGCGCCGACG GAGTCGCGCT CCAGGTTTAT CGCCAAGCCG AAAGTGTTAC
251 CCGGGAATTC GAGCATCTCA CCTTGCAATG CATCTGACAA ACCATGGATG
301 CGAACGATAC CGTCAGTTAC CGAAATTACC GTACCACAGG TACGCACTTC
351 GGCATTTACA GACAGATTTT CGATCTTGGC TTTAATCAAA TCGCTAATTT
401 CAGCAGGATT AAGCTGCATG AAAACTCTCC TAATTCGTCA TAGTCGTGTA
451 CAAGGCACTC AATTGTCCTT GTACAGACAA ATCCAAAACC TGATCACCCA
501 CTTCAACTTT TATGCCGCCA ATCAGCTCCG GTTCGATTTC GACAGAGATT
551 TTCAGCTCGC TGTCGAAACG CTTATTCAGC ATTTGCACCA ACTCGCCGAC
601 CTGTTTGTCT GTCAACGGAT AGGCACTGTA AATGACGGCA GATTGTATAT
651 GGTGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1142; ORF 278>:

```

m278.pep
1   LRAITPGAIF SIGAVKVVL I GPLPSIGRPN ASTTRPTSSR PTGTSKIRPV
51  QVTVSPSLMC SYSPNTTAPT ESRSRFIAKP KVLPGNSSIS PCIASDKPWM
101 RTIPSVTEIT VPQVRTSFT DRFSILALIK SLISAGLSCM KTLIRHSRV
151 QGTQFALYRQ IQNLITHFNF YAANQLRFDL DRDFQLAVET LIQHLHLAD
201 LFVGQRIGTV NDGRFDMVE*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 278 shows 95.9% identity over a 170 aa overlap with a predicted ORF (ORF 278.ng) from *N. gonorrhoeae*:

g278/m278

	10	20	30	40	50	60
g278.pep	LRAITPGAIFSTGAVKVVLI	GPLPSIGRPNASTTRPTNSRPTGT	SKIRPVQVT	VSPSLIC		
m278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLMC		
	10	20	30	40	50	60
	70	80	90	100	110	120
g278.pep	SYPNNTAPT	ESRSRFI	AKPKVLP	GNSSISPCIASDKP	WMRTIP	SVTEITVPRVLTSAFT
m278	SYPNNTAPT	ESRSRFI	AKPKVLP	GNSSISPCIASDKP	WMRTIP	SVTEITVPRVLTSAFT
	70	80	90	100	110	120
	130	140	150	160	170	
g278.pep	DRFSILALIRSLISAGL	SCMKTLLIRHSRVQSTQ	FALYRQIQNLITHFNF			
m278	DRFSILALIKSLISAGL	SCMKTLLIRHSRVQSTQ	FALYRQIQNLITHFYAANQLRFDF			
	130	140	150	160	170	180
m278	DRDFQLAVETLIQHLHQLADLFV	QGRIGTVNDGRFDMVE*				
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1143>:

a278.seq

1	TTGCGCGCAA	TCACGCCCGG	TGCGATTTTT	TCGATAGGGG	CGGTCAAAGT
51	TGTATTAATC	GGGCCTTTGC	CGTCGATAGG	CCGACCCAAT	GCATCAACGA
101	CGCGTCCGAC	CAGTTCGCGT	CCGACCGGCA	CTTCCAAGAT	ACGACCGGTA
151	CAGGTAACCG	TGTCGCCTTC	TTTAATATGT	TCGTGCTCGC	CCAACACTAC
201	GGCGCCGACG	GAGTCGCGCT	CCAGGTTCAT	CGCCAAGCCG	AAAGTGTTAC
251	CCGGGAATTC	GAGCATCTCA	CCTTGCAATTG	CATCTGACAA	ACCATGGATG
301	CGAACGATAC	CGTCAGTTAC	CGAAATCACC	GTACCACGGG	TACGCACTTC
351	GGCATTTACA	GACAGATTTT	CGATCTTGGC	TTTAATCAAA	TCGCTAATTT
401	CAGCAGGATT	AAGCTGCATG	AAACTCTCC	TAATTCTGTC	TAGTCGTGTA
451	CAAGGCACTC	AATTTGCCTT	GTACAGACAA	ATCCAAAACC	TGATCACCCA
501	CTTCAACTTT	TATGCCGCCA	ATCAGCTCCG	GTTTCGATTTC	GACAGAGATT
551	TTCAGCTCGC	TGTCGAAACG	CTTATTGAGC	ATTTGCGCCA	ACTCGCCGAC
601	CTGTTTGTCG	GTCACGGAT	AGGCACTGTA	AATGACGGCA	GATTTGATAT
651	GGTTGAATGA				

This corresponds to the amino acid sequence <SEQ ID 1144; ORF 278.a>:

a278.pep

1	LRAITPGAIF	SIGAVKVVLI	GPLPSIGRPN	ASTTRPTSSR	PTGTSKIRPV
51	QVTVSPSLIC	SCSPNNTAPT	ESRSRFI	AKPKVLP	GNSSISPCIASDKP
101	WMRTIP	SVTEITVPRV	RTSAFT	DRFSILALIK	SLISAGLSCM
151	KTLIRHSRV	QGTQFALYRQ	IQNLITHFNF	YAANQLRFDF	DRDFQLAVET
201	LIQHLRQLAD	LFVGQRIGTV	NDGRFDMVE*		

m278/a278 98.2% identity in 219 aa overlap

	10	20	30	40	50	60
m278.pep	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLMC		
a278	LRAITPGAIFSIGAVKVVLI	GPLPSIGRPNASTTRPTSSRPTGT	SKIRPVQVT	VSPSLIC		
	10	20	30	40	50	60
	70	80	90	100	110	120
m278.pep	SYPNNTAPT	ESRSRFI	AKPKVLP	GNSSISPCIASDKP	WMRTIP	SVTEITVPRVRTSAFT
a278	SCSPNNTAPT	ESRSRFI	AKPKVLP	GNSSISPCIASDKP	WMRTIP	SVTEITVPRVRTSAFT
	70	80	90	100	110	120

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	130	140	150	160	170	180
m278.pep	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
a278	DRFSILALIKSLISAGLSCKMTLLIRHSRVQGTQFALYRQIQNLITHFNFYAANQLRFDF					
	130	140	150	160	170	180
	190	200	210	220		
m278.pep	DRDFQLAVETLIQHLHQLADLFVQGRIQTVNDGRFDMVEX					
a278	DRDFQLAVETLIQHLHQLADLFVQGRIQTVNDGRFDMVEX					
	190	200	210	220		

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1145>:

g279.seq

```

1  atgacgcgga tttgcggctg cttgatttca acggttttga gtgtttcggc
51  aagtttgtcg gcggcgggtt tcatcaggct gcaatgggaa ggaacggata
101 ccggcagcgg cagggcgcggt ttggctccgg cttctttggc ggcagccatg
151 gtgcgtccga cggcgccggc gttgcctgca atcacgactt gtccggcgca
201 gttgaagttg acggcttcga ccacttcgcc ctgtgcggat tcggcacaaa
251 tctgcctgac ctgttcattc tccaaaccca aaatggccgc cattgcgcct
301 acgccttgcg gtacggcgga ctgcatcagt tcggcgcgca ggcggacgag
351 tttgacggca tcggcaaaat ccaatgcttc ggcggcgaca agcgcggtgt
401 attcgccgag gctgtgtccg gcaacggcgg caggcgtttt gccgcccact
451 tccaaatag

```

This corresponds to the amino acid sequence <SEQ ID 1146; ORF 279.ng>:

g279.pep

```

1  MTRICGCLIS TVLSVSASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  VRPTAAALPA ITTCPGELKL TASTTSPCAD SAQICLTCSS SKPKMAAIAP
101 TPCGTADCIS SARRRSLTA SAKSNASAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1147>:

m279.seq

```

1  ATAACGCGGA TTTGCGGCTG CTTGATTCA ACGGTTTTCA GGGCTTCGGC
51  AAGTTTGTCT GCGGCGGGTT TCATCAGGCT GCAATGGGAA GGTACGGACA
101 CGGCAGCGCG CAGGCGCGGT TTGGCACCGG CTTCTTTGGC GGCAGCCATG
151 GCGCGTCCGA CGGCGCGGCG GTTGCTGCA ATCACGATT GTCCGGGTGA
201 GTTGAAGTTG ACGGCTTCGA CCACCTCGCT TTGGGCGGCT TCGGCACAAA
251 TGGCTTTAAC CTGCTCATCT TCCAAGCCGA GAATCGCCGC CATTGCGCCC
301 ACGCTTGCG GTACGGCGGA CTGCATCAGT TCGGCGCGCA GGCGCACGAG
351 TTTGACCGCG TCGGCAAAAT TCAATGCGCC GCGGCAACG AGTGCGGTGT
401 ATTCGCCGAG GCTGTGTCCG GCAACGCGCG CAGGCGTTTT GCCGCCGCT
451 TCTAAATAG

```

This corresponds to the amino acid sequence <SEQ ID 1148; ORF 279>:

m279.pep

```

1  ITRICGCLIS TVFRASASLS AAGFIRLQWE GTDTGSGRAR LAPASLAAAM
51  ARPTAAALPA ITICPGELKL TASTTSLWAA SAQMALTCSS SKPRIAAIAP
101 TPCGTADCIS SARRRSLTA SAKFNAPAAT SAVYSPRLCP ATAAGVLPPT
151 SK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 279 shows 89.5% identity over a 152 aa overlap with a predicted ORF (ORF 279.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m279.pep	ITRICGCLISTVFRASASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
g279	MTRICGCLISTVLSVSASLSAAGFIRLQWEGTDTGSGRARLAPASLAAAMVRPTAAALPA					
	10	20	30	40	50	60
	70	80	90	100	110	120

m279.pep	ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA : :
g279	ITTCPGELKLTASTTSPCADSAQICLTCSSSKPKMAAIAPTPCGTADCISSARRRTSLTA 70 80 90 100 110 120
	130 140 150
m279.pep	SAKFNAPAATSAVYSPRLCPATAAGVLPPASKX :
g279	SAKSNASAATSAVYSPRLCPATAAGVLPPTSKX 130 140 150

a279.seq

1	ATGACNCNGA	TTTGCGGGTG	CTTGATTTCA	ACGGTTTNNNA	GGGCTTCGGC
51	GAGTTTGTCG	GCGGCGGGTT	TCATGAGGCT	GCAATTGGGAA	GGTACNGACA
101	CNNGCAGCGG	CAGGGCGCGT	TTGGCGCCGG	CTCTTTTGGC	GGCAAGCATA
151	GCGCGCTCGA	CGGCGGCGGC	ATTGCTTGCA	ATCACGACTT	GTCGCGGCGA
201	GTTGAAGTTG	ACGGCTTCAA	CCACTTCATC	CTGTGCGGAT	TCGGCGCAAA
251	TTTGTTTTAC	CTGTTTCATCT	TCCAAGCCGA	GAATCGCCGC	CATTGCGCCC
301	ACGCCTTGCG	GTACGGCGGA	CTGCATCAGT	TCGGCGCGCA	NGCGCACGAG
351	TTTGACCGCG	TCGGCAAAAT	CCAATGCGCC	GGCGGCAACN	AGTGCGGTGT
401	ATTCGCCGAN	GCTGTGTCCG	GCAACGGCGG	CAGGCGTTTT	GCCGCCCGCT
451	TCGGAATAG				

a279.pep					
1	MTXICGCLIS	TVXRASASLS	AAGFMRLQWE	GTDTGSGRAR	LAPASLAASI
51	ARSTAAALPA	ITTCPGELKL	TASTTSSCAD	SAQICFTCSS	SKPRIAAIAP
101	TPCGTADCIS	SARXRTSLTA	SAKSNAAPAAT	SAVYSPXLCP	ATAAGVLPPA
151	SE*				

		10	20	30	40	50	60
m279.pep		ITRICGCLISTVFRASASLSAAGFIRLOWEGTDTGSGRARLAPASLAAAMARPTAAALPA					
	:						
a279		MTXICGCLISTVXRASASLSAAGFMRLQWEGTDTGSGRARLAPASLAASIARSTAAALPA					
		10	20	30	40	50	60
		70	80	90	100	110	120
m279.pep		ITICPGELKLTASTTSLWAASAQMALTCSSSKPRIAAIAPTPCGTADCISSARRRTSLTA					
a279		ITTCPGELKLTASTTSSCADSAQICFTCSSSKPRIAAIAPTPCGTADCISSARXRTSLTA					
		70	80	90	100	110	120
		130	140	150			
m279.pep		SAKFNAPAATSAVYSPRLCPATAAGVLPASKX					
a279		SAKSNAPAATSAVYSPXLCPPATAAGVLPASEX					
		130	140	150			

The primer described in Table 1 for ORF 279 was used to locate and clone ORF 279. ORF 279 was cloned in pET and pGex vectors and expressed in E.coli as above-described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 2A shows the results of affinity purification and Figure 2B shows the expression in E.coli. Purified GST-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 2C), western blot (Figure 2D). These experiments confirm that 279 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 279 are provided in Figure 6. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al.

1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 279 and the amino acid sequence encoded thereby is provided herein.

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1151>:

g280.seq

```

1  atgaaacacc tcaaacttac ccttattgcc gcattgctgg ccaccgccgc
51  aactgccgca ccccttccgg ttgtaaccag tttagcgatt ttaggcgacg
101 tagccaaaca aatcggcggt gagcgcgtag ccgtacaaag cctcgtcggg
151 gccaaaccaag atactcatgc ctatcacatg accagtggcg acattaaaaa
201 aatccgcagt gcaaaactcg tcctgctcaa cggcttggga cttgaagccg
251 ccgacatcca acgcgccgtc aaacagagca aagtatccta tgccgaagcg
301 accaaaggca tccaaccctt caaagccgaa gaagaaggcg gacaccatca
351 cgaccaccat cagaccacg atcatgacca cgaaggacac caccacgacc
401 acggcgaata tgaccccccac gtctggaacg accctgttct tatgtccgac
451 tatgcccaca acgtcgctga aaccctgata aaggccgatc ccgaaggcaa
501 agtttattat caacaacgct tgggcaacta ccaaattgcag cttaaaaaac
551 tgcacagcga cgcacaagcc gcatttaatg ccgtccctgc cgccaaacgc
601 aaagtcttga cggggcacga cgcattttcc tacatgggca accgctacaa
651 catcagcttc atcgccccgc aaggcgtgag cagcgaagcc gagccgtccg
701 ccaacaagat cgcgcgcata atccggcaaa tcaaacgcga aggcatacaa
751 gccgtattta ccgaaaatat caaagacacc cgcattggtg accgcatcgc
801 caaagaaacc ggcgtcaacg tcagcggcaa actgtattcc gacgcactcg
851 gcaacgcgcc cgcagacacc tacatcgcca tgtaccgcca caacgtcgaa
901 gccttgacca acgcgatgaa gcaataa

```

This corresponds to the amino acid sequence <SEQ ID 1152; ORF 280.ng>:

g280.pep

```

1  MKHLKLTLIA ALLATAATAA PLPVVTSFSI LGDVAKQIGG ERVAVQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADIQRAV KQSKVSYAEA
101  TKGIQPLKAE EEGGHHHDH HDHHDHDEGH HHDHGEYDPH VWNDPVLMSD
151  YAQNVAETLI KADPEGVVY QQLGNVYQMQ LKKLHSDAQA AFNAVPAKR
201  KVLTHGDAFS YMGNRYNISF IAPQGVSEEA EPSAKQVAI IRQIKREGIK
251  AVFTENIKDT RMVDRIAKET GVNVSGLKLYS DALGNAPADT YIGMYRHNVE
301  ALTNAMKQ*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1153>:

m280.seq

```

1  ATGAAACACC TCAAACAC CTTATTGCC GCATTGCTGA CCGCCTCCGC
51  AACTGCCGCC CCCCTGCCGG TTGTAACCAG CTTCAGCATT TTAGGCGACG
101 TAGCCAAACA AATCGGCGGA GAGCGCGTAT CCATACAAAG TTTGGTCGGA
151 GCCAACCAAG ATACGCACGC CTATCATATG ACCAGTGGCG ACATTAAAAA
201 AATCCGCAGT GCAAAACTCG TCCTGTCTAA CGGCTTAGGA CTTGAAGCTG
251 CCGATGTGCA ACGCGCCGTC AAACAAAGCA AAGTATCCTA TACCGAAGCG
301 ACCAAAGGCA TCCAACCCCT CAAAGCCGAA GAAGAAGGCG GACACCATCA
351 CGACCACGAT CATGACCACG AAGGACACCA CCATGACCAC GCGGAATATG
401 ACCCGCACGT CTGGAACGAC CCCGTCCTTA TGTCCGCTTA TGCCCAAAAC
451 GTTGCCAAAG CCCTGATAAA GGCCGATCCC GAAGGCAAAG TTTATTATCA
501 ACAACGCTTG GGCAACTACC AAATGCAGCT CAAAAAAGT CACAGCGACG
551 CACAAGCCGC ATTTAATGCC GTCCCTGCTG CCAAACGCAA AGTCCTGACC
601 GGGCACGATG CCTTTTCCTA TATGGGCAA CGTTACCATA TCGAATTCAT
651 CGCCCCGCAA GCGTGAGCA GCGAAGCCGA GCCTTCGGCC AAACAAGTCG
701 CCGCCATCAT CCGACAAATC AAACGCGAAG GCATCAAAGC CGTCTTACC
751 GAAAACATCA AGGACACCCG TATGGTTGAC CGTATCGCCA AAGAAACCGG
801 TGTCACGTC AGCGGCAAAC TGTATTCCGA CGCACTCGGC AACCGCCCCG
851 CAGACACCTA CATCGGAATG TACCGCCACA ACATCAAAGC CTTGACCAAC
901 GCGATGAAGC AATAA

```

This corresponds to the amino acid sequence <SEQ ID 1154; ORF 280>:

m280.pep

```

1  MKHLKLTLIA ALLTASATAA PLPVVTSFSI LGDVAKQIGG ERVSIQSLVG
51  ANQDTHAYHM TSGDIKKIRS AKLVLLNGLG LEAADVQRAV KQSKVSYTEA
101  TKGIQPLKAE EEGGHHHDH HDHEGHHHDH GEYDPHVWND PVLMSAYQON
151  VAKALIKADP EGKVYYQQL GNYQMLKKL HSDAQAAFNA VPAKRKVLV

```

Homology with a predicted ORF from *N.gonorrhoeae*

m280/g280

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1155>:

a280.seq	1	ATGAAACACC	CCAAACTCAC	CCTTATCGCC	GCATTGCTGA	CCACTGCCGC
	51	AACTGCCGCC	CCCCTGCCGG	TTGTAACCAG	CTTCAGCATT	TTAGGCGACG
	101	TAGCCAAACA	ACCTGCGCGA	GAGCGCGTAT	CCATACAAAG	TTTGGTCGGA
	151	GCCAAACCAAG	ATACGCACGC	CTATCATATG	ACCAGCGGCG	ACATTAAAAA
	201	AATCCGCAGT	GCAAAACTCG	TCCTGATTAA	CGGCTTAGGA	CTTGAAGCTG
	251	CCGACATCCA	ACGTGCCGTC	AAACAGAGCA	AAGTATCCTA	TGCCGAAGCG
	301	ACCAAAGGCA	TCCAACCCCT	CAAGCGGAA	GAGAAGGCG	GACACCATCA
	351	CGACCACGAT	CATGACCACG	ACCATGACCA	GAAGGACAC	CACCACGACC
	401	ACGGCGAATA	TGACCCCCAC	GTCTGGAACG	ACCCCGTCCT	TATGTCGCGC
	451	TATGCCCAAA	ACGTCGCCGA	AGCCCTGATA	AAGGCCGACG	CCGAAGGCAA
	501	AGTTTATTAT	CAACAACGCT	TGGGCAACTA	CCAAATGCAG	CTCAAAAAAC
	551	TGCACAGTGA	CGCACAAGCC	GCATTTAATG	CCGTCCTGCG	CGCCAAACGC
	601	AAAGTCCTGA	CCGGGCACGA	TGCCTTTTCC	TATATGGGCA	AACGTTACCA
	651	TATCGAATTC	ATCGCCCCAC	AAGGTGTGAG	CAGCGAAGCC	GAGCCTTCAG
	701	CCAAACAAGT	CGCCGCCATC	ATCCGACAA	TCAAACGCGA	AGGCATCAAA
	751	GCCGTATTTA	CCGAAATAT	CAAAGACACC	CGCATGGTTG	ACCGCATCGG

801 CAAAGAAACC GGTGTCAACG TCACGGCAA ACTGTATTCC GACGCACTCG
851 GCAACGCACC CGCAGACACC TACATCGGCA TGTACCGCCA CAACATCAAA
901 GCCTTAACCA ACGCGATGAA GCAATAA

a280.pep

1	<u>MKHPKLTLLIA</u>	<u>ALLTTAATAA</u>	PLPVVTSFSI	LGDAKQIGG	ERVSQSLVG
51	ANQDTHAYHM	TSGDIKKRS	AKLVLDHNLG	LEAADIQRAV	KQSKVSYAEA
101	TKGIQPLKAE	EEGGHHHDHD	HDHHDHDMQH	HHDHGEYDPH	WVNDPVLMAA
151	YAQNVAELAI	KADPEGKVYY	QQRGLNYQMG	LKKLHSDAQA	AFNAVPAAKR
201	KVLTGHDAFS	YMGKRYHIEF	IAPQGVSSAA	EPSAKQVAAI	IRQIKREGIK
251	AVFTENIKDT	RMVDRIAKET	GVNVSGKLYS	DALGNAPADT	YIGMYRHNIK
301	ALTNAMKO*				

		10	20	30	40	50	60
m280.pep		MKHLKLT	LIAALLT	ASATAAP	LPVVT	SFSILG	DVAKQIG
a280		MKHPKLT	LIAALLT	TAATAAP	LPVVT	SFSILG	DVAKQIG
		10	20	30	40	50	60
		70	80	90	100	110	120
m280.pep		TSGDIKK	IRSAKLV	LLNGLG	LEAADV	QRAVKQ	SKVSYTE
a280		TSGDIKK	IRSAKLV	LLNGLG	LEAADV	QRAVKQ	SKVSYTE
		70	80	90	100	110	120
		130	140	150	160	170	
m280.pep		HDH----	EGHHHDH	GEYDPH	VWNDP	VLMSAY	AQNVAKA
a280		HDHHDH	DHEGHHH	DHGEYD	PHVWND	PVLMSAY	AQNVAEAL
		130	140	150	160	170	180
		180	190	200	210	220	230
m280.pep		LKKLHSD	AQAAFNA	VPAARK	VLTGHD	AFSYMGR	KRYHIEFI
a280		LKKLHSD	AQAAFNA	VPAARK	VLTGHD	AFSYMGR	KRYHIEFI
		190	200	210	220	230	240
		240	250	260	270	280	290
m280.pep		IRQIKRE	GIIKAVF	TENIKD	TRMVD	RIAKET	GVNVSG
a280		IRQIKRE	GIIKAVF	TENIKD	TRMVD	RIAKET	GVNVSG
		250	260	270	280	290	300
		300					
m280.pep		ALT	NAMKQX				
a280		ALT	NAMKQX				

q281.seq

1	atgcactacg	ccctcgcata	cgtcttctgc	ctgtccctca	gcgcgcacc
51	cgtcggcgta	ttcctcgtca	tgcgcgcat	gagcctgata	ggcgacgcat
101	tgagccacgc	cgtcctgccc	ggtgccgccc	tcggctacat	gtttgccggc
151	ttgagcctgc	ccgctatggg	tgtggcgggg	tttgccgccc	gtatgctgat
201	ggcgctgctt	gccggactcg	tcagccgctt	taccaccctg	aaagaagatg
251	ccaactttgc	cgccttttac	ctgagcagcc	tcgccatcgg	cgtaatcctc
301	atcagcaaaa	acggcagcag	cgtcgaattca	ctccacctcc	ttttcggatc
351	tgtgcttgcc	gtcgatattc	cgcgcatgca	actcatcgcc	gccgtctccg
401	gcctcagcct	cattaccctt	gccgtcatct	accgccccct	ggtgctagaa
451	agcatagacc	cccttttctt	caagtccgtc	aacggcaaaa	gcgqgctttg

g281.pcp

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1159>:

1	ATGCGCTACG	CCCTCGCATC	CGTCTTCTGC	CTGTCCCTCA	GTGCCGCACC
51	CGTCGGCGTA	TTCTCTGTCA	TGCGCCGTAT	GAGCCTGATA	GGCGACGCAT
101	TGAGCCACGC	CGTCCTGCC	GGTGCCGCCG	TCGGCTACAT	GTTTGCCGGC
151	TTGAGCTCTG	CCGCATCTGG	TTTGGGCGCG	GTAGCCCGAG	GCATGCTGAT
201	GGCACTGCTT	GCCGGACTCG	TCACGCGCTT	CACCACTCTG	AAAGAAGATG
251	CCAACTTTGC	CGCCTTTTAT	CTCAGCAGCC	TCGCCATCGG	CGTAGTCCTC
301	GTCAGCAAAA	ACGGGAGCAG	CGTCGATTTG	CTCCACCTCC	TTTTCGGCTC
351	TGTACTTGCC	GTGATATTT	CTGCCCTGCA	GCTCATCGCC	GCCGTCTCCA
401	GCCTCAGCT	CATTACCTT	CCGCTCATCT	ACCGCCCGCT	CGTACTCGAA
451	AGCATCGACC	CCTGTTTTCT	CAAATCCGTC	GCGGGCAAAG	CGGGCTTTTG
501	GCACGTCCCT	TTTCTCGTCC	TGGTCGTCAT	GAACCTCGTA	TCCGGCTTTC
551	AAGCCCTCGG	CACACTCATG	TCCGTCCGAC	TCATGATGCT	GCCAGCCATT
601	ACCGCCAGCC	TGTGGGCGAA	GCATATGGGC	GACTCATCTT	TCCTATCCGT
651	TCTGACAGCC	CTGCTGTGCG	GCTTGAGCGG	ACTGCTCATC	TCCTACCACA
701	TCGAAATTCC	TTCCGGTCCC	GCCATCATCC	TCTGTTGCAG	GCTCCTTTAT
751	CTCTTTTCCG	TCATACTCGG	CAAAGAAGGC	GCAATTCTGA	CC...

m281.pep (partial)

Computer analysis of this amino acid sequence gave the following results:

ORF 281 shows 93.5% identity over a 263 aa overlap with a predicted ORF (ORF 281.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
m281.pep	MRYALASVFCLSLSAAPVGVLVMMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGLGG					
	:					
g281	MHYALASVFCLSLSAAPVGVLVMMRRMSLIGDALSHAVLPGAAVGYMFAGLSLPAMGVGG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m281.pep	VAAGMLMALLAGLVSRTTTLKEDANFAAFYLSSLAIGVVLVSKNGSSVDLLHLLFGSVLA					
g281	FAAGMLMALLAGLVSRTTTLKEDANFAAFYLSSLAIGVILISKNGSSVDLLHLLFGSVLA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m281.pep	VDIPALQLIAAVSSLTLITLAVIYRPLVLESIDPLFLKSVGGKGGLWHVFLVLVVMNLV					

	: : :
g281	VDIPALQLIAAAVSGLTTLITLAVIYRPLVLESIDPLFLKSVNGKGGLWHVIFLILVVMNLV
	130 140 150 160 170 180
	190 200 210 220 230 240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTTALLCGLSGLLISYHIEIPSGP
	: : : : :
g281	SGFQALGIILMSVGIMMLPAITARLWARNMGTLILLSVLIALFCGLIGLLISYHIEIPSGP
	190 200 210 220 230 240
	250 260
m281.pep	AIILCCSVLYLF SVILGKEGGILT
g281	AIILCCSVLYLF SVILGKEGGILPKWFKNHRHHTTX
	250 260 270

```
a281.seq
  1  ATGCGCTACG  CCCTCGCATC  CGTCTTCTGC  CTGTCCCTCA  GTGCCGCACC
51  CGTCGGCGTA  TTCCTCGTCA  TGCGCCGTAT  GAGCCTGATA  GGGCAGCGAT  GTTGC CGCGG
101  TGAGCCACGC  CGTCTGCCCC  GGTGCCCGCG  TCGGCTACAT  GTTGC CGCGG
151  TTAAGCCTGC  CCGCCATGGG  TTTGGGCGGC  GTAGCCGCAG  GTATGCTGAT
201  GGCAGTGTCT  GCCGGAATCG  TCAGCCGCTT  CACCACCCTG  AAAGAAGATG
251  CCAACTTTGC  CGCCTTTTAT  CTCAGCAGCC  TCGCCATCGG  TGTA GCTCCTC
301  GTCAGCAAAA  ACGGCAGCAG  CGTCGATTTG  CTCACCTCC  TTTTCGGCTC
351  CGTACTTGCC  TCGCATATTC  CTGCCCTGCA  ATCATCGCC  GCCGTATCCA
401  CCCTCACACT  GCTTACCCTT  GCCGTCATCT  ACCGCCCGCT  CGTACTCGAA
451  AGCATCGACC  CCCTGTTTTCT  CAAATCTGTG  GGCGGCAAAG  GCGGGCTTTG
501  GCACGTCCTC  TTTCTCGTCT  TGGTCGT CAT  GAACCTCGTA  TCCGGCTTTC
551  AAGCCCTCGG  CACACTCATG  TCCGTCGGAC  TTATGATGCT  CAGGCCATT
601  ACCGCCCGCC  TATGGGCGAA  GCACATGGGC  GCACTCATCC  TCCTATCCGT
651  TCTGACAGCG  CTGCTGTGCG  GCTTGAGCGG  ACTGCTCATT  TCCTACCACA
701  TCGAAATTC  TTCCGGTCCC  GCCATCATCC  TCTGTTGCAG  CGTCCTTTAT
751  CTCTTTTCCG  TCATACTCGG  CAAAGAAGGC  GGCATTCTGA  CCAAATGGCT
801  CAAAACCAC  CGCACCACA  CCACCTGA
```

a281.pep

1	<u>MRYALASVFC</u>	<u>LSLSAAPGV</u>	<u>FLVMRRMSLI</u>	<u>GDALSHAVLP</u>	<u>GAAVGYMFAG</u>
51	<u>LSLPAMGLGG</u>	<u>VAAGMLMALL</u>	<u>AGLVSRTTTL</u>	<u>KEDANFAAFY</u>	<u>LSSLAIGVVL</u>
101	<u>VSKNGSSVDL</u>	<u>LHLLFGSVLA</u>	<u>VDIPALQLIA</u>	<u>AVSTLTLLTL</u>	<u>AVIYRPLVLE</u>
151	<u>SIDPLFLKSV</u>	<u>GGKGGLWHVL</u>	<u>FLVLVVMNLV</u>	<u>SGFQALGTL</u>	<u>SVGLMMLPAI</u>
201	<u>TARLWAKHMG</u>	<u>ALILLSVLTA</u>	<u>LLCGLSGLLI</u>	<u>SYHIEIPSGP</u>	<u>AIILCCSVLY</u>
251	<u>LFSVILGKEG</u>	<u>GILTKWLKNH</u>	<u>RHHTT*</u>		

		10	20	30	40	50	60
m281.pep		MRYALASVFCLSLSAAPVG	VFLVMRRMSLIGDALSHAV	LPGA	AVGYMFAGLSLP	PAMGLGG	
a281		MRYALASVFCLSLSAAPVG	VFLVMRRMSLIGDALSHAV	LPGA	AVGYMFAGLSLP	PAMGLGG	
		10	20	30	40	50	60
		70	80	90	100	110	120
m281.pep		VAAGMLMALLAGLVSRFT	TLKEDANFAAFYLSSLAIG	VVLVSKNGSSVDLLHLL	F	FGSVLA	
a281		VAAGMLMALLAGLVSRFT	TLKEDANFAAFYLSSLAIG	VVLVSKNGSSVDLLHLL	F	FGSVLA	
		70	80	90	100	110	120
		130	140	150	160	170	180
m281.pep		VDIPALQLIAAVSSLT	LITLAVIYRPLVLESID	PLFLKSVGGKGGLWHV	FLVLVVMNLV		
a281		VDIPALQLIAAVSTL	TLTAVIYRPLVLESID	PLFLKSVGGKGGLWHV	FLVLVVMNLV		
		130	140	150	160	170	180

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	190	200	210	220	230	240
m281.pep	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
a281	SGFQALGTLMSVGLMMLPAITARLWAKHMGALILLSVLTALLCGLSGLLISYHIEIPSGP					
	190	200	210	220	230	240
	250	260				
m281.pep	AIILCCSVLYLFSVILGKEGGILT					
a281	AIILCCSVLYLFSVILGKEGGILTKWLKNHRHHTTX					
	250	260	270			

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1163>:

g282.seq

```

1  atgggattgg gtatggaaat cggcaagctg attgtggctc ttttggtgct
51  gatcaatccg tttagcgcgt tgtcgcttta ccttgacctg accaacggac
101 acagcacgaa ggagcgcagg aaggtcgcgc ggacggccgc cgtcgccgtg
151 tttgccgtga ttgcggtatt tgcgctgata ggcggtgcgc tattgaaggt
201 tttgggcatc agcgtcgggt cgtttcaggt cggcggcggg attttggtgc
251 tgctgatcgc catttcgatg atgaacggca acgacaatcc cgccaagcag
301 aatctcggcg cgcagccgga aacggggcaa gcgcgccccg cccgcaatgc
351 aggggacgatt gccgtcgtgc ccatcgccat accgatcacc atcggtcggg
401 gcggtatttc gactgtgatt atttatgctt cggcagccaa aacgtacagc
451 gatatcgccg tgattatcgc ggccggtttg gtggtcagtg cgatttgcta
501 tgccatttta atcgttgccg ggaaggtcag ccgcctgctg ggcgcgacgg
551 ggctgacgat tttaaaccgc attatgggta tgatgctggc ggcggtatcg
601 gtggagatta ttgtgtcggg actgaaaacg atattccccg aactggcagg
651 ttga

```

This corresponds to the amino acid sequence <SEQ ID 1164; ORF 282.ng>:

g282.pep

```

1  MGLGMEIGKL IVALLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGALLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1165>:

m282.seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCCTGATC GCGGTCACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CCGCGGCGGG ATTTTGGTGC
251 TGCTGATCGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GCGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCGG
401 GCGGTATTTC GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGC GCGACGG
551 GGCTGACGAT TTTAAACCGC ATTATGGGTA TGATGCTGGC GCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAACG ATATTCCCCG AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1166; ORF 282.ng>:

m282.pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ ARPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMLLAAYS
201 VEIIVSGLKT IFPQLAG*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N.gonorrhoeae*

ORF 282 shows 98.6 % identity over a 217 aa overlap with a predicted ORF (ORF 282.ng) from *N. gonorrhoeae*:

m282/g282

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
g282	MGLGMEIGKLIVALLVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m282 . pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
g282	GGALLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m282 . pep	AVVPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
g282	AVVPIAIPITIGPGGISTVIIYASAAKTYSDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
	190	200	210			
m282 . pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
g282	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1167>:

a282 . seq

```

1  ATGGGATTGG GCATGGAAAT CGGCAAGCTG ATTGTGGCTT TTTTGGTGCT
51  GATTAATCCG TTTAGCGCGT TGTCGCTTTA CCTTGACCTG ACCAACGGGC
101 ACAGCACGAA GGAGCGCAGG AAGGTCGCGC GGACGGCCGC CGTTGCCGTG
151 TTTGCCGTGA TTGCGGTATT TGCGCTGATC GGCGGTACGC TGCTGAAGGT
201 TTTGGGCATC AGCGTCGGTT CGTTTCAGGT CGGCGGCGGA ATTTTGGTGT
251 TGCTGATTGC CATTTCGATG ATGAACGGCA ACGACAATCC CGCCAAGCAG
301 AATCTCGGCG CGCAGCCGGA AACGGGGCAG GTGCGCCCCG CCCGCAATGC
351 CGGAGCGATT GCCGTCGTGC CCATCGCCAT ACCGATCACC ATCGGCCCCG
401 GCGGTATTTT GACCGTGATT ATTTACGCTT CGGCGGCTAA AACATACGGC
451 GACATCGCGT TGATTATCGC GGCCGGTTTG GTGGTCAGTG CGATTTGTTA
501 TGCCATTTTA ATCGTTGCCG GGAAGGTCAG CCGCCTGCTG GGTGCGACGG
551 GGCTGACGAT TTAAACCGT ATCATGGGTA TGATGCTGGC GGCGGTATCG
601 GTGGAGATTA TTGTGTCGGG ACTGAAAATG ATATTCCCGC AACTGGCAGG
651 TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1168; ORF 282.a>:

a282 . pep

```

1  MGLGMEIGKL IVAFLVLINP FSALSPLYLDL TNGHSTKERR KVARTAAVAV
51  FAVIAVFALI GGTLLKVLGI SVGSFQVGGG ILVLLIAISM MNGNDNPAKQ
101 NLGAQPETGQ VRPARNAGAI AVVPIAIPIT IGPGGISTVI IYASAAKTYG
151 DIALIIAAGL VVSAICYAIL IVAGKVSRLG GATGLTILNR IMGMLAAVS
201 VEIIVSGLKM IFPQLAG*

```

m282/a282 99.1% identity in 217 aa overlap

	10	20	30	40	50	60
m282 . pep	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
a282	MGLGMEIGKLIVAFVLINPFSALSPLYLDLTNGHSTKERRKVARTAAVAVFAVIAVFALI					
	10	20	30	40	50	60

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	70	80	90	100	110	120
m282.pep	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQARPARNAGAI					
a282	GGTLLKVLGISVGSFQVGGGILVLLIAISMNGNDNPAKQNLGAQPETGQVRPARNAGAI					
	70	80	90	100	110	120
m282.pep	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
a282	AVVPPIAIPITIGPGGISTVIIYASAAKTYGDIALIIAAGLVVSAICYAILIVAGKVSRL					
	130	140	150	160	170	180
m282.pep	GATGLTILNRIMGMLAAVSVEIIVSGLKTIFFPQLAGX					
a282	GATGLTILNRIMGMLAAVSVEIIVSGLKMIFFPQLAGX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1169>:

```

g283.seq
1   atgaactttg ctttatccgt catcacattt accctcgctt ctttctgcc
51  cgtcccgctt gccggaaccg ccgtctttac ttggaagac ggcggcggca
101 acagctattc ggatgtgccc aaacagcttc atcccgacca gagccaaatc
151 ctcaacctgc ggacgctcca aaccaaaccg gcggtcaagc ccaaacctgc
201 cgtcgatacg aatgcggaca gtgcgaagga aaacgaaaag gatatcgccg
251 agaaaaacgg gcagcttgag gaagaaaaga aaaaaattgc cgaaaccgaa
301 cggcagaaca aagaagaaaa ctgccggatt tcaaaaatga acctgaaggc
351 ggtgggaaac tcaaatgcga aaaacaagga tgatttgatc cgtaaatata
401 ataacgccgt aaacaatac tgccgttaa
  
```

This corresponds to the amino acid sequence <SEQ ID 1170; ORF 283.ng>:

```

g283.pep
1   MNFALSVITF TLASFLPVPP AGTAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTLQTKP AVKPKPAVDT NADSAKENEK DIAEKNGQLE EEKKKIAETE
101 RQNKEENCRI SKMNLKAVGN SNAKNKDDLI RKYNNVAVNKY CR*
  
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1171>:

```

m283.seq
1   ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCCTGCC
51  CGTCCCGCCT GCCGGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAAACCTGC GGACGCGCCA AACCAAACCG GCGGTCAAAC CCGCCCAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAAGA AGAAACTGCG CGGATTTCAA AAATGAACCT
351 GAAGGCGGTG GGAAATTCAA ATGCAAAAAA CAAGGATGAT TTGATTCGGA
401 AATACAATAA CGCCGTAAAC AAATACTGCC GTTAA
  
```

This corresponds to the amino acid sequence <SEQ ID 1172; ORF 283>:

```

m283.pep
1   MNFALSVIML TLASFLPVPP AGAAVFTWKD GGGNSYSDVP KQLHPDQSQI
51  LNLRTQTQKP AVKPAQADAG KRTDGAQEN NPDTAENRQ LEEKKRIAE
101 TERQNKEENC RISKMNLKAV GNSNAKNKDD LIRKYNNAVN KYCR*
  
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m283/g283 86.1% identity in 144 aa overlap

	10	20	30	40	50	60
m283.pep	MNFALSVIMLTLASFLPVPPAGAAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
g283	MNFALSVITFTLASFLPVPPAGTAVFTWKDGGGNSYSDVPKQLHPDQSQILNLRTLQTKP					
	10	20	30	40	50	60

	70	80	90	100	110	120
m283.pep	AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRISKMNLKAV					
		:	:	:	:	:
g283	AVKPKPA-VDTNAD-SAKENEKDIAEKNQGLEEEKKRIAETERQNKEENCRISKMNLKAV					
	70	80	90	100	110	
	130	140				
m283.pep	GNSNAKNKDDLIRKYNNAVNKYCRX					
g283	GNSNAKNKDDLIRKYNNAVNKYCRX					
	120	130	140			

```
a283.seq
1  ATGAACTTTG CTTTATCCGT CATTATGTTG ACCCTCGCCT CTTTCTGCC
51  CGTCCCGCCT GCCGAGCCG CCGTCTTTAC TTGGAAGGAC GGCGGCGGCA
101 ACAGCTATTC GGATGTACCG AAACAGCTTC ATCCCGACCA AAGCCAAATC
151 TTAACCTGCG GCAGCGCCCA AACCAAACCG CGCGTCAAAC CGCCCAAAGC
201 CGACGCAGGG AAGCGCACAG ACGGCGCGGC ACAGGAAAAC AATCCCGACA
251 CTGCCGAGAA AAACCGGCAG CTTGAGGAAG AAAAGAAAAG AATTGCCGAA
301 ACCGAACGGC AGAACAAGA AGAAAACCTGC CGGATTTCAA AAATGAACCT
351 GAAAGCGGTG GGAATCTCAA ATGCAAAAAA CAAGATGATG TTGATTCGGA
401 AATACAATAA CGCCGTAAC AAATACTGCC GTTAA
```

a283.pap

1	MNFALSVIML	TLASFLPVPP	AGAAVFTWKD	GGGSYSYSDVP	KQLHPDQSQI
51	LNLRTQTQTP	AVKPAQADAG	KRTDGAQAQEN	NPDTAEKNRQ	LEEEKKRIAE
101	TERQNKKEENC	RISKMNLIKAV	GNSNAKNKDD	LIRKYNNNAVN	KYCR*

		10	20	30	40	50	60
m283.pep		MNFALSVMILTLASFLVPFPAGAAVFTWKDGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
a283		MNFALSVMILTLASFLVPFPAGAAVFTWKDGGNSYSDVPKQLHPDQSQILNLRTRQTKP					
		10	20	30	40	50	60
		70	80	90	100	110	120
m283.pep		AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
a283		AVKPAQADAGKRTDGAAQENNPDTAEKNRQLEEEKKRIAETERQNKEENCRI SKMNLKAV					
		70	80	90	100	110	120
		130	140				
m283.pep		GNSNAKNKDDLIRKYNNAVNKYCRX					
a283		GNSNAKNKDDLIRKYNNAVNKYCRX					
		130	140				

g284.seq.

1	atgccgtctg	aaactcgaaa	tcggtttcag	acggcattgg	tttacgcggc
51	aggttggggc	ttagecgtct	ttgtaacggc	attcgccttt	gcctgcacaaa
101	gagtcgcggc	ctttgcgttt	gcctttgaag	ccttcgcggc	tttttttgaa
151	actgtctttc	ttaaagcctt	ctttcttgaa	accttcgcgc	cgcgttttgc
201	cgccgaagcc	ttctttgccc	ggtttatgat	cgccgcgcgc	gcgcgcggat
251	ttctatcgc	cccagccgcc	tttgcccttc	ggcttgccgc	ctgcggattt
301	gcgtttgcgc	gccggctcca	tgccctcgat	ggtcagttcg	ggcagtttgc
351	ggttaatgta	ttttctgatt	ttgtggactt	tgacgtattc	gttcacttcg
401	gcaaacgtaa	tcgcaatacc	cgtgcggcct	cgcgcgcgcg	tgcccccgat
451	gcggtggacg	tagtcttccg	ctggtttcgg	caggtcgtaq	ttataacq

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```

501  gggtaatggt  cggtagctca  ataccgcgtg  cggcaacgtc  ggtggcaacc
551  aaaattttgc  agcggccttt  acgcaaatcc  gtcagcgtgc  ggttgcgcca
601  gccctgcggc  atatcgccgt  gcaggcagtt  ggccgcgaaa  cctttttcgt
651  acaattcatc  cgcgatgact  tcggtcatcg  ctttggtgga  cgtgaaaatc
701  acacattggt  cgatgttggc  atcgcgcagg  atgtggtcga  gcaggcggtt
751  tttgtggcgc  atatcgtcgc  agtacaacaa  ctgctcttcg  attttgcctt
801  ggccgtccac  gcgttcgact  tcgataattd  cagagtcctt  ggtcagtttg
851  cgcgccagtt  tgccgactgc  gccgtcccaa  gtggcggaga  acaataa

```

This corresponds to the amino acid sequence <SEQ ID 1176; ORF 284.ng>:

```

g284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRVAGFAF  AFEAFAGFFE
51  TVFLKAFFLE  TFAARFAAEA  FFARFMIAAP  AAGFPIAPAA  FAFRLAACGF
101 AFAGRLHAFD  GQFGQFVNV  FFDFVDFDVF  VHFGKRNNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDVNG  RYVNTACGNV  GGNQNFAAAF  TQIRQRAVAP
201 ALRHIAVQAV  GGETFFVQFI  RDDFGHRFGG  RENHTLVDPV  IAQDVVEQAV
251 FVAHIVAVQQ  LLFDLALAVH  AFDFDNFRVF  GQFARQFADC  AVPSGGEQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1177>:

```

m284.seq..
1  ATGCCGTCCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101 GAATCGCCCG  CTTTGCCTTT  GCCTTTGAAG  CCTTCGCCCG  TTTTTCGAA
151 ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTCG
201 CGCCGAAGCC  TTCTTTGCTC  GGTTCATGAT  CGCCGCGCCA  ACCGCCGAT
251 TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301 GCGTTTGGCG  GTCGGTTCCA  TGCCTTCGAT  GGTGAGTTCG  GGCAGTTTTC
351 GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401 GCAAACGTAA  TCGCAATACC  CGTGCAGCCT  GCGCGGCCCG  TCGCGCCGAT
451 GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501 GGGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACATC  GGTGGCAACC
551 AAAATTTTGC  AGCGGCCTTT  ACGCAAATCC  ATCAGCGTGC  GGTGCGCCA
601 GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  TGCGCGGAAA  CCTTTTTCGT
651 ACAGTTCATC  CGCAATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701 ACGCATTGAT  CGATATTGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751 TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801 GATCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGTCCTTT  GGTGAGTTTG
851 CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901 CTGACGGTCG  CTCGGCGTTG  CTTCCACGAT  GGTTCGATG  TCGTCGATAA
951 AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAA
1001 CGTTCAAAAT  CAACTTTGCC  GCTTTGCATC  AGGTCCATCA  GACGGCCCCG
1051 CGTGGCGACA  ATCAGATCGA  CCGGTTTGCT  CAGGCGACGG  GTTGGTAGC
1101 CGAAAGACGC  GCCGCCGACG  ATGCTGACGG  TCGGGAACCA  ACGCATATTT
1151 TTGGCATAAC  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  GTTCGCGGTT
1201 CGGGGTCAAC  ACCAAAGCAC  GCGGGCCTTT  GCCCGGTTTT  TCCTGCGGTT
1251 TGGTCAGTTT  TTGCAAAGTC  GTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1178; ORF 284>:

```

m284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE
51  TVSLKAFFLE  TFAARFAAEA  FFARFMIAAP  TAGFTIAPAA  FAFRLAACGF
101 AFAGRFHAFD  GQFGQFSVNV  FFDFVDFDVF  VHFGKRNNT  RAACAAGAPD
151 AVDVVFRLEF  QVVVDVNG  RYVDTACGNI  GGNQNFAAAF  TQIHQRAVAP
201 ALRHIAVQAV  CGETFFVQFI  RNDFGHGFVG  RENHALIDIG  IAQDMIEQAV
251 FVAHIVAVQQ  LFFDFALIVH  AFDFDDFRVF  GQFARQFADR  AVPSGGEQQS
301 LTVARRCFHD  GFDVVDKAHI  QHTVGFVQNO  HFQTFKINFA  ALHQVHQATAR
351 RGDNQIDRFA  QGTGLVAERR  AADDADGAEP  THIFGIRQRV  FLDLSRQFAG
401 RGQHQSTRAF  ARFFAAGQF  LQSR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m284/g284 92.3% identity in 298 aa overlap

646

	10	20	30	40	50	60
m284.pep	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
g284	MPSETRNR FQTALVYAAGWGLAVFVTAFAFACKRVAGFAFAFEAFAGFFETVFLKAFFLE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m284.pep	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
g284	TFAARFAAEAFFARFMIAAPAGFP IAPAAFAFRLAACGFAGRLHAFDGGQFGQFAVNV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m284.pep	FFDFVDFDV FVHFGRNRNTRAACAAGAPDAVDV FRLFRQVVVDNVGNGRYVDTACGNI					
g284	FFDFVDFDV FVHFGRNRNTRAACAAGAPDAVDV FRLFRQVVVDNVGNGRYVNTACGNV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m284.pep	GGNQNF AAAFTQIHQRAVAPALRHIAVQAVCGETFFVQFIRNDFGHGFGGRENHALIDIG					
g284	GGNQNF AAAFTQIRQRAVAPALRHIAVQAVGGETFFVQFIRDDFGHRFGGRENHTLVDVG					
	190	200	210	220	230	240
	250	260	270	280	290	300
m284.pep	IAQDMIEQAVFVAHIVAVQQLLFDFALIVHAFDFFDRVFGQFARQFADRAVPSGGEQQS					
g284	IAQDVVEQAVFVAHIVAVQQLLFDFALAVHAFDFFDRVFGQFARQFADCAVPSGGEQX					
	250	260	270	280	290	
	310	320	330	340	350	360
m284.pep	LTVARRCFHDGFDVVDKAHIQHTVGFVQNQHFQTFKINFAALHQVHQ TARRGDNQIDRFA					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1179>:

```

a284.seq
1  ATGCCGCTCTG  AAACCTCGAAA  TCGGTTTCAG  ACGGCATTGG  TTTATGCGGC
51  AGGTTGGGGC  TTAGCGGTCT  TTGTAACGGC  GTTCGCCTTT  GCCTGCAAAA
101  GAATCGCCGG  CTTTGCGTTT  GCCTTTGAAG  CCTTCGCCGG  TTTTGTGAA
151  ACCGTCTCTC  TTAAAGCCTT  CTTTCTTGAA  ACCTTCGCCG  CGCGTTTTC
201  CGCCGAAGCC  TTCTTTGCTC  GGTTTATGAT  CGCCGCGCCA  ACCGCCGGAT
251  TTACGATCGC  CCCAGCCGCC  TTTGCCTTTC  GGCTTGCCGC  CTGCGGATTT
301  GCGTTTGCGG  GTCGGTTCCA  TGCCTTCGAT  GGTCAGTTTC  GGCAGTTTTC
351  GGTTAATGTA  TTTTTCGATT  TTGTGGACTT  TGACGTATTC  GTTCACTTCG
401  GCAAACGTAA  TCGCAATACC  CGTGCGGCCT  GCGCGGCCGG  TCGCGCCGAT
451  GCGGTGGACG  TAGTCTTCCG  CCTGTTTCGG  CAGGTCGTAG  TTGATAACGT
501  GGTAATGGT  CGGTACGTCG  ATACCGCGTG  CGGCAACGTC  GGTGGCAACC
551  AAAATTTTGC  AGCGGCCTTT  GCGCAAATCC  ATCAGCGTGC  GGTTCGCGCA
601  GCCTTGCGGC  ATATCGCCGT  GCAGGCAGTT  GCGGCGGAAA  CCTTTTTCGT
651  ACAATTCATC  CGCGATGACT  TCGGTCATGG  CTTTGGTGGA  CGTGAAAATC
701  ACGCATTGAT  CGATGTCGGC  ATCGCGCAAG  ATATGATCGA  GCAGGCGGTT
751  TTTGTGGCGC  ATATCGTCGC  AGTACAGCAG  TTGTTCTTCG  ATTTTGCCTT
801  GGTCGTCCAC  GCGTTCGACT  TCGATGATTT  CAGGGTCTTT  GGTCAGTTTG
851  CGCGCCAGTT  TGCCGACCGC  GCCGTCCCAA  GTGGCGGAGA  ACAACAAAGT
901  CTGACGGTCT  TCCGGCGTGG  CTTGACGAT  GGTTCGATG  TCGTCGATAA
951  AGCCCATATC  CAACATACGG  TCGGCTTCGT  CCAAATCAG  CACTTCCAAG
1001  CGGGCGAAAT  CGACTTTGCC  GCTTTGCATC  AAGTCCATCA  GACGGCCCGG
1051  CGTGCGGACA  ATCAGATCGA  CCGGTTTGCT  CAGGGCGCGG  GTTTGGTAGC
1101  CGAACGATGC  ACCACCGACG  ATGCTGACGG  TACGGAACCA  ACGCATATTT
1151  TTGGCATACG  CCAGCGCGTT  TTTCTCGACT  TGAGCCGCCA  ATTCGCGGGT
1201  CGGCGTCAAC  ACCAACGCGC  GCGGGCCTTT  GCGCGGTTTT  TCGCTGCGTT
1251  TGTCAGTCG  CTGCAAAGTC  GGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1180; ORF 284.a>:

```

a284.pep
1  MPSETRNRFO  TALVYAAGWG  LAVFVTAFAF  ACKRIAGFAF  AFEAFAGFFE

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```

51 TVSLKAFFLE TFAARFAAEA FFARFMIAAP TAGFTIAPAA FAFRLAACGF
101 AFAGRFAHFD GQFGQFSVNV FFDFVDFDVF VHEGKRNRNT RAACAAGAPD
151 AVDVVFRLEF QVVVDNVGNG RYVDTACGNV GGNQNFAAAF AQIHQRAVAP
201 ALRHIAVQAV GGETFFVQFI RDDFGHGGG RENHALIDVG IAQDMIEQAV
251 FVAHIVAVQQ LFFDFALVVH AFDFDDFRVF GQFARQFADR AVPSGGEQQS
301 LTVFRRGFDD GFDVVDKAHI QHTVGFVQNO HFQAGEIDFA ALHQVHQTAR
351 RGDNQIDRFA QGAGLVAERC TTDDADGTEP THIFGIRQRV FLDLSRQFAG
401 RRQHQRRARAF ARFFAAGQS LQSR*

```

m284/a284 94.8% identity in 424 aa overlap

m284.pep	10	20	30	40	50	60
	MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
a284	10	20	30	40	50	60
	MPSETRNRFQTALVYAAGWGLAVFVTAFAFACKRIAGFAFAFEAFAGFFETVSLKAFFLE					
m284.pep	70	80	90	100	110	120
	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
a284	70	80	90	100	110	120
	TFAARFAAEAFFARFMIAAPTAGFTIAPAAFAFRLAACGFAGRFHAFDGGQFGQFSVNV					
m284.pep	130	140	150	160	170	180
	FFDFVDFDVFVHFGKRNRNTRAACAAGAPDAVDVFRLEFRQVVVDNVGNRGYVDTACGNI					
a284	130	140	150	160	170	180
	FFDFVDFDVFVHFGKRNRNTRAACAAGAPDAVDVFRLEFRQVVVDNVGNRGYVDTACGNV					
m284.pep	190	200	210	220	230	240
	GGNQNFAAAFQIHRQAVAPALRHIAVQAVCGGETFFVQFIRNDFGHGFGGRENHALIDIG					
a284	190	200	210	220	230	240
	GGNQNFAAAFQIHRQAVAPALRHIAVQAVGGETFFVQFIRDDFGHGGGRENHALIDVG					
m284.pep	250	260	270	280	290	300
	IAQDMIEQAVFVAHIVAVQQLFFDFALIVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
a284	250	260	270	280	290	300
	IAQDMIEQAVFVAHIVAVQQLFFDFALVVHAFDFDDFRVFGQFARQFADRAVPSGGEQQS					
m284.pep	310	320	330	340	350	360
	LTVARRCFHDGFDVVDKAHIQHTVGFVQNHQFQTFKINFALHQVHQTARRGDNQIDRFA					
a284	310	320	330	340	350	360
	LTVFRRGFDDGFDVVDKAHIQHTVGFVQNHQFQAGEIDFAALHQVHQTARRGDNQIDRFA					
m284.pep	370	380	390	400	410	420
	QGTGLVAERRAADDADGAEPHTHIFGIRQRVFLDLSRQFAGRGQHQSTRAFARFFAAGQF					
a284	370	380	390	400	410	420
	QGAGLVAERCTTDDADGTEPHTHIFGIRQRVFLDLSRQFAGRRQHQRRARAFARFFAAGQS					
m284.pep	LQSRX					
a284	LQSRX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1181>:

```

g285.seq
1  atgaccgata ccacaccgac agataccgat ccgaccgaaa acggcacgcg
51  caaaatgccg tctgaacacc gccccgcccc gccggcaaaa aaacgccgcc
101 cgctgctgaa gctgtcggcg gcactgctgt ctgtcctgat tttggcagta

```

```

151  tgtttcctcg gctggatcgc cggtagcgaa gcaggtttgc gcttcgggct
201  gtaccaaata ccgtcctggt tcggcgtaaa catttcctcc caaaacctca
251  aaggcacact gctcgacggc ttcgacggcg acaactggtc gatagaaacc
301  gagggggcag accttaaaat cagccgcttc cgcttcgctg ggaaccgctc
351  cgaactgatg cggcgacgcc tgacatcac cgacatctcc gccggcgaca
401  tcgccatcgt aaccaaaccc actccgccta aagaagaacg cccgcctcaa
451  ggctgcccgc acagcataga cctgcccgcg gctgtctatc tcgaccgctt
501  cgagacgggc aaaatcagca tgggcaaaac cttgacaaa caaacgctct
551  atctcgaacg cctcaacgcg gcataccggt acgaccgtaa agggcacccg
601  ctcgacctga agggcgccga cagccggtgg agcagttcgt cggggtcagc
651  ctcggtcggc ttgaaaaaac cgtttgccct cgataccgcc atttacacca
701  aaggcggatt cgaaggcgaa accatacaca gtacggcgcg gctgagcggc
751  agcctgaagg atgtgcgcgc cgaactgacg atcgacggcg gcaatatccg
801  cctctcgga aaatccgtca tccaccggtt tgccgaatca ttggataaaa
851  cattggaaga agtactggtc aaaggattca acatcaatcc gtccgccttc
901  gtgccttccc tgccgatgac cgggctgaat ttcgacctga ccgcatccc
951  gtcgttttca gacggcatcg cgctggaagg ctgctcgat ttggaaaaca
1001 ccaaagccgg ctttgccgac cgcaacggca tcccgtccg tcagggtttg
1051 ggcggttttg tcatccggca ggacggcacg gtgcatatcg gcaatacgtc
1101 cgccgccctg ctcgacggcg gcggcatcag gctgtcgggc aaaaacgaca
1151 ccgaaaaaga catccttgat ttaaatatag gcatcaactc cgtcggcgcg
1201 gaagacgtgc tgcaaacggc gttcaaaggc aggttggacg gcagcatcgg
1251 catcgcgggc acgaccgcct cgcccaaaat ctcttggcaa ctcggcaccg
1301 gcacggcacg cacggacggc agcctcccca tcgaagcga ccccgcaaac
1351 gaacagcgga aactggtgtt cgacaccgtc aacatctccg ccggggaagg
1401 cagcctgacc gcgcaaggct atctcgagct gtttaaagac cgctgctca
1451 agctggacat ccgttcccgc gcattcgacc ctccgcgat cgatccgcaa
1501 tttccggcag gcaatatcaa cggttcgatt catcttgccg gtgaatcggc
1551 aaaagagaaa ttacgggca aaatgcgttt ttgcccgtt acgttcaacg
1601 gcgtgccgat tgccggcagc gccgacattg ttacgagtc ccgccacctt
1651 ccgcgcgcgc cgctcgattt gcggttgggg cggaaacatc taaaacaga
1701 cggcggttcc ggcaaaaaag gcgaccggct taacctcaat ataccgcac
1751 ccgatttatc ccgtttcggt ttcggactcg cggggtcttt aaatgcacg
1801 ggacaccttt ccggcgattt ggacggcggc atccgaacct ttgaaaccga
1851 cctttccggc acggcgcgca acttacacat cggcaaacg gcagacatcc
1901 gttcgctcga tttaccctc aaaggctcac ccggcacaag ccgcccgatg
1951 cgcgcggata tcaaggcgcg ccgcctttcc ctgtcggcg gcgcggcggt
2001 tgtcgatacc gccggcctga cgctggaagg tacgggcgcg cagcagcgca
2051 tccgcacaca cgcgcgatg acgctggacg gcaaacggtt caaactcgat
2101 ttggacgctt caggcggcat caacagggaa cttaccgat ggaaggcag
2151 catcggcac ctcgacatcg gcggcgcat caacctcaag ctgcaaaacc
2201 gtatgacgct cgaagccggt gcggaacacg tggcggaag tgccggaat
2251 tggcaggcaa tggcggcgag cctcaacctg caaaccttt ctggggacg
2301 gaaaaccggc atatcggcaa aaggcggcgc acgcggcctg cacatcgccg
2351 agttgcacaa tttcttcaaa ccgccttccg aacacaatct ggttttaaac
2401 ggcgactggg atgtgcctca cgggcacaa gcgcgcggct acctcaatat
2451 cagccggcaa agcggcgatg ccgtattgcc cggcgggcag gctttgggtt
2501 tgaacgcatt ttccctgaaa acgcgctttc aaaacgaccg catcggaatc
2551 ctgcttgacg gcggcgcgcg tttcgacggg attaacgcgg atttgggcat
2601 cggaacgcc ttcggcggca atatggcaaa tacaccgctc gccggcagga
2651 ttacagcctc cttcccgcac ttgggcgat tgaagccctt tctgccgcg
2701 gccgcgcaaa acattaccg cagcctgaat gcctccgcgc aaatcggcg
2751 acgggtaaat caacggcaat atcaccgtcg ggcaaacgg ctccttcgat
2801 accgcacctt tggcgggcag gctcaacctg accgttgccg atgccgaagc
2901 attccgcaac ttcctaccgg tcggacaaac cgtcaaaggc agcctgaatg
2951 cgcccgtaac cctcgcgggc agcatcgccg acccgcaact ggcggcgagt
3001 atcaacggcg acaagctcta ttaccgcaac caaacccaag gcatcatctt
3051 ggacaacggc tcgctgcgtt cgcatattgc aggcaggaaa tgggtaatcg
3101 acagcctgaa attccggcac gaaggacgg cggaactctc cggcacggtc
3151 agcatggaaa acagcgtgcc cgatgtcgat atcggcggcg tgttcgacaa
3201 ataccgcatc ctgtcccgcc ccaaccgcgc cctgacgggt tccggcaaca
3251 cccgcctgcg ctattcgccg caaaaaggca tatccgttac cggtatgatt
3301 aaaactgatc aggggctggt cggttcgcaa aaatcctcga tgccgtccgt
3351 cggcgacgat gtcgtcgat tgggcgaagt caagaaagag gccggcgcat
3401 cgctccccgt caatatgaac ctgactttag acctcaatga cggcatccgc

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3451 ttctccggct acggcgcgga cgttaccata ggcggcaaac tgacctgac
3501 cgcgcaaccg ggcggaaatg tgcgtggggt gggcacggtc cgcgtcatca
3551 aaggcggtta caaagcatac gggcaggatt tagacattac caaaggcaca
3601 gtctcctttg tcggcccgct caacgacccc aacctgaaca tccgcgccga
3651 acgcccgcct tccccgcgtg gtgcgggctg ggaaatattg ggcagcctca
3701 acagcccgcg cattacgctg acggcaaacg aaccgatgag tgaaaaagac
3751 aagctctcct ggctcatcct caaccgtgcc ggcagcgcca gcagcgcgga
3801 caatgccgcc ctgtccgcag ccgcaggcgc gctgcttgcc gggcaaatca
3851 acgaccgcat cgggctggtg gatgatttgg gctttaccag caagcgcgagc
3901 cgcaacgcgc aaaccggcga actcaacccc gccgaacagg tgctgaccgt
3951 cggcaaacaa ctgaccggca aactctacat cggctacgaa tacggcatct
4001 ccagcgcgga acagtccgtc aaactgattt accggctgac ccgcgccata
4051 caggcggttg cccgtatcgg cagccggttc tcgggcggcg agctgacata
4101 caccatacgt ttcgaccgcc tcttcggttc ggacaaaaaa gactccgcag
4151 gaaacggcaa agggaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1182; ORF 285.ng>:

```

g285.pep
  1  MTDTTPTD TD PTENGTRKMP SEHRPAPPK KRRPLLKLSA ALLSVLILAV
51  CFLGWIAGTE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGNWNSIET
101 EGADLKISRF RFAWKPELSE RSLHITDIS AGDIAIVTKP TPPKEERPPQ
151 GLPDSIDLPA AVYLDRFETG KISMGTFDK QTVYLERLNA AYRYDRKGHR
201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGFEGE TIHSTARLSG
251 SLKDVRAELT IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGS LD LENTKAGFAD RINGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGTGTARTDG SLPIASDPAN
451 EQRKLVFDTV NISAGEGSLT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 FPAGNINGSI HLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIVKTGGGF GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLGG IRTFETDLG TARNLHIGKA ADIRSLDFTL KGSPGTSRPM
651 RADIKGGRLS LSGGAAVVDT AGLTLEGTGA QHRIRTHAAM TLDGKPFKLD
701 LDASGGINRE LTRWKSGSIGI LDIGGAFNLK LQNRMTLEAG AEHVAASAAN
751 WQAMGGSNLN QHFSWDRKTG ISAKGGARGL HIAELHNFFK PPFHNLVLN
801 GDWDVAYGHN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIGNA FGGNMANTPL GGRITASLPD LGALKPFLPA
901 AAQNTGSLN ASAQIGGRVG SPSVNAAVNG SSNYKGKINGN ITVGQSRSF
951 TAPLGGRNLN TVADAEAFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAEISGTV
1051 SMENSVPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSMPSVGDD VVVLGEVKKE AAASLPVNMN LTLDLNDGIR
1151 FSGYGADVTI GGLTLTAQP GGNVRGVGTV RVIKGRYKAY GQDLIDITKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YGISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRLFGSDKK DSAGNGKGK*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1183>:

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m285.seq
  1  ATGACCGATA CCGACCGAC AGATACCGAT CCGACCGAAA ACGGCACGCG
51  CAAAATGCCG TCTGAACACC GCCCTACCCC GCCGGCAAAA AAACGCCGCC
101 CGTTGCTGAA GCTGTCGGCG GCACTGCTGT CTGTCTGTAT TTTGGCAGTA
151 TGTTTCCTCG GCTGGCTCGC CGGTACGGAA GCAGGTTTGC GCTTCGGGCT
201 GTACCAAATC CCGTCTTGTT TCGGCGTAA CATTTCCTCC CAAAACCTCA
251 AAGGCACGCT GCTCGACGGC TTCGACGGCG ACAACTGGTC GATAGAAACC
301 GAGGGGGCAG ACCTTAAAT CAGCCGCTTC CGCTTCGCGT GGAAACCGTC
351 CGAACTGATG CGCCGCAGCC TGCACATTAC CGAAATTTCG GCCGCGGACA
401 TCGCCATCGT TACCAAACCG ACTCCGCTTA AAGAAGAACG CCCGCGGCTC
451 AGCCTTCCCG ACAGCATAGA CCTGCCTGCC GCCGTCTATC TCGAGCGCTT
501 CGAGACGGGC AAAATCAGCA TGGGCAAAGC CTTTGACAAA CAAACCGTCT
551 ATCTCGAACG GCTGGATGCT TCATACCGTT ACGACCGCAA AGGACACCGC
601 CTTGACCTGA AGGCCGCCGA CACGCCGTGG AGCAGTTCGT CGGGGCGGCG
651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTAGCGCGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG

```

801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GGCCGCCTTC
901 GTGCCCTTCC TGCCCGATGC CGGACTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG TTCGCTCGAT TTGGAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCCGTCCG TCAGGTTTTA
1051 GGCGGCTTTG TCATCCGGCA GGACGGCACG GTGCATATCG GCAATACGTC
1101 CGCCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTTGGACG GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCAAAAT CTCTTGGAAC CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCAGCAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACG CTTCGCGCAT CGATCCGCAA
1501 CTTCGGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
1551 AAAAGAGAAA TTCACAGGCA AAATGCGGTT TTTACCCGGC ACGTTCACG
1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGGCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAACAAGAG
1701 CCGCGGCTTC GGCAAAAAAG GCGACCGGCT TAACCTCAAT ATCACC GCAC
1751 CCGATTATAT CCGTTTCGGT TTCGGACTCG CCGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGTGATTT GGACGGCGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCCGATA
1951 CGCGCCGACA TCAAAGGCAG CGCCTTTTCG CTGTGCGGCG GAGCGGCGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACC GCA
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGTT CAAATTCGAT
2101 TTGGACGCTT CAGGCGGCAT CAACAGGGAA CTTACCCGAT GGAAAGGCAG
2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
2201 GTATGACGCT CGAAGCCGGT GCGGAACGCG TGGCGGCAAG TCGCGCAAAT
2251 TGGCAGGCAA TGGGCGGCAG CCTCAACCTG CAACACTTTT CTTGGGATAA
2301 AAAAACCGGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
2351 AGTTGCACAA TTTCTTCAAA CCGCCCTTCG AACACAATCT GGTTTTAAAC
2401 GGCGACTGGG ATGTCGCCTA CCGGCGCAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG CATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCCG ATTTGGGCAT
2601 CGCCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GGCGGCAGGA
2651 TTACCGCCTC CCTTCCCGAC TTGGGCGCAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTAGGC TCTCCGTCG TCAATGCCGC CGTCAACGGC AGCACTCACT
2801 ACGGGAATA CAACGGCAAC ATCACCCTCG GGCAAAGCCG CTCTTTCGAT
2851 ACCGCGCCTT TGGGCGGCAG GCTCAACCTG ACCGTTGCCG ATGCCGAAGT
2901 ATTCCGCAAC TTCTTACCGG TCGGACAAAC CGTCAAAGGC AGCCTGAATG
2951 CGCCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACTCTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
3101 ACAGCCTGAA ATTCCGGCAC GAAGGGACGG CGGAACCTC CGGTACGGTC
3151 GGTATGGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTGCGCG CAAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGGATC AGGGGCTGTT CGGTTTCGAA AAATCCTCGA TGCCGTCGCT
3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGTCCCGCT CAATATGAAC CTGACTTTAG ACCTCAATGA CCGCATCCGC
3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCGAAAC TGACCTGAC
3501 CGCCAATCG GCGGAAGCG TACGGGGCGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCCGCT CAACGATCCC AACCTCAACA TCCGCGCCGA
3651 ACGCCGCTT TCCCCGTCG GTGCGGGCGT GGAATATTTG GGCAGCCTCA
3701 ACAGCCCGCG CATACGCTG ACGGCAAAAC AACCATGAG TGAAAAAGAC
3751 AAGCTCTCTT GGCTCATCCT CAACCGCGCC GGCAGCGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCTGCAG CCGCAGGTGC GCTGCTTGCC GGGCAAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGGCGA ACTCAACCCC GCCGAACAGG TGCTGACCGT
3951 CGCAAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAATGATTT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTTC TCGGGCGGCG AGCTGACATA

651

4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
 4151 GAAACGGCAA AGGAAATAA

This corresponds to the amino acid sequence <SEQ ID 1184; ORF 285>:

```
m285.pep
1  MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
51  CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
101 EGADLKISRF RFAWKPSSELM RRS�HITEIS AGDIAIVTKP TPPKEERPPL
151 SLPDSIDLPA AVYLDRLFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
201 LDLKAADTPW SSSSGAASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
251 SLKDVRÆELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPAAF
301 VPSLPDAGLN FDLTAIPSFS DGIALEGSLD LENTKAGFAD RNGIPVRQVL
351 GGFVIRQDGT VHIGNTSAAI LGRGGIRLSG KIDTEKDILD LNIGINSVGA
401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPPIAGS ADIVYESRHL
551 PRAAVDLRLG RNIIKTGDDG GKKGDRNLN ITAPDLSRFG FGLAGSLNVR
601 GHLSGDLDDG IRTFETDLSG AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
651 RADIKGSRLS LSGGAHVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
701 LDASGGINRE LTRWKGSIIG LDIGGAFNLK LQNRMTLEAG AERVAASAAN
751 WQAMGGSINL QHFSWDKKTG ISAKGGAHGL HIAELHNFEK PPFEHNLVLN
801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
851 LLDGGARFGR INADLGIANA FGGNMANAPL GGRITASLPD LGALKPFLLA
901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVGQSRSEF
951 TAPLGGRLNL TVADAEVFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSCTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFGSQ KSSMPSVGDD VVVLGEVKKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTTLTAQS GGSVRGVGTV RVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSEKD
1251 KLSWLILNRA GSGSSGDNAI LSAAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNGKKG*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m285/g285 96.5% identity in 1389 aa overlap

      10      20      30      40      50      60
m285.pep MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      MTDTTPTDTDPTENGTRKMPSEHRPAPPAKKRRPLLKLSAALLSVLILAVCFLGWIAGE
      10      20      30      40      50      60

      70      80      90     100     110     120
m285.pep AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
      70      80      90     100     110     120

      130     140     150     160     170     180
m285.pep RRS�HITEISAGDIAIVTKPTTPKEERPPLSLPDSIDLPAAYLDRLFETGKISMKGAFDK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      RRS�HITDISAGDIAIVTKPTTPKEERPQGLPDSIDLPAAYLDRLFETGKISMKGTFDK
      130     140     150     160     170     180

      190     200     210     220     230     240
m285.pep QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g285      QTVYLERLNAAARYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGFEGE
      190     200     210     220     230     240

      250     260     270     280     290     300
m285.pep TIHSTARLSGSLKDVRÆELADGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
```

[illegible]

	:	:	:	:	:	:
g285	AAQNITGSLN	SAQIGGRVGS	PSVNAAVNGSS	SNYGKINGNIT	VGQSRSFDTA	PLGGRNLNL
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
m285.pep	TVADAEVFRN	FLPVGQTVKGS	LNAAVTLGGS	ADPHLGGSING	DKLYYRNQTQ	GIIILDNG
	:	:	:	:	:	:
g285	TVADAEAFRN	FLPVGQTVKGS	LNAAVTLGGS	ADPHLGGSING	DKLYYRNQTQ	GIIILDNG
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
m285.pep	SLRSHIAGRK	WVIDSLKFRHE	GTAELSGTVGM	ENSGPDVDIG	AVFDKYRILSR	PNRRLTV
	:	:	:	:	:	:
g285	SLRSHIAGRK	WVIDSLKFRHE	GTAELSGTVSM	ENSVDPVDIG	AVFDKYRILSR	PNRRLTV
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
m285.pep	SGNTRLRYSP	QKGISVTGMIK	TDQGLFGSQKS	SMPSVGDDVV	VLGEVKKEAA	APLPVNMN
	:	:	:	:	:	:
g285	SGNTRLRYSP	QKGISVTGMIK	TDQGLFGSQKS	SMPSVGDDVV	VLGEVKKEAA	ASLPVNMN
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
m285.pep	LTLDLNDGIR	FAGYGADVTIG	GKLTTLTAQSG	GSVRVGTVRV	IKGRYKAYGQ	DLDTKTGT
	:	:	:	:	:	:
g285	LTLDLNDGIR	FSGYGADVTIG	GKLTTLTAQPG	GNVRVGTVRV	IKGRYKAYGQ	DLDTKTGT
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
m285.pep	VSVFGPLNDP	NLNIRAERRLS	PVGAGVEILGS	LNSPRITLTAN	EPMSEKDKLS	WLILNRA
	:	:	:	:	:	:
g285	VSVFGPLNDP	NLNIRAERRLS	PVGAGVEILGS	LNSPRITLTAN	EPMSEKDKLS	WLILNRA
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
m285.pep	GSGSSGDNA	ALSAAAGALLA	GQINDRIGLV	DDLGFTSKR	SRNAQTGELN	PAEQVLTVGK
	:	:	:	:	:	:
g285	GSGSSGDNA	ALSAAAGALLA	GQINDRIGLV	DDLGFTSKR	SRNAQTGELN	PAEQVLTVGK
	1270	1280	1290	1300	1310	1320
	1330	1340	1350	1360	1370	1380
m285.pep	LTGKLYIGYE	YSISISSAEQSV	KLIYRLTRAIQ	AVARIGSRSSG	GELTYTIRFDR	FGSGDKK
	:	:	:	:	:	:
g285	LTGKLYIGYE	GYSISISSAEQSV	KLIYRLTRAIQ	AVARIGSRSSG	GELTYTIRFDR	LFGSGDKK
	1330	1340	1350	1360	1370	1380
	1390					
m285.pep	DSAGNGKGKX					
g285	DSAGNGKGKX					

a285.seq	1	ATGACCGATA	CCGCACCGAC	AGATACCGAT	CCGACCGAAA	ACGGCACGCG
	51	CAAAATGCCG	TCTGAACACC	GCCCTACCCC	CGCGGCAAAA	AAACGCCGCC
	101	CGTGTCTGAA	GCTGTGGCG	GCACTGCTGT	GCTGCTTATAT	TTTGGCAGTA
	151	TGTTTCTCTG	GCTGGCTCGC	CGGCACGGAA	GCGGGTTTGC	GCTTCGGGCT
	201	GTACCAAATC	CCGTCTTGTT	TCGGCGTAAA	CATTTCTCTC	CAAAACCTCA
	251	AAGGCACGCT	GCTCGACGGC	TTTCGACGGC	ACAACGTGTC	GATAGAAACC
	301	GAGGGGGCAG	ACCTTAAAA	CAGCCGCTTC	CGCTTCGCGT	GGAAACCGTC
	351	CGAACTGATG	CGCCGCAGCC	TGCACATTAC	CGAAATTTCC	CCCGCCGACA
	401	TCGCCATCGT	TACCAAACCG	ACTCCGCCTA	AAGAAGAACG	CCCGCCGCTC
	451	AGCCTTCCCG	ACAGCATAGA	CCTGCCTGCC	GCGTCTATC	TCGACCGCTT
	501	CGAGACGGGC	AAATACAGCA	TGGGCAAAGC	CTTTGACAAA	CAAACCGTCT
	551	ATCTCGAACG	GCTGGATGCT	TCATACCGTT	ACGACCGCAA	AGGACACCGC
	601	CTCGACCTGA	AGGCTGCCGA	CACGCCGTGG	AGCAGTTTCT	CGGGTCTCAG

651 CTCGGTCGGC TTGAAAAAAC CGTTTGCCCT CGATACCGCC ATTTACACCA
701 AAGGCGGACT CGAAGGCAAA ACCATACACA GTACGGCTCG GCTGAGCGGC
751 AGCCTGAAGG ATGTGCGCGC CGAACTGGCG ATCGACGGCG GCAATATCCG
801 CCTCTCGGGA AAATCCGTCA TCCACCCGTT TGCCGAATCA TTGGATAAAAA
851 CATTGGAAGA AGTACTGGTC AAAGGGTTCA ACATCAATCC GTCCGCCTTC
901 GTGCCTTCCC TGCCCGATGC CGGGCTGAAT TTCGACCTGA CCGCCATCCC
951 GTCGTTTTCA GACGGCATCG CGCTGGAAGG CTCGCTCGAT TTGAAAAACA
1001 CCAAAGCCGG CTTTGCCGAC CGCAACGGCA TCCCGTCCG TCAGGTTTTA
1051 GGCAGCTTTG TCATCCGGCA GGACGGCAG GTGCATATCG GCAATACGTC
1101 CGTCGCCCTG CTCGGACGGG GCGGCATCAG GCTGTCGGGC AAAATCGACA
1151 CCGAAAAAGA CATCCTCGAT TTAAATATAG GCATCAACTC CGTCGGCGCG
1201 GAAGACGTAC TGCAAACCGC GTTCAAAGGC AGGTGAGAC GCAGCATCGG
1251 CATCGGTGGC ACGACCGCCT CGCCCAAAAT CTCTTGCAA CTCGGCATCG
1301 GCACGGCGCG CACGGACGGC AGCCTCGCCA TTGCAAGCGA CCCCACAAAC
1351 GGACAGCGGA AACTGGTGCT CGACACCGTC AACATCGCCG CCGGGCAAGG
1401 CAGCCTGACC GCGCAAGGCT ATCTCGAGCT GTTTAAAGAC CGCTGCTCA
1451 AGCTGGACAT CCGTTCCCGC GCATTGACAC CTTGCGCAT CGATCCGCAA
1501 CTTCCGGCAG GCAATATCAA CGGCTCAATA AACCTTGCCG GCGAACTGGC
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1601 GCGTACCGAT TGCCGGCAGT GCCGACATTG TTTACGAGTC CCGCCACCTT
1651 CCGCGTGCCG CCGTCGATTT GCGGCTGGGG CGGAACATTA TTAAAAACA
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1751 CCGATTTATC CCGTTTCGGT TTCGGACTCG CGGGGTCTTT AAATGTACGC
1801 GGACACCTTT CCGGCGATTT GGACGGTGGC ATCCGAACCT TTGAAACCGA
1851 CCTTTCCGGC GCGGCGCGCA ACCTGCACAT CGGCAAGGCG GCAGACATCC
1901 GTTCGCTCGA TTTCACGCTC AAAGGTTGCG CCGACACAAG CCGCCGATA
1951 CGCGCCGACA TCAAAGGCAG CCGCCTTTCG CTGTCGGGCG GAGCGGAGGT
2001 TGTCGATACC GCCGACCTGA TGCTGGACGG CACGGGCGTG CAGCACCAGC
2051 TCCGCACACA CGCCGCCATG ACGCTGGATG GCAAACCGT CAAATTCGAT
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2151 CATCGGCATC CTCGACATCG GCGGCGCATT CAACCTCAAG CTGCAAAACC
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2301 AAAAACCAGC ATATCGGCAA AAGGCGGCGC ACACGGTCTG CATATCGCCG
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2401 GGCGACTGGG ATGTGCGCTA CCGGCGAAAC GCGCGCGGCT ACCTCAATAT
2451 CAGCCGGCAA AGCGGCGATG CCGTATTGCC CCGCGGGCAG GCTTTGGGTT
2501 TGAACGCATT TTCCCTGAAA ACGCGCTTTC AAAACGACCG TATCGGAATC
2551 CTGCTTGACG GCGGCGCGCG TTTCGGGCGG ATTAACGCCG ATTTGGACAT
2601 CGGCAACGCC TTCGGCGGCA ATATGGCAA TGCACCGCTC GCGGCGAGGA
2651 TTACCGCCTC CTTTCCCGAC TTGGGCACAT TGAAGCCCTT TCTGCCCGCC
2701 GCCGCGCAAA ACATTACCGG CAGCCTGAAT GCCGCGCGC AAATCGGCGG
2751 ACGGGTCGGC TCTCCGTCCG TCAATGCCGC CGTCAACGGC AGCAGCAACT
2801 ACGGGAAAT CAACGGCAAC ATCACCCTCG GGCAAGCCG CTCTTTCGAT
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2951 CCGCCGTAAC CCTCGGCGGC AGCATCGCCG ATCCGCACTT GGGCGGCAGC
3001 ATCAACGGCG ACAAACCTTA TTACCGCAAC CAAACCCAAG GCATCATCTT
3051 GGACAACGGC TCGCTGCGTT CGCATATCGC GGGCAGGAAA TGGGTAATCG
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3151 GGTATGAAA ACAGCGGACC CGATGTCGAT ATCGGCGCGG TGTTCGACAA
3201 ATACCGCATC CTGTCCCGCC CCAACCGCCG CCTGACGGTT TCCGGCAACA
3251 CCCGCTGCG CTATTCGCCG CAAAAAGGCA TATCCGTTAC CGGGATGATT
3301 AAAACGATC AGGGGCTGTT CGGTTTCGCA AAATCCTCGA TGCCGTCCGT
3351 CGGCGACGAT GTCGTCGTAT TAGGCGAAGT CAAAAAGAG GCGGCGGCAC
3401 CGCTCCCGT CAATATGAAC CTGACTTTAG ACCTCAATGA CGGCATCCG
3451 TTCGCCGGCT ACGGCGCGGA CGTTACCATA GCGGCAAAAC TGACCTGAC
3501 CGCCCAATCG GCGGAAGCG TGCGGGGCGT GGGCACGGTC CGCGTCATCA
3551 AAGGGCGTTA TAAGGCATAC GGGCAGGATT TGGACATTAC CAAAGGCACG
3601 GTCTCCTTTG TCGGCCCGCT CAACGACCCC AACCTCAACA TCCGCGCCGA
3651 ACGCGCCTT TCCCCGTCG GTGCGGGCGT GGAATATTG GGCAGCCTCA
3701 ACAGTCCGCG CATTACGCTG ACGGCAAACG AACCGATGAG TGAAAAAGAC
3751 AAGCTCTCCT GGCTCATCCT CAACCGCGCC GGCAGTGGCA GCAGCGGCGA
3801 CAATGCCGCC CTGTCCGAG CCGCCGGCGC GCTGCTTGCC GGGCAAATCA
3851 ACGACCGCAT CGGGCTGGTG GATGATTTGG GCTTTACCAG CAAGCGCAGC
3901 CGCAACGCGC AAACCGCGCA ACTCAACCCC GCCGAACAGG TGCTGACCGT

655

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3951 CGGCAAACAA CTGACCGGCA AACTCTACAT CGGCTACGAA TACAGCATCT
4001 CCAGCGCGGA ACAGTCCGTC AAAGTATT ACCGGCTGAC CCGCGCCATA
4051 CAGGCGGTTG CCCGTATCGG CAGCCGTTTC TCGGGCGGCG AGCTGACATA
4101 CACCATACGT TTCGACCGCT TCTCCGGTTC GGACAAAAA GACTCCGCCG
4151 GAAACAGCAA AGGAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1186; ORF 285.a>:

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a285.pep
  1 MTDTAPTDTD PTENGTRKMP SEHRPTPPAK KRRPLLKLSA ALLSVLILAV
  51 CFLGWLAGE AGLRFGLYQI PSWFGVNISS QNLKGTLLDG FDGDNWSIET
 101 EGADLKISRF RFAWKPSSELM RRSLLHITEIS AGDIAIVTKP TPPKEERPPPL
 151 SLPDSIDLPA AVYLDREFETG KISMKGAFDK QTVYLERLDA SYRYDRKGHR
 201 LDLKAADTPW SSSSGSASVG LKKPFALDTA IYTKGGLEGK TIHSTARLSG
 251 SLKDVRAELA IDGGNIRLSG KSVIHPFAES LDKTLEEVLV KGFNINPSAF
 301 VPSLPDAGLN FDLTAIPFSF DGIALEGLSD LENTKAGFAD RNGIPVRQVL
 351 GSFVIRQDGT VHIGNTSVAL LGRGGIRLSG KIDTEKDILD LNIGINSVGA
 401 EDVLQTAFKG RLDGSIGIGG TTASPKISWQ LGIGTARTDG SLAIASDPAN
 451 GQRKLVLDTV NIAAGQGSIT AQGYLELFKD RLLKLDIRSR AFDPSRIDPQ
 501 LPAGNINGSI NLAGELAKEK FTGKMRFLPG TFNGVPIAGS ADIVYESRHL
 551 PRAAVDLRLG RNIIKTDGGF GKKGDRLNLN ITAPDLSRFG FGLAGSLNVR
 601 GHLSGDLGG IRTFETDLGS AARNLHIGKA ADIRSLDFTL KGSPDTSRPI
 651 RADIKGSRLS LSGGAEVVDI ADLMLDGTGV QHRIRTHAAM TLDGKPFKFD
 701 LDASGGINRE LTRWKGSIIGI LDIGGAFNLK LQNRMTLEAG AERVAASAAN
 751 WQAMGGSLNL QHFSWDKKTG ISAKGGAHGL HIAELHNFFK PPFENLVLN
 801 GDWDVAYGRN ARGYLNISRQ SGDAVLPGGQ ALGLNAFSLK TRFQNDRIGI
 851 LLDGGARFGR INADLDIGNA FGGNMANAPL GGRITASLPD LGTLKPFPLPA
 901 AAQNITGSLN AAAQIGGRVG SPSVNAAVNG SSNYGKINGN ITVQSRFSFD
 951 TAPLGGRLNL TVADAEVFRN FLPVGQTVKG SLNAAVTLGG SIADPHLGGS
1001 INGDKLYYRN QTQGIILDNG SLRSHIAGRK WVIDSLKFRH EGTAELSGTV
1051 GMENSGPDVD IGAVFDKYRI LSRPNRRLTV SGNTRLRYSP QKGISVTGMI
1101 KTDQGLFSGQ KSSMPSVGDD VVVLGEVKE AAAPLPVNMN LTLDLNDGIR
1151 FAGYGADVTI GGKLTTLAQ SSVRGVGT VVIKGRYKAY GQDLDTKGT
1201 VSFVGPLNDP NLNIRAERRL SPVGAGVEIL GSLNSPRITL TANEPMSKED
1251 KLSWLILNRA GSGSSGDNA LSAAGALLA GQINDRIGLV DDLGFTSKRS
1301 RNAQTGELNP AEQVLTVGKQ LTGKLYIGYE YSISSAEQSV KLIYRLTRAI
1351 QAVARIGSRS SGGELTYTIR FDRFSGSDKK DSAGNSKKG*

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m285/a285 99.4% identity in 1389 aa overlap

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          10      20      30      40      50      60
m285.pep MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
|||||
a285     MTDTAPTDTDPTENGTRKMPSEHRPTPPAKKRRPLLKLSAALLSVLILAVCFLGWLAGE
          10      20      30      40      50      60

          70      80      90      100     110     120
m285.pep AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
|||||
a285     AGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGDNWSIETEGADLKISRFRFAWKPSSELM
          70      80      90      100     110     120

          130     140     150     160     170     180
m285.pep RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAVYLDREFETGKISMKGAFDK
|||||
a285     RRSLLHITEISAGDIAIVTKPTPPKEERPPSLPDSIDLPAAVYLDREFETGKISMKGAFDK
          130     140     150     160     170     180

          190     200     210     220     230     240
m285.pep QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGAASVGLKKPFALDTAIYTKGGLEGK
|||||
a285     QTVYLERLDASYRYDRKGHRDLKAADTPWSSSSGSASVGLKKPFALDTAIYTKGGLEGK
          190     200     210     220     230     240

          250     260     270     280     290     300
m285.pep TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLEEVLVKGFNINPAAF
|||||

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656

a285	TIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIHPFAESLDKTLLEEVLVKGFNINPSAF
	250 260 270 280 290 300
m285.pep	310 320 330 340 350 360
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a285	VPSLPDAGLNFDLTAIPSFSDGIALEGSLENTKAGFADRNGIPVRQVLGSFVIRQDGT
	310 320 330 340 350 360
m285.pep	370 380 390 400 410 420
	VHIGNTSAALLGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
a285	VHIGNTSVALGRGGIRLSGKIDTEKDILDNLNIGINSVGAEDVLQTAFKGRLDGSIGIGG
	370 380 390 400 410 420
m285.pep	430 440 450 460 470 480
	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGSILTAQGYLELFKD
a285	TTASPKISWQLGIGTARTDGLAIASDPANGQRKLVLDTVNIAAGQGSILTAQGYLELFKD
	430 440 450 460 470 480
m285.pep	490 500 510 520 530 540
	RLKLDIRSRADFPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
a285	RLKLDIRSRADFPSRIDPQLPAGNINGSINLAGELAKEKFTGKMRFLPGTFNGVPIAGS
	490 500 510 520 530 540
m285.pep	550 560 570 580 590 600
	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLRSRFGFGLAGSLNVR
a285	ADIVYESRHLPRAAVDLRLGRNIIKTDGGFGKKGDRNLNITAPDLRSRFGFGLAGSLNVR
	550 560 570 580 590 600
m285.pep	610 620 630 640 650 660
	GHLSGDLGGIRTFFETDLGAARNLHIGKAADIRSLDFTLKGSPTSRPIRADIKGSRLS
a285	GHLSGDLGGIRTFFETDLGAARNLHIGKAADIRSLDFTLKGSPTSRPIRADIKGSRLS
	610 620 630 640 650 660
m285.pep	670 680 690 700 710 720
	LSGGAHVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
a285	LSGGAHVDTADLMLDGTGVQHRIRTHAAMTLDGKPFKFDLDASGGINRELTRWKSGSIGI
	670 680 690 700 710 720
m285.pep	730 740 750 760 770 780
	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSNLQHFSWDKKTGISAKGGAHGL
a285	LDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMGGSNLQHFSWDKKTGISAKGGAHGL
	730 740 750 760 770 780
m285.pep	790 800 810 820 830 840
	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
a285	HIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYLNISRQSGDAVLPGGQALGLNAFSLK
	790 800 810 820 830 840
m285.pep	850 860 870 880 890 900
	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
a285	TRFQNDRIGILLDGGARFGRINADLGIANAFGGNMANAPLGGRITASLPDLGALKPFLPA
	850 860 870 880 890 900
m285.pep	910 920 930 940 950 960
	AAQNITGSLNAAQIGGRVGSFVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLNL
a285	AAQNITGSLNAAQIGGRVGSFVNAAVNGSSNYGKINGNITVGQSRSFDTAPLGGRNLNL

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a285	AAQNITGSLNAAAQIGGRVGS	PSVNA	AVNGSSNY	KINGNIT	VGQSR	SFDTAP	LGGRLNL
	910	920	930	940	950	960	
m285.pep	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGSIAD	PHLGG	SINGDKLYYRNQTQGIILDNG
a285	TVADAEVFRN	FLPVGQ	TVKGS	LNAAVT	LGGSIAD	PHLGG	SINGDKLYYRNQTQGIILDNG
	970	980	990	1000	1010	1020	
m285.pep	SLRSHIAGR	KWVIDSL	KFRHEG	TAE	LSGT	VMENSG	PDVDIGAVFDKYRILSRPNRRLTV
a285	SLRSHIAGR	KWVIDSL	KFRHEG	TAE	LSGT	VMENSG	PDVDIGAVFDKYRILSRPNRRLTV
	1030	1040	1050	1060	1070	1080	
m285.pep	SGNTRLRYS	PQKGIS	VTGMIK	TDQGL	FGSQ	KSSMPS	VGDDVVVLGEVKKEAAAPLPVNMN
a285	SGNTRLRYS	PQKGIS	VTGMIK	TDQGL	FGSQ	KSSMPS	VGDDVVVLGEVKKEAAAPLPVNMN
	1090	1100	1110	1120	1130	1140	
m285.pep	LTLDLNDG	IRFAGY	GADVTI	GGKLT	LTAQ	SGGS	SVRGVGTVRVIKGRYKAYGQDLITKGT
a285	LTLDLNDG	IRFAGY	GADVTI	GGKLT	LTAQ	SGGS	SVRGVGTVRVIKGRYKAYGQDLITKGT
	1150	1160	1170	1180	1190	1200	
m285.pep	VSVFVG	PLNDP	NLNIRA	ERRLS	SPVG	AGVEIL	GSLNSPRITLTANEPMSEKDKLSWLIILNRA
a285	VSVFVG	PLNDP	NLNIRA	ERRLS	SPVG	AGVEIL	GSLNSPRITLTANEPMSEKDKLSWLIILNRA
	1210	1220	1230	1240	1250	1260	
m285.pep	GSGSSG	DNAALS	AAAGAL	LAGQIN	DRIGL	VDDL	LGFTSKRSRNAQTGELNP
a285	GSGSSG	DNAALS	AAAGAL	LAGQIN	DRIGL	VDDL	LGFTSKRSRNAQTGELNP
	1270	1280	1290	1300	1310	1320	
m285.pep	LTGKLYI	GYEYSI	SSAEQ	SVKLI	YRLTR	AIQAV	ARIGSRSSGGELTYTIRFDRFSGSDKK
a285	LTGKLYI	GYEYSI	SSAEQ	SVKLI	YRLTR	AIQAV	ARIGSRSSGGELTYTIRFDRFSGSDKK
	1330	1340	1350	1360	1370	1380	
m285.pep	DSAGNG	KGKX					
a285	DSAGNS	KGKX					
	1390						

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1187>:

g285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG ATCGCCGGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCGTC CTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACGCTGCTCG ACGGCTTCGA CGGCACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAA CCGTCCGAAC
251 TGATGCGCCG CAGCCTGCAC ATCACCAGCA TCTCCGCCGG CGACATCGCC
301 ATCGTAACCA AACCGACTCC GCCTAAAGAA GAACGCCCGC CTCAAGGCCT
351 GCCCACAGC ATAGACCTGC CCGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAACCTTTG ACAAACAAAC CGTCTATCTC
451 GAACGCCTCA ACGCGGCATA CCGTTACGAC CGTAAAGGGC ACCGCCTCGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG

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551 TCGGGCTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGATTGGAAG GCGAAACCAT ACACAGTACG GCGCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGACGATCGA CGCGGCAAT ATCCGCCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTTGA TAAACATTG
751 GAAGAAGTAC TGGTCAAAGG ATTCAACATC AATCCGTCCG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTCGA CCTGACCGCC ATCCCGTCGT
851 TTTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTCAAG TTTTGGGCGG
951 CTTTGTCTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGCCG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CCGGCAAAAT CGACACCGAA
1051 AAAGACATCC TTGATTTAAA TATAGGCATC AACTCCGTCT GCGCGGAAGA
1101 CGTGCTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GCGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CACCGGCACG
1201 GCACGCACGG ACGGCAGCCT cgcCATCGCA AGCGACCCCG CAAACGAACA
1251 CGGAAACTAG GTGTTGACAC CCGTCAACAT CTCGCGCGGG GAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCTTTCG CGCATCGATC CGCAATTTCC
1401 GGCAGGCGat atCAACGGTT CGATTCATCT TGCCGTGAA CTGGCAAAAG
1451 AGAAATTTAC GGGCAAAATG CGTTTTTTCG CCGGTACGTT CAACGGCGTG
1501 CCGATTGCCG GCAGCGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 CGCCGCGCTC GATTTGCGGT TGGGGCGGAA CATCGTCAAA ACAGACGGCG
1601 GCTTTCGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCGGGC GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCACGGC GCGCAACTTA CACATCGGCA AAGCGGCAGA CATCGGTTCC
1801 CTCGATTTTA CCTCAAAGG CTCACCCGGC ACAAGCCGCC CGATGCGCGC
1851 CGATATCAAG GCGGCGCGCC TTTCCCTGTC GGGCGGCGCG GCGGTGTCTG
1901 ATACCGCCGG CCTGACGCTG GAAGGTACGG GCGCGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGACGGCAAA CCGTTCAAA TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGAAA GGCAGCATCG
2051 GCATCTTCGA CATCGCGCGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACACGTGGCG GCAAGTGGCG CAAATGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GACAGGAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACGCGCG GCCTGCACAT CGCCGAGTTG
2251 CACAATTTCT TCAAACCGCC CTTGCAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC ACAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGCG GCGCGTTTCG GACGGATTAA CGCCGATTG GGCATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATACAC CGCTCGGCGG CAGGATTACA
2551 GCCTCCCTTC CCGACTTGGG CGCATGGAAG CCCTTTCTGC CCGCCGCCGC
2601 GCAAAACATT ACCGGCAGCC TGAATGCCTC CGCGCAATC GCGGACGGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCGTCA ACGGTAGCAG CAACTACGGG
2701 AAAATCAACG GCAATATCAC CGTCGGGCAA AGCCGTCCT TCGATACCGC
2751 ACCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGCATTC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTTCG GCGGCAGCAT CGCCGACCCG CACTTGGGCG GCAGTATCAA
2901 CGGCGACAAG CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTTCGAT ATTGCAGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTTCC GGCACGAAGG GACGGCGGAA CTCTCCGGCA CGGTACGAT
3051 GGAACACAGC GTGCCCGATG TCGATATCGG CGCGGTGTTT GACAAATACC
3101 GCATCTGTGC CCGCCCAAC CGCCGCTGA CCGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGTA TGATTAAAAAC
3201 TGATCAGGGG CTGTTTCGTT CGCAAAAATC CTCGATGCCG TCCGTGCGCG
3251 ACGATGTCGT CGTATTGGGC GAAGTCAAGA AAGAGCGCGG GGCATCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCTC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCGC
3401 AACCGGGCGG AAATGTGCGT GGGGTGGGCA CCGTCCGCGT CATCAAAGGG
3451 CGTTACAAAG CATACGGGCA GGATTTAGAC ATTACCAAAG GCACAGTCTC
3501 CTTTGTCTGG CCGCTCAACG ACCCAACCT GAACATCCG GCCGAACGCC
3551 GCCTTTCCCG CGTCGGTGCG GCGTGGAATA TATTGGGCAG CCTCAACAGC
3601 CCGCGCATTG CGCTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCCTGGCTC ATCCTCAACC GTGCCGGCAG CGGCAGCAGC GGCACAATG
3701 CCGCCCTGTC CGCAGCCGCA GCGCGCTGC TTGCGGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGGAACCTA ACCCCGCCGA ACAGGTGCTG ACCGTGCGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACGG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTTCGCCGT ATCGGCAGCC GTTCGTGCGG CGCGGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTCTTC GGTTCGGACA AAAAGACTC CGCAGGAAAC
4051 GGCAAGGGA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1188; ORF 285-1.ng>:
g285-1.pep

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1  LKLSAALLSV LILAVCFLGW IAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFEDGDN WSIETEGADL KISRFRFAWK PSELMRRSLH ITDISAGDIA
101 IVTKPTPPKE ERPPQGLPDS IDLPAAVYLD RFETGKISMG KTFDKQTVYL
151 ERLNAAYRYD RKGHRLDLKA ADTPWSSSSG SASVGLKPPF ALDTAIYTKG
201 GFEGETIHST ARLSGSLKDV RAELTIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGTGT
401 ARTDGSIAIA SDPANEQRKL VFDTVNISAG EGSLLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQFPAGD INGSIHLAGL LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIVK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGTARNL HIGKAADIRS
601 LDFTLKSGPG TSRPMRADIK GGRLSLSGGA AVVDTAGLTL EGTGAQHRIR
651 THAAMTLDGK PFKLDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAEHVA ASANWQAMG GSLNLQHFSW DRKTGISAKG GARGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGHNARGYL NISRQSGDAV LPPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIGNAFGGNM ANTPLGGRIT
851 ASLPDLGALK PFLPAAAQNI TGSLNASHAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRLNLTVADA EAFRNFLPVG QTVKGSINAA
951 VTGGGSIADP HLGGSINGDK LYYRNQTQGI ILDNGSLRSH IAGRKWVIDS
1001 LKFRHEGTAE LSGTVSMENS VPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGSV VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAASL
1101 PVMNMLTLDL NDGIRFSGYG ADVTIGGKLT LTAQPGGNVR GVGTVRVIK
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEGYISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRLF GSDKKDSAGN
1351 GKKG*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1189>:

m285-1.seq

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1  CTGAAGCTGT CGGCGGCACT GCTGTCTGTC CTGATTTTGG CAGTATGTTT
51  CCTCGGCTGG CTCGCCGTA CGGAAGCAGG TTTGCGCTTC GGGCTGTACC
101 AAATCCCCTC TTGGTTCGGC GTAAACATTT CCTCCCAAAA CCTCAAAGGC
151 ACCTGCTCGC ACGGCTTCGA CGGCGACAAC TGGTCGATAG AAACCGAGGG
201 GGCAGACCTT AAAATCAGCC GCTTCCGCTT CGCGTGGAAG CCGTCCGAAC
251 TGATGCGCGC GACGCTGCAC ATTACCGAAA TTTCCGCGCG CGACATCGCC
301 ATCGTTACCA AACCGACTCC GCCTAAAGAA GAACGCCCCG CGCTCAGCCT
351 TCCCGACAGC ATAGACCTGC CTGCCGCCGT CTATCTCGAC CGCTTCGAGA
401 CGGGCAAAAT CAGCATGGGC AAAGCCTTTG ACAAACAACG CGTCTATCTC
451 GAACGGCTGG ATGCTTCATA CCGTTACGAC CGCAAAGGAC ACCGCCTTGA
501 CCTGAAGGCC GCCGACACGC CGTGGAGCAG TTCGTCGGGG GCGGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGACTCGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA CGGCAGCCT
651 GAAGGATGTG CGGCGCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAAAT CGTCATCCAC CCGTTTGGCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGGCCG CTTCTGTCGC
801 TTCCCTGCCC GATGCCGGAC TGAATTTCTG CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGTTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTC CCGACCGCAA CGGCATCCCC GTCCGTCAGG TTTTAGGCGG
951 CTTTGTATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCGCGG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCATTTTAAA TATAGGCATC AACTCCGTCG CGCGGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCACGAC CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCACGG ACGGCAGCCT CGCCATTGCA AGCGACCCAG CAAACGGACA
1251 GCGGAACTG GTGCTCGACA CCGTCAACAT CGCCGCGGGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCGCGCATTT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA CTGGCAAAAG
1451 AGAAATTAC AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCCG GCAGTGCCGA CATTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCCGCGTC GATTTGCGGC TGGGGCGGAA CATTATTAAT ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCAGAT
1651 TTATCCCGTT TCGGTTTTCG ACTCGCGGGT TCTTTAAATG TACGCGGACA
1701 CTTTTCGGGT GATTTGGACG GCGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CCGGCGCGGC GCGCAACCTG CACATCGGCA AGGCGGCAGA CATCGGTTCC
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCAGC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTGCTGTGC GGGCGGAGCG GCGGTTGTCT
1901 ATACCGCGCA CCTGATGCTG GACGGCACGG GCGTGCAGCA CCGCATCCGC
1951 ACACACGCGG CCATGACGCT GGATGGCAA CCGTTCAAT TCGATTGGA
2001 CGCTTCAGGC GGCATCAACA GGGAACTTAC CCGATGGAAG GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGCGG CAAATTGGCA

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2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GGCACACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTTCT TCAAAACCGCC CTTTCAAAAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GCAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAGCGG CGATGCCGTA TTGCCCGGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAAC GACCGCATCG GAATCCTGCT
2451 TGACGGCGCG GCGCGTTTCG GCGGGATTAA CGCCGATTTC GGCATCGCCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CGCATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCGC CGCGCAAAATC GCGGACGCGG
2651 TAGGCTCTCC GTCCGTCAAT GCCGCCGTCA ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCTC ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCCCTC GCGGCAGCAT CGCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGCGACAAA CTCTATTACC GCAACCAAAC CCAAGGCATC ATCTTGACA
2951 ACGGCTCGCT GCGTTCGCAT ATCGCGGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAGG GACGGCGGAA CTCTCCGGTA CGGTCCGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCGCCTGA CGGTTTCCGG CAACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAATAA
3201 GGATCAGGGG CTGTTCCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGGC GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGCTTCGC
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTACGG GCGTGGGCA CGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CACACGGGCA GGATTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTCCGG CCGCTCAACG ATCCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCG CGTCGGTCCG GCGTGGAAA TATTGGGCG CCTCAACAGC
3601 CCGCGCATTA CGTGACGGC AAACGAACCG ATGAGTGAAA AAGACAAGCT
3651 CTCTTGGGTC ATCCTCAACC GCGCCGGCAG CGGACGACG GGCAGCAATG
3701 CGCCCTCTC TGCAGCCGCA GGTGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CCGGCAAAAC GCGGAACCTA ACCCGCCGCA ACAGGTGCTG ACCGTCGGCA
3851 AACAACTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 CGGGAACAGT CCGTCAAACT GATTACCAGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTCGGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGCTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 GGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1190; ORF 285-1>:

m285-1.pep

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1 LKLSAALLSV LILAVCF LGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51 TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPPLSLPDS IDLPAAVYLD RFETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRLDLKA ADTPWSSSSG AASVGLKKKF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFN I NPAAFPVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGGFVI RQDGTVHIGN TSAALLGRGG IRLSGKIDTE
351 KDILDNLNIG NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGSIAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKG DRLNLITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA AVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASANWQAMG GSLNLQHFSW DKKTGISAKV GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL GIANAFGGNM ANAPLGGRIT
851 ASLPDLGALK PFLPAAQNI TGSLNAAAI GGRVGSPPSVN AAVNGSSNYG
901 KINGNITVGQ SRSDTAPLG GRNLTVADA EVFRNFLPVG QTVKGSNLAA
951 VTLGGSIAADP HLGGSINGDK LYRNQTQGI ILDNGLSLRS HIGRKKVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGSVR GVGTVRVIKG
1151 RYKAYGQDLD ITKGTVSFVG PLNDPNLNIR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDKLSWL ILNRAGSGSS GDNAALSAAG GALLAGQIND
1251 RIGLVDDLGF TSKRSRNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 GKGK*

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g285-1/m285-1 96.5% identity in 1354 aa overlap

10 20 30 40 50 60

661

g285-1.pep	LKLSAALLSVLILAVCF LGW IAGTEAGLRFG LYQIPSWFGVNISSQN LKGTLLDGF DGDN
m285-1	LKLSAALLSVLILAVCF LGW IAGTEAGLRFG LYQIPSWFGVNISSQN LKGTLLDGF DGDN
	10 20 30 40 50 60
g285-1.pep	70 80 90 100 110 120
m285-1	70 80 90 100 110 120
g285-1.pep	WSIETEGADLKISRFRFAWKPS ELMRRSLHITDISAGDIAIVTKPTPPKEERPPQGLPDS
m285-1	WSIETEGADLKISRFRFAWKPS ELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS
	70 80 90 100 110 120
g285-1.pep	130 140 150 160 170 180
m285-1	130 140 150 160 170 180
g285-1.pep	IDLPAAYLDRFETGKISMGKTFDKQTVYLERLNAARYDRKGHRLDLKAADTPWSSSSG
m285-1	IDLPAAYLDRFETGKISMGKAFDKQTVYLERLDASYRYDRKGHRLDLKAADTPWSSSSG
	130 140 150 160 170 180
g285-1.pep	190 200 210 220 230 240
m285-1	190 200 210 220 230 240
g285-1.pep	SASVGLKKPFALDTAIYTKGFEGETIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
m285-1	AASVGLKKPFALDTAIYTKGLEGKTIHSTARLSGSLKDVRAELTIDGGNIRLSGKSVIH
	190 200 210 220 230 240
g285-1.pep	250 260 270 280 290 300
m285-1	250 260 270 280 290 300
g285-1.pep	PFAESLDKTL EEVLVKGFNINPSAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK
m285-1	PFAESLDKTL EEVLVKGFNINPAAFVPSLPDAGLNFDLTAIPSFSDGIALEGS LDLENTK
	250 260 270 280 290 300
g285-1.pep	310 320 330 340 350 360
m285-1	310 320 330 340 350 360
g285-1.pep	AGFADRNGIPVRQVLGGFVIRQDGT VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGI
m285-1	AGFADRNGIPVRQVLGGFVIRQDGT VHIGNTSAALLGRGGIRLSGKIDTEKDILDLNIGI
	310 320 330 340 350 360
g285-1.pep	370 380 390 400 410 420
m285-1	370 380 390 400 410 420
g285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGTGTARTDGS LAIASDPANEQRKL
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGTTASPKISWQLGIGTARTDGS LAIASDPANGQRKL
	370 380 390 400 410 420
g285-1.pep	430 440 450 460 470 480
m285-1	430 440 450 460 470 480
g285-1.pep	VFDTVNISAGEGSLTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQFPAGDINGSIHLAGE
m285-1	VLDTVNIAAGQGS LTAQGYLELFKDRLLKLDIRSRAFDPSRIDPQLPAGNINGSINLAGE
	430 440 450 460 470 480
g285-1.pep	490 500 510 520 530 540
m285-1	490 500 510 520 530 540
g285-1.pep	LAKEKFTGKMRF LPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIVKTDGGFGKKGD
m285-1	LAKEKFTGKMRF LPGTFNGVPIAGSADIVYESRHLPRAAVDLRLGRNIKT DGGFGKKGD
	490 500 510 520 530 540
g285-1.pep	550 560 570 580 590 600
m285-1	550 560 570 580 590 600
g285-1.pep	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDL DGGIRT FETDLSGTARNLHIGKAADIRS
m285-1	RLNLNITAPDLSRFGFGLAGSLNVRGHLSGDL DGGIRT FETDLSGAARNLHIGKAADIRS
	550 560 570 580 590 600
g285-1.pep	610 620 630 640 650 660
m285-1	610 620 630 640 650 660
g285-1.pep	LDFTLKGSPGTSRPMRADIKGGRSLSGGA AVVDTAGLTLEGTGAQHRIRTHAAMTLDGK
m285-1	LDFTLKGSPDTSRPIRADIKGSRSLSGGA AVVDTADLMLDGTGVQHRIRTHAAMTLDGK
	610 620 630 640 650 660
g285-1.pep	670 680 690 700 710 720
m285-1	670 680 690 700 710 720
g285-1.pep	PFKLDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGA EHVAASAANWQAMG
m285-1	PFKFDLDASGGINRELTRWKSGSIGILDIGGAFNLKLQNRMTLEAGA ERVAASAANWQAMG
	670 680 690 700 710 720
g285-1.pep	730 740 750 760 770 780
m285-1	730 740 750 760 770 780
g285-1.pep	GSLNLQHFSWDRKTGISAKGGARGHLHIAELHNFFKPPFEHNLVLNGDWDVAYGHNARGYL
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL

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	730	740	750	760	770	780
	790	800	810	820	830	840
g285-1.pep	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIGNAFGGNM					
m285-1	NISRQSGDAVLPGGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLGIANAFGGNM					
	790	800	810	820	830	840
	850	860	870	880	890	900
g285-1.pep	ANTPLGGRITASLPDLGALKPFLPAAAQONITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
m285-1	ANAPLGGRITASLPDLGALKPFLPAAAQONITGSLNAAQIGGRVGSPSVNAAVNGSSNYG					
	850	860	870	880	890	900
	910	920	930	940	950	960
g285-1.pep	KINGNITVGQSRSFDTAPLGGRLNLTVADAEAFRNFLPVGQTVKGSINAAVTLGGSIA DP					
m285-1	KINGNITVGQSRSFDTAPLGGRLNLTVADAEVFRNFLPVGQTVKGSINAAVTLGGSIA DP					
	910	920	930	940	950	960
	970	980	990	1000	1010	1020
g285-1.pep	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWWIDSLKFRHEGTAELSGTVSMENS					
m285-1	HLGGSINGDKLYYRNQTQGIILDNGSLRSHIAGRKWWIDSLKFRHEGTAELSGTVGMENS					
	970	980	990	1000	1010	1020
	1030	1040	1050	1060	1070	1080
g285-1.pep	VPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
m285-1	GPDVIDIGAVFDKYRILSRPNRRLTVSGNTRLRYSPQKGISVTGMIKTDQGLFGSQKSSMP					
	1030	1040	1050	1060	1070	1080
	1090	1100	1110	1120	1130	1140
g285-1.pep	SVGDDVVVLGEVKKEAAASLPVNMNLTLDLNDGIRFSGYGADVTTIGGKLTTLTAQPGGNVR					
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTTIGGKLTTLTAQSGGSVR					
	1090	1100	1110	1120	1130	1140
	1150	1160	1170	1180	1190	1200
g285-1.pep	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
m285-1	GVGTVRVIKGRYKAYGQDLDTKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS					
	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
g285-1.pep	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
m285-1	PRITLTANEPMSEKDKLSWLILNRAGSGSSGDNAALSAAGALLAGQINDRIGLVDDLGF					
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
g285-1.pep	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYGISSAEQSVKLIYRLTRAIQAVAR					
m285-1	TSKRSRNAQTGELNPAEQVLTVGKQLTGKLYIGYEYSISSAEQSVKLIYRLTRAIQAVAR					
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
g285-1.pep	IGSRSSGGELTYTIRFDRLFSGDKKDSAGNGKGK					
m285-1	IGSRSSGGELTYTIRFDRFSGDKKDSAGNGKGKX					
	1330	1340	1350			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1191>:

a285-1.seq

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1  CTGAAGCTGT  CGGCGGCACT  GCTGTCTGTT  CTGATTTTGG  CAGTATGTTT
51  CCTCGGCTGG  CTCGCCGCA  CGGAAGCGGG  TTTGCGCTTC  GGGCTGTACC
101  AAATCCCGTC  TTGGTTCGGC  GTAAACATTT  CCTCCCAAAA  CCTCAAAGGC
151  ACGCTGCTCG  ACGGCTTCGA  CGCGGACAAC  TGGTCGATAG  AAACCGAGGG
201  GGCAGACCTT  AAAATCAGCC  GCTTCCGCTT  CGCGTGGAAG  CCGTCCGAAC
251  TGATGCGCGC  CAGCCTGCAC  ATTACCGAAA  TTTCCGCCGG  CGACATCGCC
301  ATCGTTACCA  AACCGACTCC  GCCTAAAGAA  GAACGCCCGC  CGCTCAGCCT
351  TCCCGACAGC  ATAGACCTGC  CTGCCGCCGT  CTATCTCGAC  CGCTTCGAGA
401  CGGGCAAAAT  CAGCATGGGC  AAAGCCTTG  ACAAACAAAC  CGTCTATCTC
451  GAACGGCTGG  ATGCTTCATA  CCGTTACGAC  CGCAAAGGAC  ACCGCCTCGA

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501 CCTGAAGGCT GCCGACACGC CGTGGAGCAG TTCGTCGGGG TCAGCCTCGG
551 TCGGCTTGAA AAAACCGTTT GCCCTCGATA CCGCCATTTA CACCAAAGGC
601 GGA CTGGAAG GCAAAACCAT ACACAGTACG GCTCGGCTGA GCGGCAGCCT
651 GAAGGATGTG CGCGCCGAAC TGGCGATCGA CGGCGGCAAT ATCCGCTCT
701 CGGGAAAATC CGTCATCCAC CCGTTTGCCG AATCATTGGA TAAAACATTG
751 GAAGAAGTAC TGGTCAAAGG GTTCAACATC AATCCGTCGG CCTTCGTGCC
801 TTCCCTGCCC GATGCCGGGC TGAATTTTCA CCTGACCGCC ATCCCGTCGT
851 TTTCAGACGG CATCGCGCTG GAAGGCTCGC TCGATTTGGA AAACACCAAA
901 GCCGGCTTTG CCGACCGCAA CGGCATCCCC GTCCGTGAGG TTTTAGGCAG
951 CTTTGTGATC CGGCAGGACG GCACGGTGCA TATCGGCAAT ACGTCCGTCTG
1001 CCCTGCTCGG ACGGGGCGGC ATCAGGCTGT CGGGCAAAAT CGACACCGAA
1051 AAAGACATCC TCGATTTAAA TATAGGCATC AACTCCGTCTG GCGCGGAAGA
1101 CGTACTGCAA ACCGCGTTCA AAGGCAGGTT GGACGGCAGC ATCGGCATCG
1151 GTGGCAGCAG CGCCTCGCCC AAAATCTCTT GGCAACTCGG CATCGGCACG
1201 GCGCGCAGCG ACGGCAGCCT CGCCATTGCA AGCGACCCCG CAAACGGACA
1251 GCGGAAACTG GTGCTCGACA CCGTCAACAT CGCCGCGCGG CAAGGCAGCC
1301 TGACCGCGCA AGGCTATCTC GAGCTGTTTA AAGACCGCCT GCTCAAGCTG
1351 GACATCCGTT CCCGCGCATT CGACCCTTCG CGCATCGATC CGCAACTTCC
1401 GGCAGGCAAT ATCAACGGCT CAATAAACCT TGCCGGCGAA TGGCAAAAG
1451 AGAAATTACAG AGGCAAAATG CGGTTTTTAC CCGGCACGTT CAACGGCGTA
1501 CCGATTGCGG CGAGTGCCGA CATTTGTTTAC GAGTCCCGCC ACCTTCCGCG
1551 TGCCGCGGTC GATTTGCGGC TGGGGCGGAA CATTATTAAA ACAGACGGCG
1601 GCTTCGGCAA AAAAGGCGAC CGGCTTAACC TCAATATCAC CGCACCCGAT
1651 TTATCCCGTT TCGGTTTCGG ACTCGCGGGG TCTTTAAATG TACGCGGACA
1701 CCTTTCCGGC GATTTGGACG GTGGCATCCG AACCTTTGAA ACCGACCTTT
1751 CGCGCGCGGC GCGCAACCTG CACATCGGCA AGCGGCGAGA CATCCGTTTCG
1801 CTCGATTTCG CGCTCAAAGG TTCGCCCCGAC ACAAGCCGCC CGATACGCGC
1851 CGACATCAAA GGCAGCCGCC TTTCGCTGTC GGGCGGAGCG GAGGTTGTCTG
1901 ATACCGCGCA CTGATGCTG GACGGCACGG CGGTGCAGCA CCGCATCCGC
1951 ACACACGCCG CCATGACGCT GGATGGCAA CCGTTCAAAT TCGATTTGGA
2001 CGCTTCAGGC GGCATCAACA GGAACCTTAC CCGATGGAAA GGCAGCATCG
2051 GCATCCTCGA CATCGGCGGC GCATTCAACC TCAAGCTGCA AAACCGTATG
2101 ACGCTCGAAG CCGGTGCGGA ACGCGTGGCG GCAAGTGGCG CAAATTGGCA
2151 GGCAATGGGC GGCAGCCTCA ACCTGCAACA CTTTCTTGG GATAAAAAAA
2201 CCGGCATATC GGCAAAAGGC GCGGCACACG GTCTGCATAT CGCCGAGTTG
2251 CACAATTCTT TCAAACCGCC CTTCGAACAC AATCTGGTTT TAAACGGCGA
2301 CTGGGATGTC GCCTACGGGC GAAACGCGCG CGGCTACCTC AATATCAGCC
2351 GGCAAAAGCG CGATGCCGTA TTGCCCCGCG GGCAGGCTTT GGGTTTGAAC
2401 GCATTTTCCC TGAAAACGCG CTTTCAAAC GACCGTATCG GAATCCTGCT
2451 TGACGGCGGC GCGCGTTTCG GCGGGATTAA CGCCGATTTC GACATCGGCA
2501 ACGCCTTCGG CGGCAATATG GCAAATGCAC CGCTCGGCGG CAGGATTACC
2551 GCCTCCCTTC CCGACTTGGG CACATTGAAG CCCTTTCTGC CCGCCGCGCG
2601 GCAAAACATT ACCGGCAGCC TGAATGCCG CCGCAAAATC GCGGACGGG
2651 TCGGCTCTCC GTCCGTCAAT GCCGCCGTC ACGGCAGCAG CAACTACGGG
2701 AAAATCAACG GCAACATCAC CGTCGGGCAA AGCCGCTCTT TCGATACCGC
2751 GCCTTTGGGC GGCAGGCTCA ACCTGACCGT TGCCGATGCC GAAGTATTCC
2801 GCAACTTCCT ACCGGTCGGA CAAACCGTCA AAGGCAGCCT GAATGCCGCC
2851 GTAACCTCTG GCGGCAGCAT CGCCGATCCG CACTTGGGCG GCAGCATCAA
2901 CCGGCACAAA CTCTATTACC GCAACCAAA CCAAGGCATC ATCTTGGACA
2951 ACGGCTCGCT GCGTTTCGAT ATCGCGGCA GGAATGGGT AATCGACAGC
3001 CTGAAATTCC GGCACGAAG GACGGCGGAA CTCTCCGTA CGGTCGGTAT
3051 GGAAAACAGC GGACCCGATG TCGATATCGG CGCGGTGTTC GACAAATACC
3101 GCATCCTGTC CCGCCCCAAC CGCCGCTGA CGGTTTCGG CACACCCGC
3151 CTGCGCTATT CGCCGCAAAA AGGCATATCC GTTACCGGGA TGATTAAAC
3201 GGATCAGGGG CTGTTTCGTT CGCAAAATC CTCGATGCCG TCCGTCGGCG
3251 ACGATGTCGT CGTATTAGG GAAGTCAAAA AAGAGGCGGC GGCACCGCTC
3301 CCCGTCAATA TGAACCTGAC TTTAGACCTC AATGACGGCA TCCGTTTCG
3351 CGGCTACGGC GCGGACGTTA CCATAGGCGG CAAACTGACC CTGACCGCCC
3401 AATCGGGCGG AAGCGTGCGG GCGGTGGGCA CGGTCCGCGT CATCAAAGGG
3451 CGTTATAAGG CATAAGGGCA GGATTTGGAC ATTACCAAAG GCACGGTCTC
3501 CTTTGTGCGC CCGCTCAACG ACCCAACCT CAACATCCGC GCCGAACGCC
3551 GCCTTTCCCC CGTCGGTGCG GCGGTGGAAA TATTGGGCG CCTCAACAGT
3601 CCGCGCATTG CGTGACGGC AAACGAACCG ATGAGTGAAG AAGACAAGCT
3651 CTCTTGCTC ATCTCAACC GCGCCGCGAG TGGCAGCAG GCGGACAATG
3701 CCGCCCTGTC CGCAGCCGCC GCGCGCTGC TTGCCGGGCA AATCAACGAC
3751 CGCATCGGGC TGGTGGATGA TTTGGGCTTT ACCAGCAAGC GCAGCCGCAA
3801 CGCGCAAAAC GCGCAACTCA ACCCGCCGGA ACAGGTGCTG ACCGTCGGCA
3851 AACAACCTGAC CGGCAAACTC TACATCGGCT ACGAATACAG CATCTCCAGC
3901 GCGGAACAGT CCGTCAAACT GATTTACCGG CTGACCCGCG CCATACAGGC
3951 GGTGCCCCGT ATCGGCAGCC GTTCGTGCGG CGGCGAGCTG ACATACACCA
4001 TACGTTTCGA CCGTTCTCC GGTTCGGACA AAAAAGACTC CGCCGGAAC
4051 AGCAAAGGAA AATAA

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This corresponds to the amino acid sequence <SEQ ID 1192; ORF 285-1.a>:

664

a285-1.pep

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1  LKLSAALLSV LILAVCFLGW LAGTEAGLRF GLYQIPSWFG VNISSQNLKG
51  TLLDGFDDGN WSIETEGADL KISRFRFAWK PSELMRRSLH ITEISAGDIA
101 IVTKPTPPKE ERPPSLPDS IDLPAAYLDR FETGKISMV KAFDKQTVYL
151 ERLDASYRYD RKGHRDLKA ADTPWSSSSG SASVGLKKPF ALDTAIYTKG
201 GLEGKTIHST ARLSGSLKDV RAELAIDGGN IRLSGKSVIH PFAESLDKTL
251 EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIAL EGSLDLENTK
301 AGFADRNGIP VRQVLGSFVI RQDGTVHIGN TSVALLGRGG IRLSGKIDTE
351 KDILDLNIGI NSVGAEDVLQ TAFKGRLDGS IGIGGTTASP KISWQLGIGT
401 ARTDGLAIA SDPANGQRKL VLDTVNIAAG QGSLTAQGYL ELFKDRLLKL
451 DIRSRAFDPS RIDPQLPAGN INGSINLAGE LAKEKFTGKM RFLPGTFNGV
501 PIAGSADIVY ESRHLPRAAV DLRLGRNIIK TDGGFGKKGD RLNLNITAPD
551 LSRFGFGLAG SLNVRGHLGS DLDGGIRTFE TDLSGAARNL HIGKAADIRS
601 LDFTLKGSPD TSRPIRADIK GSRLSLSGGA EVVDTADLML DGTGVQHRIR
651 THAAMTLDGK PFKFDLDASG GINRELTRWK GSIGILDIGG AFNLKLQNRM
701 TLEAGAERVA ASAANWQAMG GSNLNLQHFSW DKKTGISAKG GAHGLHIAEL
751 HNFFKPPFEH NLVLNGDWDV AYGRNARGYL NISRQSGDAV LPGGQALGLN
801 AFSLKTRFQN DRIGILLDGG ARFGRINADL DIGNAFGGNM ANAPLGGRIT
851 ASLPDLGTLK PFLPAAQNI TGSNLAAQI GGRVGSPSVN AAVNGSSNYG
901 KINGNITVGQ SRSFDTAPLG GRNLTVADA EVFRNFPVG QTVKGS LNAA
951 VTLGGSADP HLGGSLGDK LYRNQQTQGI ILDNGLSLRH IAGRWVIDS
1001 LKFRHEGTAE LSGTVGMENS GPDVDIGAVF DKYRILSRPN RRLTVSGNTR
1051 LRYSPQKGIS VTGMIKTDQG LFGSQKSSMP SVGDDVVVLG EVKKEAAAPL
1101 PVNMNLTLDL NDGIRFAGYG ADVTIGGKLT LTAQSGGVR GVGTVRVIKG
1151 RYKAYQDLD ITKGTVSFVG PLNDPNLNR AERRLSPVGA GVEILGSLNS
1201 PRITLTANEP MSEKDLKSWL ILNRAGSGSS GDNAALSAAA GALLAGQIND
1251 RIGLVDDLGF TSKRSNAQT GELNPAEQVL TVGKQLTGKL YIGYEYSISS
1301 AEQSVKLIYR LTRAIQAVAR IGSRSSGGEL TYTIRFDRFS GSDKKDSAGN
1351 SKGK*

```

a285-1/m285-1 99.3% identity in 1354 aa overlap

	10	20	30	40	50	60
a285-1.pep	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
m285-1	LKLSAALLSVLILAVCFLGWLAGTEAGLRFGLYQIPSWFGVNISSQNLKGTLLDGFDDGN					
	70	80	90	100	110	120
a285-1.pep	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
m285-1	WSIETEGADLKISRFRFAWKPSSELMRRSLHITEISAGDIAIVTKPTPPKEERPPSLPDS					
	130	140	150	160	170	180
a285-1.pep	IDLPAAYLDRFETGKISMVKAQFQTVYLERLDASYRYDRKGRHLDLKAADTPWSSSSG					
m285-1	IDLPAAYLDRFETGKISMVKAQFQTVYLERLDASYRYDRKGRHLDLKAADTPWSSSSG					
	190	200	210	220	230	240
a285-1.pep	SASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
m285-1	AASVGLKKPFALDTAIYTKGGLEGKTIHSTARLSGSLKDVRAELAIDGGNIRLSGKSVIH					
	250	260	270	280	290	300
a285-1.pep	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIALEGS LDLENTK					
m285-1	PFAESLDKTL EEVLVKGFNI NPSAFVPSLP DAGLNFDLTA IPSFSDGIALEGS LDLENTK					
	310	320	330	340	350	360
a285-1.pep	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
m285-1	AGFADRNGIPVRQVLGSFVIRQDGTVHIGNTSVALLGRGGIRLSGKIDTEKDILDLNIGI					
	370	380	390	400	410	420
a285-1.pep	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL					
m285-1	NSVGAEDVLQTAFKGRLDGSIGIGGTTASPKISWQLGIGTARTDGLAIASDPANGQRKL					
	430	440	450	460	470	480

665

a285-1.pep	VLDTVNIAAGQGS	LTAAQGYLELFKDRLLK	LDIRSRAFDPSRIDPQLPAGNINGSIN	LAGE	
m285-1	VLDTVNIAAGQGS	LTAAQGYLELFKDRLLK	LDIRSRAFDPSRIDPQLPAGNINGSIN	LAGE	
	430	440	450	460	470 480
a285-1.pep	LAKEKFTGKMRFLPG	TFN	GVPIAGSADIVYESRHL	PRAAVDLRLGRNIIKTDGGFGKKG	D
m285-1	LAKEKFTGKMRFLPG	TFN	GVPIAGSADIVYESRHL	PRAAVDLRLGRNIIKTDGGFGKKG	D
	490	500	510	520	530 540
a285-1.pep	RLN	LNITAPDLSRFGFGLAGSLNVRGHL	SGDLGGIRT	FETDL	SGAARNLHIGKAADIRS
m285-1	RLN	LNITAPDLSRFGFGLAGSLNVRGHL	SGDLGGIRT	FETDL	SGAARNLHIGKAADIRS
	550	560	570	580	590 600
a285-1.pep	LDFTLKGSPDTSRPI	RADIKGSRLSLSGGAEVVD	TADLMLDGTGVQHRIR	THAAMTLDGK	
m285-1	LDFTLKGSPDTSRPI	RADIKGSRLSLSGGAEVVD	TADLMLDGTGVQHRIR	THAAMTLDGK	
	610	620	630	640	650 660
a285-1.pep	PFKFDLDASGGINREL	TRWKG	SIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG		
m285-1	PFKFDLDASGGINREL	TRWKG	SIGILDIGGAFNLKLQNRMTLEAGAERVAASAANWQAMG		
	670	680	690	700	710 720
a285-1.pep	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
m285-1	GSLNLQHFSWDKKTGISAKGGAHGLHIAELHNFFKPPFEHNLVLNGDWDVAYGRNARGYL				
	730	740	750	760	770 780
a285-1.pep	NISRQSGDAVLP	GGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM			
m285-1	NISRQSGDAVLP	GGQALGLNAFSLKTRFQNDRIGILLDGGARFGRINADLDIGNAFGGNM			
	790	800	810	820	830 840
a285-1.pep	ANAPLGGRITASLPDLGLTKPFLPAAQAQ	NITGSLNAAAQIGGRVGS	PSVNAAVNGSSNYG		
m285-1	ANAPLGGRITASLPDLGLTKPFLPAAQAQ	NITGSLNAAAQIGGRVGS	PSVNAAVNGSSNYG		
	850	860	870	880	890 900
a285-1.pep	KINGNITVQSR	SFDTAPLGGRLNLT	VADAEVFRN	FLPVGQTVKGS	LNAAVTLGGS
m285-1	KINGNITVQSR	SFDTAPLGGRLNLT	VADAEVFRN	FLPVGQTVKGS	LNAAVTLGGS
	910	920	930	940	950 960
a285-1.pep	HLGGSINGDKLYYRNQ	TQGII	LDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS		
m285-1	HLGGSINGDKLYYRNQ	TQGII	LDNGSLRSHIAGRKWVIDSLKFRHEGTAELSGTVGMENS		
	970	980	990	1000	1010 1020
a285-1.pep	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRL	RYSPQKGISVTGMIKTDQGLFGSQKSSMP			
m285-1	GPDVDIGAVFDKYRILSRPNRRLTVSGNTRL	RYSPQKGISVTGMIKTDQGLFGSQKSSMP			
	1030	1040	1050	1060	1070 1080
a285-1.pep	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLT	LTAAQSGGSVR			
m285-1	SVGDDVVVLGEVKKEAAAPLPVNMNLTLDLNDGIRFAGYGADVTIGGKLT	LTAAQSGGSVR			
	1090	1100	1110	1120	1130 1140
a285-1.pep	GVGTVRVIKGRYKAYGQDL	DITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS			
m285-1	GVGTVRVIKGRYKAYGQDL	DITKGTVSFVGPLNDPNLNIRAERRLSPVGAGVEILGSLNS			
	1150	1160	1170	1180	1190 1200

666

	1150	1160	1170	1180	1190	1200
	1210	1220	1230	1240	1250	1260
a285-1.pep	PRITLTAN	EPMS	EKDKLS	WLILNR	AGSGSS	GDNAALS
m285-1	PRITLTAN	EPMS	EKDKLS	WLILNR	AGSGSS	GDNAALS
	1210	1220	1230	1240	1250	1260
	1270	1280	1290	1300	1310	1320
a285-1.pep	TSKRSR	NAQTG	ELNPAE	QVLTVG	KQLTGK	LYIGYE
m285-1	TSKRSR	NAQTG	ELNPAE	QVLTVG	KQLTGK	LYIGYE
	1270	1280	1290	1300	1310	1320
	1330	1340	1350			
a285-1.pep	IGSRSS	GGELTY	TIRFDR	FSGSDK	KDSAGN	SKGKX
m285-1	IGSRSS	GGELTY	TIRFDR	FSGSDK	KDSAGN	SKGKX
	1330	1340	1350			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1193>:

```

g286.seq
1  atgcagaaca ccggtaccat gatgatcaaa ccgaccgccc tgctcctgcc
51  ggctttatth ttctttccgc acgcatacgc gcctgccgcc gacctttccg
101 aaaacaaggc ggcgggtttc gcattgttca aaagcaaaag ccccgacacc
151 gaatcagtc aattaaaacc caaattcccc gtccgcacgc acacgcagga
201 cagtgaatc aaagatatgg tcgaagaaca cctgccgctc atcacgcagc
251 agcaggaaga ggttttggat aaggaacaga cgggattcct tggcgaagaa
301 gcaccggaca acgttaaaac aatgctccgc agcaaaggct atttcagcag
351 caaggtcagc ctgacggaaa aagacggagc ttatacgggt cacatcacac
401 cgggcccgcg caccaaaatc gccaacgtcg gcgtcgccat cctcggcgac
451 atcctttcag acggcaacct cgccgaatac taccgcaacg cgctggaaaa
501 ctggcagcag ccggtaggca gcgatttcga tcaggacagt tgggaaaaaca
551 gcaaaacttc cgtcctcggc gcggtaacgc gcaaaggcta ccgcttgcc
601 aagctcggca acaccggggc ggccgtcaac cccgataccg ccaccgcoga
651 ttgaaacgtc gtcgtggaca gcggccgccc cattgccttc ggcgactttg
701 aaatcacccg cacacagcgt taccgccaac aaaccgtctc cggcctggcg
751 cgcttccaac cgggcacgcc ctacgacctc gacctgctgc tcgacttcca
801 acaggcgctc gaacaaaacg ggcattatth cggcgcgctc gtacaagccg
851 acttcgaccg cctcccaagg ggaccgcgtc cccgtcaaaag tcagcgtaac
901 cgaggtcaaa cgccacaaac tcgaaaccgg catccgcctc gattcggaat
951 acggtttggg cggcaaaaat gcctacgact attacaacct cttcaacaaa
1001 ggctatatcg gctcggtcgt ctgggatatg gacaaatacg aaaccacgct
1051 tgccgccggc atcagccagc cgcgcaacta tcggggcaac tactggacaa
1101 gcaacgtttc ctacaacctg tcgaccaccc aaaacctcga aaaacgcgcc
1151 ttctccggcg gcatctggtg tgtgcgcgac cgcgcgggca tcgatgccag
1201 gctggggggc gaatttctcg cagaaggccg gaaaatcccc ggctcggatg
1251 tcgatttggg caacagccac gccacgatgc tgaccgcctc ttggaaacgc
1301 cagctgctca acaacgtgct gcaccccgaa aacggccatt acctcgacgg
1351 caaaatcggg acgactttgg gcacattcct gtcctccacc gcgctaatec
1401 gcacctctgc ccgcgcaggt tatttcttca cgcccgaaaa caaaaaactc
1451 ggcacgttca tcatacgcg acaagcgggt tacaccgttg cagcgacaaa
1501 tgccgatgtc ccctcggggc tgatgttccg cagcggcggc gcgtcttccg
1551 tgcgcggtta cgaacttga

```

This corresponds to the amino acid sequence <SEQ ID 1194; ORF 286.ng>:

```

g286.pep
1  MQNTGTMMIK PTALLLPALF FFPAYAPAA DLSENKAAGF ALFKSKSPDT
51  ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKD GAYTV HITPGPRTKI ANVGVAAILGD
151 ILSDGNLA EY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKGYPLA
201 KLGNTRAAVN PDTATADLNV VVDSGRPIAF GDFEITGTQR YPEQTVSGLA
251 RFQPGTPYDL DLLLD FQQA EQNGHYS GAS VQADFRLPR GPRPRQSQRN
301 RGQTPQTRNR HPPRF GIRFG RQNRLRL LQP LQQRLYRLGR LGYGQIRNHA
351 CRRHQPA AQL SGQLLDK QRF LQPFDPKPR KTRLLRRHLV CARPRGHR CQ
401 AGGGISRRRP ENPRLGCRFG QQPRHDADRL LETPAAQ QRA APRKRPLPRR

```

667

451 QNRDDFGHIP VLHRANPHLC PRRFLHARK QKTRHVHHTR TSGLHRCTRO
501 CRCPLGADV PRRRVFRARL RT*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1195>:

m286.seq

```

1 ATGCACGACA CCCGTACCAT GATGATCAAA CCGACCGCCC TGCTCCTGCC
51 GGCTTTATTT TTCTTTCCGC ACGCATACGC GCCTGCCGCC GACCTTTCCG
101 AAAACAAGGC GCGGGTTTC GCATTGTTCA AAAACAAAAG CCCCACACAC
151 GAATCAGTCA AATTAAACC CAAATTCCCC GTCCTCATCG ACACGCAGGA
201 CAGTGAAATC AAAGATATGG TCGAAGAACA CCTGCCGCTC ATCAGCAGC
251 AGCAGGAAGA AGTATTGAC AAGGAACAGA CGGGCTTCCT CGCCGAAGAA
301 GCGCCGGACA ACGTTAAAC GATGCTCCGC AGCAAAGGCT ATTTACAGCAG
351 CAAAGTCAGC CTGACGGAAA AAGACGGAGC TTATACGGTA CACATCACAC
401 CGGGCCCGCG CACCAAAATC GCCAACGTCG GCGTCGCCAT CCTCGGCGAC
451 ATCCTTTCAG ACGGCAACCT CGCCGAATAC TACCGCAACG CGCTGGAAAA
501 CTGGCAGCAG CCGGTAGGCA GCGATTTCGA TCAGGACAGT TGGGAAAACA
551 GCAAAACTTC CGTCTCGGC GCGGTAACGC GCAAAGCCTA CCCGCTTGCC
601 AAGCTCGGCA ATACGAGGC GGCCGTCAAC CCCGATACCG CCACCGCCGA
651 TTTGAACGTC GTCGTGGACA GCGGCCGCC CATCGCCTTC GCGACTTTG
701 AAATCACCGG CACACAGCGT TACCCCGAAC AAATCGTCTC CGGCCTTGCG
751 CGTTTCCAGC CCGGTATGCC GTACGACCTC GACCTGCTGC TCGACTTCCA
801 ACAGGCGCTC GAACAAAACG GGCATTATTC CGGCGCGTCC GTACAAGCCG
851 ACTTCGACCG CCTCCAAGC GACCGCGTCC CCGTCAAAGT CAGCGTAACC
901 GAGGTCAAAC GCCACAAACT CGAAACCGGC ATCCGCCTCG ATTCGGAATA
951 CGGTTTGGGC GGCAAAATCG CCTACGACTA TTACAACCTC TTCAACAAAG
1001 GCTATATCGG TTCGTCGTC TGGGATATGG ACAAATACGA AACCACGCTT
1051 GCCGCCGGCA TCAGCCAGCC GCCTCAACTAT CCGGGCAACT ACTGGACAAG
1101 CAACGTTTCC TACAACCGTT CGACCACCCA AAACCTCGAA AAACGCGCCT
1151 TCTCCGGCGG CGTCTGGTAT GTGCGCGACC GCGCGGGCAT CGATGCGCAGG
1201 CTGGGGGCGG AATTCTCTCG AGAAGGCGCG AAAATCCCCG GCTCGGCTGT
1251 CGATTTGGGC AACAGCCACG CCACGATGCT GACCGCCTCT TGGAAACGCC
1301 AGCTGCTCAA CAACGTGCTG CATCCCGAAA ACGGCCATTA CCTCGACGGC
1351 AAAATCGGTA CGACTTTGGG CACATTCTTG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGTGCAGGTT ATTTCTTAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGT ACACCGTTGC CCGCGACAAT
1501 GCGGACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGACT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCA ACGCGCCCTC CTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCTTTCCGG CGCGGTGTTT CACGATATGG GCGATGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCCGGA CTGGGCGTGC
1751 GCTGGTTTCA CCGGCTTGC CCGTTTTCTT TCGACATCGC CTACGGGCAC
1801 AGCGATAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1196; ORF 286>:

m286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLPKPKF VLIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKDGAIVT HITPGPRTKI ANVGVAIGLD
151 ILSDGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLGNTQAAVN PDTATADLVN VVDSGRPIAF GDFEITGTQR YPEQIVSGLA
251 RFQPGMPYDL DLLLDFQQAL EQNGHYS GAS VQADFDRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYNNL FNKGYSVSV WDMDKYETTL
351 AAGISQPRNY RGNYSWTSNV YNRSTTQNL KRAFSGGVWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSAVDLG NSHATMLTAS WKRLNNVL HPENGHYLDG
451 KIGTTLTGFL SSTALIRTS RAGYFFTPEN KKLGTFIIR QAGYTVARDN
501 ADVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTLSGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSPLA PFSFDIAYGH
601 SDKKIRWHIS LGTRF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m286/g286 95.9% identity in 293 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTM	IKPTALLLP	ALFFFP	HAYAPAA	DLSENKA	AGFALFK
g286	MQNTGT	MIKPTALLLP	ALFFFP	HAYAPAA	DLSENKA	AGFALFK
	10	20	30	40	50	60
m286.pep	VLIDTQ	DSEIKDM	VEEHLPL	ITQQQEE	VLDKEQT	GFLAEEA
g286	VRIDTQ	DSEIKDM	VEEHLPL	ITQQQEE	VLDKEQT	GFLAEEA
	70	80	90	100	110	120
m286.pep	LTEKDG	AYTVHIT	PGPRTK	IANVGV	AILGDI	LSDGNLA
g286	LTEKDG	AYTVHIT	PGPRTK	IANVGV	AILGDI	LSDGNLA
	130	140	150	160	170	180
m286.pep	WENSKT	SVLGAV	TRKAYP	LAKLGNT	QAAVNPD	TATADLN
g286	WENSKT	SVLGAV	TRKGYP	LAKLGNT	RAAVNPD	TATADLN
	190	200	210	220	230	240
m286.pep	YPEQIV	SGLARF	QPGMPY	DLDLLLD	FQQALEQ	NGHYSGA
g286	YPEQTV	SGLARF	QPGT	PYDLDLLLD	FQQALEQ	NGHYSGA
	250	260	270	280	290	299
m286.pep	TEVKRH	KLETGIR	LDSEYGL	GKGKIAY	DYYNLFN	KGYIGSV
g286	RGQTPQ	TRNRHPP	RFGRQNR	LRLLOPL	QQRLYRL	GLGYQIR
	300	310	320	330	340	359
m286.pep	RGQTPQ	TRNRHPP	RFGRQNR	LRLLOPL	QQRLYRL	GLGYQIR
g286	RGQTPQ	TRNRHPP	RFGRQNR	LRLLOPL	QQRLYRL	GLGYQIR
	310	320	330	340	350	360

a286.seq

1	ATGCACGACA	CCCGTACCAT	GATGATTAAA	CCGACCGCCC	TGCTCCTGCC
51	GGCTTTATTT	TTCTTTCCGC	ACGCATACGC	GCCTGCCGCC	GACCTTTCCG
101	AAAACAAGGC	GGCGGGTTTC	GCATTGTTCA	AAAACAAAAG	CCCCGACACC
151	GAATCAGTTA	AATTAACAC	CAAAATCCCC	GTCCGCATCG	ACACGCAGGA
201	TAGTGAAATC	AAGATATTGG	TCGAAGAACA	CTGCGCGTC	ATCACGCAGC
251	AGCAGGAAGA	AGTATTGGAC	AAGGAACAGA	CGGCTTTCCT	CGCGGAAGAA
301	GCACCGGACA	ACGTTAAAAC	AATGCTCCGC	AGCAAAGGCT	ATTTCAGCAG
351	CAAAGTCAGC	CTGACGGAAA	AAGACGGAGC	TTATACGGTA	CACATCACAC
401	CGGGCCCCGC	CACCAAAATC	GCCAACGTCG	GCCTCGCCAT	CCTCGGCGAC
451	ATCCTTTTCAG	ACGGCAACCT	CGCCGAATAC	TACCGCAACG	CGCTGGAAAA
501	CTGGCAGCAG	CCGGTAGGCA	GTGATTTCGA	TCAGGACAGT	TGGGAAAAACA
551	GCAAAACTTC	CGTCCTCGGC	GCGGTAACGC	GCAAAGCCTA	CCCGCTTGCC
601	AAGCTCGGCA	ACACCCGGGC	GGCCGTCAAC	CCCGATACCG	CCACCGCCGA
651	TTTGAACCTG	GTCGTGGACA	GCGGCCCGCC	CATCGCCTTC	GGCGACTTTG
701	AAATTACCGC	CGCGAGCGT	TACCCCGAAC	AAATCGTCTC	CGGCTTTGGC
751	CGCTTCCAAC	CAGGCACGCC	TACGACCTC	GACCTGCTGC	TGCACTTCCA
801	ACAGGCGCTC	GAACAAAACG	GGCATTATTC	CGGCGCGTCC	GTACAAGCCG
851	ACTTCGACCG	CCTCCAAGGC	GACCGCGTCC	CCGTCAAAGT	CAGCGTAACC
901	GAGGTCAAAC	GCCACAAGCT	CGAAACCGGC	ATCCGCCTCG	ATTCGGAATA
951	CGGTTTGGGC	GGCAAAATCG	CCTACGACTA	TTACAACCTC	TTCAACAAGG
1001	GCTATATCGG	TTCGGTCTGC	TGGGATATTG	ACAAATACGA	AACCAACGTT
1051	GCCGCCGGCA	TCAGCCAGCC	CGCGAACTAT	CGGGGCAACT	ACTGGACAAG
1101	CAACGTTTCC	TACAACCGTT	CGACCACCCA	AAACCTCGAA	AAACCGCGCT
1151	TCTCCGGGCG	CATCTGGTAT	GTGCGCGACC	GCGCGGGCAT	CGATGCCAGG
1201	CTGGGGGCGG	AGTTTCTCGC	AGAAGGCGCG	AAAATCCCCG	GCTCGGATAT
1251	CGATTTGGCG	AACAGCCACG	CCACGATGCT	GACCGCCTCT	TGGAAACGCC
1301	AGCTGCTCAA	CAACGTGCTG	CATCCCGAAA	ACGGCCATTA	CTCTGACGGG

669

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1351 AAAATCGGTA CGACTTTGGG CGCATTCTCG TCCTCCACCG CGCTGATCCG
1401 CACCTCTGCC CGCGCAGGTT ATTTCTTCAC GCCCGAAAAC AAAAACTCG
1451 GCACGTTTAT CATACGCGGA CAAGCGGGTT ACACCGTTGC CCGCGACAAT
1501 GCCAACGTTT CTTCAGGGCT GATGTTCCGC AGCGGCGGCG CGTCTTCCGT
1551 GCGCGGTTAC GAACTCGACA GCATCGGGCT TGCCGGCCCG AACGGATCGG
1601 TCCTGCCCCG ACGCGCCCTC TTGGTGGGCA GCCTGGAATA CCAACTGCCG
1651 TTTACGCGCA CCCTTTCCGG CGCGGTGTTC CACGATATGG GCGACGCCGC
1701 CGCCAATTTC AAACGTATGA AGCTGAAACA CGGTTCGGGA CTGGGCGTGC
1751 GCTGGTTCAG CCCGCTCGCG CCGTTTTCCT TCGACATCGC CTACGGGCAC
1801 AGCGACAAGA AAATCCGCTG GCACATCAGC TTGGGAACGC GCTTCTAA

```

This corresponds to the amino acid sequence <SEQ ID 1198; ORF 286.a>:

a286.pep

```

1 MHDTRTMMIK PTALLLPALF FFPHAYAPAA DLSENKAAGF ALFKNKSPDT
51 ESVKLKPKFP VRIDTQDSEI KDMVEEHLPL ITQQQEEVLD KEQTGFLAEE
101 APDNVKTMLR SKGYFSSKVS LTEKD GAYTV HITPGPRTKI ANVGVAI LGD
151 ILS DGNLAEY YRNALENWQQ PVGSDFDQDS WENSKTSVLG AVTRKAYPLA
201 KLG NTRAAVN PDTATADLN VVDSGRPIAF GDFEITGTOR YPEQIVSGLA
251 RFQPGT PYDL DLLLDFQQA LEQNGHYS GASVQADFDRLQG DRVPVKVSVT
301 EVKRHKLETG IRLDSEYGLG GKIAYDYYNL FNKG YIGSVV WMDMKYETTL
351 AAGISQPRNY RGNWTSNVS YNRSTTQNLE KRAFSGGIWY VRDRAGIDAR
401 LGAEFLAEGR KIPGSDIDLG NSHATMLTAS WKRQLLN NVL HPENGHYLDG
451 KIGTTLGAFL SSTALIRTS A RAGYFFTPEN KKLGTFIIRG QAGYTVARDN
501 ANVPSGLMFR SGGASSVRGY ELDSIGLAGP NGSVLPERAL LVGSLEYQLP
551 FTRTSLGAVF HDMGDAAANF KRMKLKHGSG LGVRWFSP LA PFSFDIAYGH
601 SDDKIRWHIS LGTRF*

```

m286/a286 98.7% identity in 615 aa overlap

	10	20	30	40	50	60
m286.pep	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPFP					
a286	MHDTRTMMIKPTALLLPALFFFPHAYAPAADLSENKAAGFALFKNKSPDTESVKLKPFP					
	10	20	30	40	50	60
m286.pep	70	80	90	100	110	120
	VLIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
a286	VRIDTQDSEIKDMVEEHLPLITQQQEEVLDKEQTGFLAEEAPDNVKTMLRSKGYFSSKVS					
	70	80	90	100	110	120
m286.pep	130	140	150	160	170	180
	LTEKD GAYTVHITPGPRTKIANVGVAI LGDILSDGNLAEYYRNALENWQQPVGSDFDQDS					
a286	LTEKD GAYTVHITPGPRTKIANVGVAI LGDILSDGNLAEYYRNALENWQQPVGSDFDQDS					
	130	140	150	160	170	180
m286.pep	190	200	210	220	230	240
	WENSKTSVLGAVTRKAYPLAKLGNTQAAVNPDATADLN VVDSGRPIAFGDFEITGTOR					
a286	WENSKTSVLGAVTRKAYPLAKLGNTAAVNPDATADLN VVDSGRPIAFGDFEITGTOR					
	190	200	210	220	230	240
m286.pep	250	260	270	280	290	300
	YPEQIVSGLARFQPGMPYDL DLLLDFQQA LEQNGHYS GASVQADFDRLQGDRVPVKVSVT					
a286	YPEQIVSGLARFQPGT PYDL DLLLDFQQA LEQNGHYS GASVQADFDRLQGDRVPVKVSVT					
	250	260	270	280	290	300
m286.pep	310	320	330	340	350	360
	EVKRHKLETGIRLDSEYGLGGKIAYDYYNLFNKG YIGSVVWMDMKYETTLAAGISQPRNY					
a286	EVKRHKLETGIRLDSEYGLGGKIAYDYYNLFNKG YIGSVVWMDMKYETTLAAGISQPRNY					
	310	320	330	340	350	360
	370	380	390	400	410	420

670

m286.pep	RGNYWTSNVSYNRSTTQNLEKRAFSGGVWYVRDRAGIDARLGAEFLAEGRKIPGSAVDLG
a286	RGNYWTSNVSYNRSTTQNLEKRAFSGGIWIYVRDRAGIDARLGAEFLAEGRKIPGSDIDLG
	370 380 390 400 410 420
m286.pep	NSHATMLTASWKRLNNVLHPENGHYLDGKIGTTLGTFLSSTALIRTSARAGYFFTPEN
a286	NSHATMLTASWKRLNNVLHPENGHYLDGKIGTTLGAFLSSTALIRTSARAGYFFTPEN
	430 440 450 460 470 480
m286.pep	KKLGTFIIRGQAGYTVARDNADVPSGLMFRSGGASSVRGYELDSIGLAGPNSVLPERAL
a286	KKLGTFIIRGQAGYTVARDNANVPSGLMFRSGGASSVRGYELDSIGLAGPNSVLPERAL
	490 500 510 520 530 540
m286.pep	LVGSLLEYQLPFFTRTLSGAVFHDMGDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
a286	LVGSLLEYQLPFFTRTLSGAVFHDMGDAAANFKRMKLKHGSGLGVRWFSPPLAPFSFDIAYGH
	550 560 570 580 590 600
m286.pep	SDKKIRWHISLGTRFX
a286	SDKKIRWHISLGTRFX
	610

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1199>:

g287.seq

1	atgttttaaac	gcagtgatgat	tgcaatggct	tgtatttttc	ccctttcagc
51	ctgtgggggc	ggcgggtggcg	gatcgcccga	tgtcaagtcg	gcggacacgc
101	cgtcaaaacc	ggccgcccc	gttgttgctg	aaaatgccgg	ggaaggggtg
151	ctgccgaaaag	aaaagaaaga	tgaggaggca	gcgggcggtg	cgccgcaagc
201	cgatacgag	gacgcaaccg	ccggagaagg	cagccaagat	atggcggcag
251	tttcggcaga	aaatacaggc	aatggcggtg	cggcaacaac	ggacaacccc
301	aaaaatgaag	acgcgggggc	gcaaaatgat	atgccgcaaa	atgccgccga
351	atccgcaa	caaacaggga	acaaccaacc	cgccggttct	tcagattccg
401	ccccgcgctc	aaaccctgcc	cctgcgaatg	gcggtagcga	ttttggaagg
451	acgaacgtgg	gcaattctgt	tgtgattgac	ggaccgtcgc	aaaatataac
501	gttgaccac	tgtaaaggcg	attcttgtaa	tggtgataat	ttattggatg
551	aagaagcacc	gtcaaaatca	gaatttgaaa	aattaagtga	tgaagaaaaa
601	attaagcgat	ataaaaaaga	cgagcaacgg	gagaattttg	tcggtttggt
651	tgctgacagg	gtaaaaaagg	atggaactaa	caaatatata	atcttctata
701	cggacaaaacc	acctactcgt	tctgcacggg	cgaggagggtc	gcttccggcc
751	gagattccgc	tgattcccgt	caatcaggcc	gatacgtga	ttgtggatgg
801	ggaagcggtc	agcctgacgg	ggcattccgg	caatatcttc	gcgccgaag
851	ggaattaccg	gtatctgact	tacggggcgg	aaaaattgcc	cggcgatcg
901	tatgccctcc	gtgtgcaagg	cgaaccggca	aaaggcgaaa	tgcttggtgg
951	cacggccgtg	tacaacggcg	aagtgtctga	tttccatatg	gaaaacggcc
1001	gtccgtaccc	gtccggaggc	aggtttgccg	caaaagtcga	tttcggcagc
1051	aaatctgtgg	acggcattat	cgacagcggc	gatgatttgc	atatgggtac
1101	gcaaaaattc	aaagccgcca	tcgatggaaa	cggctttaag	gggacttggg
1151	cggaaaatgg	cggcggggat	gtttccggaa	ggttttacgg	cccggccggc
1201	gaggaaatgg	cgggaaaata	cagctatcgc	ccgacagatg	ctgaaaaggg
1251	cggattccgc	gtgtttgccg	gcaaaaaaga	tcgggattga	

This corresponds to the amino acid sequence <SEQ ID 1200; ORF 287.ng>:

g287.pep

1	MFKRSVIAMA	CIFPLSACGG	GGGGSPDVKS	ADTPSKPAAP	VVAENAGEGV
51	LPKEKKDEEA	AGGAPQADTQ	DATAGEGSQD	MAAVSAENTG	NGGAATTDNP
101	KNEDAGAQN	MPQNAAESAN	QTGNNQPAGS	SDSAPASNPA	PANGGSDFR

671

151	TNVGNSVVID	GPSQNITLTH	CKGDSCNGDN	LLDEEAPSKS	EFEKLSDEEK
201	IKRYKKDEQR	ENFVGLVADR	VKKDGTNKYI	IFYTDPKPTR	SARSRRSLPA
251	EIPLIPVNQA	DTLIVDGEAV	SLTGHSGNIF	APEGNYRYLT	YGAEKLPGGS
301	YALRVQGEPA	KGEMLVGTAV	YNGEVLHFHM	ENGRPYPSGG	RFAAKVDFGS
351	KSDVGIIISG	DDLHMGTKQK	KAAIDGNGFK	GTWTENGGGD	VSGRFYGPAG
401	EEVAGKYSYR	PTDAEKGGF	VFAGKKDRD*		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1201>:

```
m287.seq
1      ATGTTTAAAC  GCAGCGTAAT  CGCAATGGCT  TGTATTTTTC  CCCTTTCAGC
51     TCGCGGGGCG  GCGCGTGGCG  GATCGCCCGA  TGTCAAGTCG  GCGGACACGC
101    TGTCAA AAC  TGCCGCCCT  GTTGTTCCTG  AAAAAGAGAC  AGAGGCAAAG
151    GAAGATGCGC  CACAGGCAGG  TTCTCAAGGA  CAGGGCGCGC  CATCCGCACA
201    AGGCAGTCAA  GATATGGCGG  CGGTTTCGGA  AGAAAATACA  GGCAATGGCG
251    GTGCGGTAAC  AGCGGATAAT  CCCAAAAATG  AAGACGAGGT  GGCACAAAA
301    GATATGCCGC  AAAATGCCGC  CGGTACAGAT  AGTTCGACAC  CGCATACAC
351    CCCGGATCCG  AATATGCTTG  CCGGAAATAT  GGAAAATCAA  GCAACGGATG
401    CCGGGGAATC  GTCTCAGCCG  GCAAACCAAC  CGGATATGGC  AAATGCGGCG
451    GACGGAATGC  AGGGGGACGA  TCCGTCCGGA  GGCGGGGCAA  ATGCCGGCAA
501    TACGGCTGCG  CAAGGTGCAA  ATCAAGCCGG  AAACAATCAA  GCCCGCGGTT
551    CTTCAGATCC  CATCCCCGCG  TCAAACCCGT  CACCTGCGAA  TTGGCGGTAGC
601    AATTTTGGA  GGGTTGATT  GGCTAATGGC  GTTTTGATTG  ACGGGCCGTC
651    GCAAAATATA  ACGTTGACCC  ACTGTAAAGG  CGATTCTTGT  AGTGGCAATA
701    ATTTCTTGGA  TGAAGAAGTA  CAGCTAAAT  CAGAATTGGA  AAAATTAAGT
751    GATGCAGACA  AATAAGTAA  TTACAAGAAA  GATGGGAAGA  ATGATAAATT
801    TGTCGGTTTG  GTTGCCGATA  GTGTGCAGAT  GAAGGGAATC  AATCAATATA
851    TTATCTTTTA  TAAACCTAAA  CCCACTTCAT  TTGCGCGATT  TAGGCGTTCT
901    GCACGTCGA  GGCGGTCGCT  TCCGGCCGAG  ATGCCGCTGA  TTCCCGTCAA
951    TCAGGCGGAT  ACGCTGATT  TCGATGGGGA  AGCGGTCAGC  CTCGAGGGGG
1001   ATTCCGGCAA  TATCTTCGCG  CCCGAAGGGA  ATTACCGGTA  TCTGACTTAC
1051   GGGGCGGAAA  AATTGCCCGG  CGGATCGTAT  GCCCTTCGTG  TTCAAGGCGA
1101   ACCGGCAAAA  GGCGAAATGC  TTGCGGGCCG  GGCCGTGTAC  AACGGCGAAG
1151   TACTGCATTT  CCATACGGAA  AACGGCCGTC  CGTACCCGAC  CAGGGGCAGG
1201   TTTGCGCAA  AAGTCGATT  CGGCAGCAA  TCTGTGGACG  CAGATTACGA
1251   CAGCGGCGAT  GATTTGCATA  TGGGTACGCA  AAAATTCAAA  GCCGCCATCG
1301   ATGGAACGG  CTTTAAGGGG  ACTTGGACGG  AAAATGGCAG  CGGGGATGTT
1351   TCCGGAAGT  TTTACGCCCC  GGCCGGCGAG  GAAGTGGCGG  GAAAATACAG
1401   CTATCGCCCG  ACAGATGCGG  AAAAGGGCGG  ATTCGGCGTG  TTTGCCGGCA
1451   AAAAAGACGA  GGATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1202; ORF 287>:

m287.pep	1	MFKRSVIAMA	CIFALSACGG	GGGGSPDVKS	ADTLSPKPAAP	VVSEKETEAK
	51	EDAPQAGSQG	QGAPSAQGSQ	DMAAVSEENT	GNGGAVTADN	PKNEDEVAQN
	101	DMPQNAAGTD	SSTPNHTPDP	NMLAGNMENQ	ATDAGESSDP	ANQPFMANAA
	151	DGMQGDPSA	GGQAGNATAA	QGANQAGNNQ	AAGSSDPIPA	SNPAPANGGS
	201	NFGRVDLANG	VLIDGPSQNI	TLTHCKGDSC	SGNNFLDEEV	QLKSEFEKLS
	251	DADKISNYKK	DGKNDKFVGL	VADSVQMKGI	NQYIIFYKPK	PTSFARFRRS
	301	ARSRRSLPAE	MPLIPVNQAD	TLIVDGEAVS	LTGHSIGNIFA	PEGNYRYLTY
	351	GAEKLPGGSY	ALRVQGEPAK	GEMLAGAQQV	NGEVLHFHTE	NGRPYPTRGR
	401	FAAKVDFGSK	SVDDIIDSGD	DLHMGTGKFK	AAIDGNGFKG	TWTENGSGDV
	451	SGKIFYGPAGE	EVAGKYSYRP	TDAEKGGEFGV	FAGKKEQD*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m287/g287 70.1% identity in 499 aa overlap

```

              10      20      30      40      49
m287.pep    MFKRSVIAMACIFALSACGGGGGSPDVKSADTL SKPAAPVVSE-----KETEA
             ||||| ||||| ||||| ||||| ||||| :| |
g287        MFKRSVIAMACIFPLSACGGGGGSPDVKSADTPSKPAAPVVAENAGEGVLPKEKKDEEA
              10      20      30      40      50      60

```

	50	60	70	80	90	100	109
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT					
g287	:	::			:		
	AGGAPQADTQD--ATAGEGSQDMAAVSAENTGNGGAATTDNPKNEDAGAQN	DMPQNAA--					
		70	80	90	100	110	
m287.pep	110	120	130	140	150	160	169
	DSSTPNHTPDPNMLAGNMENQATDAGESSQPANQPDMANAADGMQGD	DP	SAGGQ	NAGNTA			
g287	-----						
m287.pep	170	180	190	200	210	220	229
	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFG	RVDLANGVLIDGPSQ	NITLTHCKGDS				
g287	: : :			:	: :		: :
	-ESANQTGNNQAGSSDSAPASNPAPANGGSDFGR	TNVGNSVVIDGPSQ	NITLTHCKGDS				
	120	130	140	150	160	170	
m287.pep	230	240	250	260	270	280	289
	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKD	GKNDKFVGLVADSVQ	MKGINQYIIFYKP				
g287	: :		: :		: :		: :
	CNGDNLLEEAPSKSEFEKLSDEEKIKRYKKDE	QRENFVGLVADRVK	KDGTNKYIIFYTD				
	180	190	200	210	220	230	
m287.pep	290	300	310	320	330	340	349
	KPTSFARFRRSARSRRLPAEMPLIPVNQADTL	LIVDGEAVSLTGHSGN	IFAPEGNYRYLT				
g287	:						
	KPPT-----RSARSRRLPAEIP	LIPVNQADTL	LIVDGEAVSLTGHSGN	IFAPEGNYRYLT			
	240	250	260	270	280	290	
m287.pep	350	360	370	380	390	400	409
	YGAEKLPGGSYALRVQGEPAKGEMLAGAAVYN	GEVLHFHTENGRPY	PTRGRFAAKVD	FGS			
g287			: :			: :	
	YGAEKLPGGSYALRVQGEPAKGEMLVGTAVYN	GEVLHFHMENGRPY	PSGGRFAAKVD	FGS			
	300	310	320	330	340	350	
m287.pep	410	420	430	440	450	460	469
	KSVDGIIDSDDLHMG	TQKFKA	AIDGNGFKGTWTENG	SGDVSGKFYGPAGEE	VAGKYSYR		
g287			: :				
	KSVDGIIDSDDLHMG	TQKFKA	AIDGNGFKGTWTENG	GGDVSGRFRYPAGEE	VAGKYSYR		
	360	370	380	390	400	410	
m287.pep	470	480	489				
	PTDAEKG	GGVFAGKKEQDX					
g287		: :					
	PTDAEKG	GGVFAGKKDRDX					
	420	430					

a287.seq

1	ATGTTTAAAC	GCAGTGTGAT	TGCAATGGCT	TGTATTGTTG	CCCTTTCAGC
51	CTGTGGGGGC	GGCGGTGGCG	GATCGCCCGA	TGTTAAGTCG	GCGGACACGC
101	TGTCAAAACC	TGCCGCCCTT	GTTGTTACTG	AAGATGTCGG	GGAAGAGGTG
151	CTGCCGAAAG	AAAAGAAAGA	TGAGGAGCGC	GTGAGTGGTG	CGCCGCAAGC
201	CGATACGCAG	GACGCAACCG	CCGGAAAAGG	CGGTCAAGAT	ATGGCGGCAG
251	TTTCGGCAGA	AAATACAGGC	AATGGCGGTG	CGGCAACAAC	GGATAATCCC
301	GAAAATAAAG	ACGAGGGACC	GCAAAATGAT	ATGCCGCAA	ATGCCGCCGA
351	TACAGATAGT	TCGACACCGA	ATCACACCCC	TGCACCGAAT	ATGCCAACCA
401	GAGATATGGG	AAACCAAGCA	CCGGATGCCG	GGGAATCGGC	ACAACCGGCA
451	AACCAACCGG	ATATGGCAAA	TGCGCGGCAG	GGAATGCAGG	GGGACGATCC
501	GTCGGCAGGG	GAAAATGCCG	GCAATACGGC	AGATCAAGCT	GCAAATCAAG
551	CTGAAAACAA	TCAAGTCGGC	GGCTCTCAA	ATCCTGCCTC	TTCAACCAAT
601	CCTAACGCCA	CGAATGGCGG	CAGCGATTTT	GGAAGGATAA	ATGTAGCTAA
651	TGGCATCAAG	CTTGACAGCG	GTTTCGGAAA	TGTAACGTTG	ACACATTGTA
701	AAGACAAAGT	ATGCGATAGA	GATTTCTTAG	ATGAAGAAGC	ACCACCAAAA
751	TCAGAATTTG	AAAAATTAAG	TGATGAAAGAA	AAAATTAATA	AATATAAAAA

801	AGACGAGCAA	CGAGAGAATT	TTGTCGGTTT	GGTTGCTGAC	AGGGTAGAAA
851	AGAATTGGAAC	TAACAAATTAC	GTCAATCATTT	ATAAAGACAA	GTCCGCTTCA
901	TCTTTCATCTG	CGCGATTATCAG	CGGTTCTGTCA	CGGTCTGAGGC	GGTCGCTTCC
951	GGCCGAGATG	CGCGTGATTC	CCGTCAATCA	GGCGGATACG	GTGATTGTCTG
1001	ATGGGGAAGC	GGTCAGCCTG	ACGGGGCATT	CCGGCAATAT	CTTCGCGCCC
1051	GAAGGGAATT	ACCGGTATCT	GACTTACGGG	GCGGAAAAAT	TGTCGGGCGG
1101	ATCGTATGCC	CTCAGTGTGC	AAGGCGAAGC	GGCAAAGGC	GAATATCTTG
1151	CGGGCACGGC	CGTGTACAAC	GGCGAAGTGC	TGCATTTCCA	TATGGAAATC
1201	GGCCGTCGGT	CCCGTCCGG	AGCGAGGTTT	GCGCAAAAG	TCGATTTCTG
1251	CAGCAAATCT	GTGGACGGCA	TTATCGACAG	CGGCGATGAT	TTGCATATGG
1301	GTACGCAAAA	ATTCAAAGCC	GTTATCGATG	GAACAGGCTT	TAAGGGGACT
1351	TGGACGAAAA	ATGGCCGGCG	GGATGTTTTC	GGAAGGTTTT	ACGGCCCGGC
1401	CGGCGAAGAA	GTGGCGGGAA	AATACAGCTA	TGCGCCGACA	GATGCGGAAA
1451	AGGGCGGATT	CGGCGTGTTT	GCCGGCAAAA	AAGAGCAGGA	TTGA

a287.pap

1	<u>MFKRSVIAMA</u>	CIVALSACGG	GGGGSPDVKS	ADTLSPAAP	VVTEDVGEEV
51	LPKEKKDEEA	VSGAPQADTQ	DATAGKGGQD	MAAVSAENTQ	NGGAATTDNPF
101	ENKDEGPQND	MPQNAADTDS	STPNHTPAPN	MPTRDMGNQA	PDAGESAQPA
151	NQPDMANAAD	GMQGDDPSAG	ENAGNTADQA	ANQAENNQVG	GSQNPASSTN
201	PNATNGGSDF	GRINVANGIK	LDSGSENVTL	THCKDKVCDR	DFLDEEAPPK
251	SEFEKLSDEE	KINKYKKDEQ	RENFVGLVAD	RVEKNGTNKY	VIIYKDKSAS
301	SSSRFRFSA	RSRRSLPAEM	PLIPVNQADT	LIVDGEAVSL	TGHSNGNIFAP
351	EGNYRYLTYG	AAKLSGGSYA	LSVQGEPAKT	ELMAGTAVSN	GEVLHFHMEN
401	GRPSPSGGRF	AAKVDFGSKS	VDGIIDSGDD	LHMGTKQFKA	VIDGNGFKGT
451	WTENGGGDVS	GRFYGPAGEE	VACKYSYRPT	DAEKGGFVGF	AGKKEQD*

	10	20	30	40	49
m287.pep	MFKRSVIAMACIFALSACGGGGGGSPDVKSADTL	SKPAA	PVVSE-----	KETEA	
a287	MFKRSVIAMACIVALSACGGGGGGSPDVKSADTL	SKPAA	PVVTTEDV	GEEVLPKEKKDEEA	
	10	20	30	40	50
	60	70	80	90	100
m287.pep	KEDAPQAGSQGGAPSAQGSQDMAAVSEENTGNGGAVTADNPKNEDEVAQN	DMPQNAAGT			
a287	VSGAPQADTQ--DATAGKGGQDMAAVSAENTGNGGAATT	DNPENKDEGPQNDMPQNAADT			
	70	80	90	100	110
	120	130	140	150	160
m287.pep	DSSTPNHTPDPNMLAGNMENQATDAGESSQFANQP	PDMAADGMQGGDDPSAGGQ	NAGNTA		
a287	DSSTPNHTPAPNMPTRDMGNQAPDAGESAQFANQP	PDMAADGMQGGDDPSAG-ENAGNTA			
	120	130	140	150	160
	170	180	190	200	210
m287.pep	AQGANQAGNNQAAGSSDPIPASNPAPANGGSNFR	GRVDLANGVLIDGPSQ	NITLTHCKGDS		
a287	DQAANQAENNQVGGSQNPASSTNPNATNGGSD	FGRINVANGIKLDSGSENVTLTHCKDKV			
	180	190	200	210	220
	230	240	250	260	270
m287.pep	CSGNNFLDEEVQLKSEFEKLSADAKISNYKKDGKNDKFVGLVADSVQMKGINQYII	IFYKP			
a287	CD-RDFLDEEAPPKSEFEKLSDEEKINKYKKDEQRENFVGLVADRVEKNGTNKYVII	YKD			
	240	250	260	270	280
	290	300	310	320	330
m287.pep	KP--TSFARFRRSARSRRLPAEMPLIPVNQADTL	LIVDGEAVSLTGHS	GNIFAPEGNYRY		
a287	KSASSSSARFRRSARSRRLPAEMPLIPVNQADTL	LIVDGEAVSLTGHS	GNIFAPEGNYRY		
	300	310	320	330	340
	350				

674

	350	360	370	380	390	400
m287.pep	LTYGAEKLPGGSYALRVQGEPAKGEMLAGAAVYNGEVLHFHTENGRPYPTRGRFAAKVDF					
	: :					
a287	LTYGAEKLSGGSYALSVQGEPAKGEMLAGTAVYNGEVLHFHMENGRPSPSGGRFAAKVDF					
	360	370	380	390	400	410
	410	420	430	440	450	460
m287.pep	GSKSVDGIIDSDDLHMGTKQFKAAIDGNGFKGTWTENGSGDVSGKFYGPAGEEVAGKYS					
	: : :					
a287	GSKSVDGIIDSDDLHMGTKQFKAVIDGNGFKGTWTENGSGDVSGRFYGPAGEEVAGKYS					
	420	430	440	450	460	470
	470	480	489			
m287.pep	YRPTDAEKGFGVFAGKKEQDX					
a287	YRPTDAEKGFGVFAGKKEQDX					
	480	490				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1205>:

```
g288.seq
1  atgcacaccg gacaggcggt aagccggggt ctgtctcgga cagtcatcc
51  tctaggcata ccgttgccgg tatgtcaag caacctacc gaacgctcg
101 cgggcagcgt cattgcgttc tgtttggtct tgctccgaat ggggtttgg
151 ctgccgcata ttgttaccaa atgcgcgggt cgcccttacc gcacctttt
201 acccttgcct gtgtgcccaa agcagccatc ggcggttttg ctttctgtt
251 cactttccgt cgcgttaccg gccccggccg ttaaccggca ttctacctg
301 cggagcccgg actttctctc ccgatgcct tacgcgatac gcggcgactg
351 tctgcccgtc ccgtgtgcgg cgcgattat aacacgaaac gcaaaaatgc
401 cgttgtaaac ggtacaggtt tcagacggca tacagcctaa actacacacc
451 ctgtttcagg ctgaccttga tgaagccgtc caagtcgcgg tccaataccg
501 cttttgagtt gccgacttcg taacctgtac qcaagtcctt gatcgcgtg
```

This corresponds to the amino acid sequence <SEQ ID 1206; ORF 288.ng>:

g288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	RPAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAARIITRN	AKMPSETVQV	SDGIQPKLHT
151	LFOAGFDEAV	QVAVQYGFVV	ADFVACTOVF	DA*	

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1207>:

```
m288.seq
1  ATGCACACCG GACAGGCGGT AAGCCGGGTT CTGTCTCGGA CAGTCATTCC
51  TCTAGGCATA CCGTTACCGG TATGCTCAAG CAACCTACCC GAACGCTCGG
101 CGGGCAGCGT CATTCGCTTC TGT'TTGGTCT TGCTCCGAAT GGGG'TTGGC
151 CTGCCGCATA TTGTTACCAA ATGCGCGGTG CGCCCTTACC GCACCT'TTC
201 ACCCTTACCT GTGCTGCCAA AGCAGCCATC GGCGGT'TTG CTTTCTGTTC
251 CACTTTCGGT CGCGTTACCG CGCCCGGCCG TTAACCGGCA TTCTACCCTG
301 CGGAGCCCGG ACTTTCCTCC CCGTATGCCT TACGCGATAC GCGGCGACTG
351 TCTGCCCGTC CCGTGTGCGG CGCGGATTAT AACACGAAAC ACAAAAATGC
401 CGTCTGAAAC GGTACAGGTT TCAGACGGCA TACAGCCTAA ACTACACGCC
451 CTGTTTCAGG CTGGCTTCGA TGAAGCCGTC CAAGTCGCCA TCCAATACCC
501 CTTTGGTGTT GCCGACTTCG TAGCCTGTAC GCAAGTCTTT GATACGTGA
```

This corresponds to the amino acid sequence <SEO ID 1208; ORF 288>:

m288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	RPAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAARIITRN	TKMPSETVQV	SDGIQPKLHA
151	LFOAGFDEAV	QVAIQYGFV	ADFVACTOVE	DT*	

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m288/g288 97.8% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGFLPHIVTKCAV					
g288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGFLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
g288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : :					
g288	PCAARIITRNAKMPSETVQVSDGIQPKLHTLFQAGFDEAVQVAVQYGFVADFVACTQVF					
	130	140	150	160	170	180
m288.pep	DTX					
	:					
g288	DAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1209>:

a288.seq

1	ATGCACACCG	GACAGGCGGT	AAGCCGGGTT	CTGTCTCGGA	CAGTCATTCC
51	TCTAGGCATA	CCGTTGCCGG	TATGCTCAAG	CAACCTACCC	GAACGCTCGG
101	CGGGCAGCGT	CATTGCGTTC	TGTTTGGTCT	TGCTCCGAAT	GGGGTTTGGC
151	CTGCCGCATA	TTGTTACCAA	ATGCGCGGTG	CGCCCTTACC	GCACCTTTTC
201	ACCCTTGCCCT	GTGCTGCCAA	AGCAGCCATC	GGCGGTTTTC	CTTTCTGTTC
251	CACTTTCCGT	CGCGTTACCG	CGCCCGGCCG	TTAACCGGCA	TTCTACCCTG
301	CGGAGCCCGG	ACTTTCCTCC	CCGTATGCCT	TACGCGATAC	GCGGCGACTG
351	TCTGCCCGTC	CCGTGTGCGG	CGCGGATTAT	AACACGAAAC	GCAAAAATGC
401	CGTCTGAAAC	GGTACAGGTT	TCAGACGGCA	TACAGCCTAA	ACTACAGGCC
451	CTGTTTCAGG	CTGGCTTCGA	TAAAGCCGTC	CAAGTCGCCG	TCCAATACGG
501	CTTTGGTGTT	GCCGACTTCG	TAGCCTGTGC	GCAAGTCTTT	AATGCGTGA

This corresponds to the amino acid sequence <SEQ ID 1210; ORF 288.a>:

a288.pep

1	MHTGQAVSRV	LSRTVIPLGI	PLPVCSSNLP	ERSAGSVIAF	CLVLLRMGFG
51	LPHIVTKCAV	RPYRTFSPLP	VLPKQPSAVL	LSVPLSVALP	RPAVNRHSTL
101	RSPDFPPRMP	YAIRGDCLPV	PCAARIITRN	AKMPSETVQV	SDGIQPKLHA
151	LFQAGFDKAV	QVAVQYGFV	ADFVACAQVF	NA*	

m288/a288 97.2% identity in 181 aa overlap

	10	20	30	40	50	60
m288.pep	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGFLPHIVTKCAV					
a288	MHTGQAVSRVLSRTVIPLGIPLPVCSSNLPERSAGSVIAFCLVLLRMGFGFLPHIVTKCAV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m288.pep	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
a288	RPYRTFSPLPVLPKQPSAVLLSVPLSVALPRPAVNRHSTLRSPDFPPRMPYAIRGDCLPV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m288.pep	PCAARIITRNTKMPSETVQVSDGIQPKLHALFQAGFDEAVQVAIQYGFVADFVACTQVF					
	: : :					

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```

a288      PCAARIITRNAKMPSETVQVSDGIQPKLHALFQAGFDKAVQVAVQYGFVADVFVACAQVF
              130      140      150      160      170      180

m288.pep   DTX
            ::
a288      NAX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1211>:

```

g290.seq
1   atggcaaaaa tgatgaaatg ggcggctggt ggcggcggtcg cgcggcgacgc
51  gggtttggggc ggatggtctt atctgaagcc cgaaccgcag gctgcttata
101 ttacggaagc  ggtcaggcgc ggcgatatca gccggacggt ttccgcgacg
151 ggcgagattt  cgccgtccaa cctggtatcg gtcggcgcgcg aggtctcggg
201 gcagattaaa  aagctttatg tcaaaactcg gcaacaggtc aaaaaggcg
251 atttgattgc  ggaaatcaat tcgaccacgc agaccaacac gatcgatatg
301 gaaaaatcca  aattggaaac gtatcaggcg aagctggtgt ccgcacagat
351 tgcattgggc  agcgcggaaa aaaaatataa gcgtcaggcg gcgttgtgga
401 aggatgatgc  gacctctaaa gaagatttgg aaagcgcgca ggatgcgctt
451 gccgccgcca  aagccaatgt tgccgagttg aaggctttaa tcagacagag
501 caaaatttcc  atcaataccg ccgagtcgga tttgggctac acgcgcatta
551 ccgcgacgat  ggacggcacg gtggtggcga ttcccgtgga agaggggcag
601 actgtgaacg  cggcgcgagc tacgccgacg attgtccaat tggcgaatct
651 ggatatgatg  ttgaacaaaa tgcagattgc cgagggcgat attaccaagg
701 tgaaggcggg  gcaggatatt tcgtttacga ttttgtccga accggatacg
751 ccgattaagg  cgaagctcga cagcgtcgac cccgggctga ccacgatgtc
801 gtcgggcggc  tacaacagca gtacggatac ggcttccaat gcggtctatt
851 attatgcccg  ttcgtttgtg ccgaatccgg acggcaaaact cgccacgggg
901 atgacgacgc  agaatacggg tgaaatcgac ggtgtgaaaa atgtgttgct
951 tattccgtcg  ctgaccgtga aaaatcgcgg cggcaaggcg ttcgtacgcg
1001 tgttgggtgc  ggacggcaag gcagtggaaac gcgaaatccg gaccggtatg
1051 aaagacagta  tgaataccga agtgaaaagc ggggtgaaag agggggacaa
1101 agtggcatc  tccgaaataa ccgccgccga gcagcaggaa agcggcgaa
1151 gcgccttagg  cggcccgccg cgccgataa

```

This corresponds to the amino acid sequence <SEQ ID 1212; ORF 290.ng>:

```

g290.pep
1   MAKMMKWAAV AAVAAAAVWG GWSYLKPEPQ AAYITEAVRR GDISRTVSAT
51  GEISPSNLVS VGAQASGOIK KLYVKLGQOV KKGDLIAEIN STTQTNTIDM
101 EKSKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATSK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESDLGY TRITATMDGT VVAIPVEEQG
201 TVNAAQSTPT IVQLANLDM LNKMQIAEGD ITKVKAGQDI SFTILSEPD
251 PIKAKLDSVD PGLTMSGGG YNSSTDASN AVYYYARFV PNPDGKLTG
301 MTTQNTVEID GVKNVLLIPS LTVKNRGGKA FVRVLGADGK AVEREIRTGM
351 KDSMNTEVKS GLKEGDKVVI SEITAAEQQE SGERALGGPP RR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1213>:

```

m290.seq (partial)
1   ..GTATCGGTCG GCGCGCAGGC ATCGGGGCAG ATTAAGATAC TTTATGTCAA
51  ACTCGGGCAA CAGGTTAAAA AGGGCGATT TATTGCGGAA ATCAATTCTGA
101 CCTCGCAGAC CAATACGCTC AATACGGAAA AATCCAAGTT GGAAACGTAT
151 CAGGCGAAGC TGGTGTCTGC ACAGATTGCA TTGGGCAGCG CGGAGAAGAA
201 ATATAAGCGT CAGGCGGCGT TATGGAAGGA AAACGCGACT TCCAAAGAGG
251 ATTTGGAAAG CGCGCAGGAT GCGTTTGCCG CCGCCAAAGC CAATGTTGCC
301 GAGCTGAAGG CTTTAATCAG ACAGAGCAA ATTTCCATCA ATACCGCCGA
351 GTCGGAATTG GGCTACACGC GCATTACCGC AACGATGGAC GGCACGGTGG
401 TGGCGATTCT CGTGAAGAG GGGCAGACTG TGAACGCGGC GCAGTCTACG
451 CCGACGATTG TCCAATTGGC GAATCTGGAT ATGATGTTGA ACAAATGCA
501 GATTGCCGAG GGCGATATTA CCAAGGTGAA GGCGGGGCAG GATATTTCGT
551 TTACGATTTT GTCCGAACCG GATACGCCGA TTAAGGCGAA GCTCGACAGC
601 GTCGACCCCG GGCTGACCAC GATGTCGTCG GGCGGTTACA ACAGCAGTAC
651 GGATACGGCT TCCAATGCGG TCTACTATTA TGCCCGTTTCG TTTGTGCCGA

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```

701 ATCCGGACGG CAAACTCGCC ACGGGGATGA CGACGCAGAA TACGGTTGAA
751 ATCGACGGCG TGAAAAATGT GCTGATTATT CCGTCGCTGA CCGTGAAAAA
801 TCGCGGCGGC AAGGCGTTTG TGCGCGTGTT GGGTGCGGAC GGCAAGGCGG
851 CGGAACGCGA AATCCGGACC GGTATGAGAG ACAGTATGAA TACCGAAGTA
901 AAAAGCGGGT TGAAAGAGGG GGACAAAGTG GTCATCTCCG AAATAACCGC
951 CGCCGAGCAA CAGGAAAGCG GCGAACGCGC CCTAGGCGGC CCGCCGCGCC
1001 GATAA

```

This corresponds to the amino acid sequence <SEQ ID 1214; ORF 290>:

```

m290.pep (partial)
1  ..VSVGAQASGQ IKILYVKLGQ QVKKGDLIAE INSTSQNTNL NTEKSKLETY
51  QAKLVSAQIA LGSAEKKYKR QAALWKENAT SKEDLESAQD AFAAAKANVA
101 ELKALIRQSK ISINTAESEL GYTRITATMD GTVVAILVEE GQTVNAAQST
151 PTIVQLANLD MMLNKMQIAE GDITKVKAGQ DISFTILSEP DTPIKAKLDS
201 VDPGLTTMSS GGYNSSTDTA SNAVYYYARS FVPNPDGKLA TGMTTQNTVE
251 IDGVKNVLLI PSLTVKNRGG KAFVRVLGAD GKAAEREIRT GMRDSMNTEV
301 KSGLKEGDKV VISEITAAEQ QESGERALGG PPRR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m290/g290 96.1% identity in 334 aa overlap

```

m290.pep                                10      20      30
                                VSVGAQASGQIKILYVKLGQQVKKGDLIAE
                                |||
g290      PQAAYITEAVRRGDISRTVSATGEISPSNLVSVGAQASGQIKKLYVKLGQQVKKGDLIAE
      30      40      50      60      70      80

m290.pep      40      50      60      70      80      90
INSTSQNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKQAALWKENATSKEDLESAQD
|||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g290      INSTTQTNTIDMEKSKLETYQAKLVSAQIALGSAEKKYKQAALWKDDATSKEDLESAQD
      90      100     110     120     130     140

m290.pep      100     110     120     130     140     150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:||||:||||:| |||:||||:| |||:||||:| |||:||||:| |||:||||:|
g290      ALAAAKANVAELKALIRQSKISINTAESDLGYTRITATMDGTVVVAIPVEEGQTVNAAQST
      150     160     170     180     190     200

m290.pep      160     170     180     190     200     210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
|||||
g290      PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVDPGLTTMSS
      210     220     230     240     250     260

m290.pep      220     230     240     250     260     270
GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
|||||
g290      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLLIPSLTVKNRGG
      270     280     290     300     310     320

m290.pep      280     290     300     310     320     330
KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
|||||
g290      KAFVRVLGADGKAVEREIRTGMKDSMNTEVKSGLKEGDKVVISEITAAEQQESGERALGG
      330     340     350     360     370     380

m290.pep      PPRRX
              ||||
g290      PPRRX
      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1215>:

```
a290.seq
1   ATGGCAAAAA TGATGAAATG GCGCGCTGTT GCGGCGGTCG CCGCGGCAGC
51  GGTTTGGGGC GGATGGTCTT ATCTGAAGCC CGAGCCGCAG GCTGCTTATA
101 TTACGGAAAC GGTGAGGCGC GCGGACATCA GCCGGACGGT TTCTGCAACA
151 GGGGAGATTT CGCCGTCCAA CCTGGTATCG GTCGGCGCGC AGGCATCGGG
201 GCAGATTAAG AAACCTTATG TCAAACCTCGG GCAACAGGTT AAAAAGGGCG
251 ATTTGATTGC GGAAATCAAT TCGACCTCGC AGACCAATAC GCTCAATACG
301 GAAAAATCCA AATTGGAAAC GTATCAGGCG AAGCTGGTGT CGGCACAGAT
351 TGCATTGGGC AGCGCGGAGA AGAAATATAA GCGTCAGGCG GCGTTGTGGA
401 AGGATGATGC GACCGCTAAA GAAGATTTGG AAAGCGCACA GGATGCGCTT
451 GCCGCCGCCA AAGCCAATGT TGCCGAGCTG AAGGCTCTAA TCAGACAGAG
501 CAAAATTTCC ATCAATACCG CCGAGTCGGA ATTGGGCTAC ACGCGCATTA
551 CCGCAACGAT GGACGGCAGC GTGGTGCGCA TTCTCGTGGA AGAGGGGCAG
601 ACTGTGAACG CGGCGCAGTC TACGCCGACG ATTGTCCAAT TGGCGAATCT
651 GGATATGATG TTGAACAAAA TGCAGATTGC CGAGGGCGAT ATTACCAAGG
701 TGAAGGCGGG GCAGGATATT TCGTTTACGA TTTTGTCCGA ACCGGATACG
751 CCGATTAAGG CGAAGCTCGA CAGCGTCGAC CCCGGGCTGA CCACGATGTC
801 GTCGGGCGGC TACAACAGCA GTACGGATAC GGCTTCCAAT GCGGTCTACT
851 ATTATGCCCG TTCGTTTGTG CCGAATCCGG ACGGCAAACT CGCCACGGGG
901 ATGACGACGC AGAATACGGT TGAAATCGAC GGTGTGAAAA ATGTGCTGAT
951 TATTCCGTCG CTGACCGTGA AAAATCGCGG CCGCAGGGCG TTTGTGCGCG
1001 TGTGTTGGTGC AGACGGCAAG GCGGCGGAAC GCGAAATCCG GACCGGTATG
1051 AGAGACAGTA TGAATACCGA AGTAAAAAGC GGGTTGAAAG AGGGGGACAA
1101 AGTGGTCATC TCCGAAATAA CCGCCGCCGA GCAGCAGGAA AGCGGCGAAC
1151 GCGCCCTAGG CGGCCGCCCG CGCCGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1216; ORF 290.a>:

```
a290.pep
1   MAKMMKWA AV AAVAAA VWG GWSYLKPEPQ AAYITETVRR GDISRTVSAT
51  GEISPSNLVS VQAQASGQIK KLYVKLGQOV KKGDILAEIN STSQTNTLNT
101 ESKKLETYQA KLVSAQIALG SAEKKYKRQA ALWKDDATAK EDLESAQDAL
151 AAAKANVAEL KALIRQSKIS INTAESELGY TRITATMDGT VVAILVEEGQ
201 TVNAAQSTPT IVQLANLDM LNMQIAEGD ITKVKAGQDI SFTILSEPDT
251 PIKAKLDSVD PGLTTMSSGG YNSSTDASN AVYYYARSFV PNPDGKLATG
301 MTTQNTVEID GVKNVLIIPS LTVKNRGGRA FVRVLGADGK AAEREIRTGM
351 RDSMNTEVKS GLKEGDKVVI SEITAEQQE SGERALGGPP RR*

m290/a290 98.2% identity in 334 aa overlap

m290.pep
10 20 30
VSVGAQASGQIKILYVKLGQOVKKGDILAE
|||||

a290
30 40 50 60 70 80
PQAAYITETVRRGDISRTVSATGEISPSNLVS VQAQASGQIKKLYVKLGQOVKKGDILAE

m290.pep
40 50 60 70 80 90
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKENATSKEDLESAQD
|||||

a290
90 100 110 120 130 140
INSTSQTNTLNTEKSKLETYQAKLVSAQIALGSAEKKYKRQAALWKDDATAKEDLESAQD

m290.pep
100 110 120 130 140 150
AFAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST
|:|||||

a290
150 160 170 180 190 200
ALAAAKANVAELKALIRQSKISINTAESELGYTRITATMDGTVVAILVEEGQTVNAAQST

m290.pep
160 170 180 190 200 210
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVD PGLTTMSS
|||||

a290
210 220 230 240 250 260
PTIVQLANLDMMLNKMQIAEGDITKVKAGQDISFTILSEPDTPIKAKLDSVD PGLTTMSS

220 230 240 250 260 270
```


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```

m290.pep      GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               |||||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          GGYNSSTDASNAVYYYARSFVNPDPGKLATGMTTQNTVEIDGVKNVLIIPSLTVKNRGG
               270      280      290      300      310      320

               280      290      300      310      320      330
m290.pep      KAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               :|||||||||||||||||||||||||||||||||||||||||||||||||||||
a290          RAFVRVLGADGKAAEREIRTGMRDSMNTEVKSGLKEGDKVVI SEITAAEQQESGERALGG
               330      340      350      360      370      380

m290.pep      PPRRX
               |||||
a290          PPRRX
               390

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1217>:

```

g292.seq
1   atgaaaacca agttaatcaa aatcttgacc ccctttaccg tcctgccgct
51  gctggcttgc gggcaaacgc ccgtttccaa tgccaacgcc gaatccgccg
101 tcaaagccga atccgccggc aaatccgttg ccgcttcttt gaaagcgcg
151 ttggaaaaaa cctattccgc ccaagatttg aaagtgttga gcgtcagcga
201 aacaccggtc aaaggcattt acgaagtcgt cgtcagcggc aggcagatta
251 tctacaccga tgccgaaggc ggctatatgt tcgtcggcga actcatcaac
301 atcgacacgc gcaaaaacct gaccgaagaa cgcgccgccg atttgaacaa
351 aatcgacttc gcctccctgc ctttggacaa agccatcaaa gaagtacgcg
401 gcaacggcaa gctgaaagtc gccgtcttct ccgaccccca ttgtccgttc
451 tgcaaacgct tggaacatga gtttgaaaaa atgaccgacg tgacggttta
501 cagctttatg atgcccattg ccggcctgca cccagatgcc gcgcgcaagg
551 cgcaaactct atggtgtcag cccgaccgtg ccaaagcgtg gacggattgg
601 atgcgtaaag gcaaattccc ggtcggcggc agcatctgcg acaatcccgt
651 cgcggaacc acttccttgg gcgaacagtt cggcttcaac ggcacgccga
701 cccttcgtct tccccaacgg gcgcacccaa agcggttaca gcccgatgcc
751 ccaactggag gaaatcatcc gcaaaaacca gcagtaaacc cgcaatga

```

This corresponds to the amino acid sequence <SEQ ID 1218; ORF 292.ng>:

```

g292.pep
1   MKTKLIKILT PFTVLPLLAC GQTPVSNANA ESAVKAESAG KSAVASLKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFGVELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLRLPQR AHPKRLQPDA
251 PTGGNHPQKP AVNPQ*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1219>:

```

m292.seq
1   ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
51  GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCTCTTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAAA GAAGTGCCCG
401 GCAACGGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTTC
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATTG CCGGCCTGCA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATTCCC GGTCCGGCGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACAATT CCGCTTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCAACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC

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751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

This corresponds to the amino acid sequence <SEQ ID 1220; ORF 292>:

```

m292.pep
  1 MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSVASLKR
 51 LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAEG GYMFVGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLV AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m292/g292 98.7% identity in 238 aa overlap

	10	20	30	40	50	60
m292.pep	MKTKLIKILTPFTVLPLLACGQTPVSNANAEPKAVKAESAGKSVASLKRLEKTYSAQDL					
g292	MKTKLIKILTPFTVLPLLACGQTPVSNANAESAVKAESAGKSVASLKRLEKTYSAQDL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m292.pep	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
g292	KVLVSSETPVKGIYEVVVSQRQIIYTDAEGGYMFVGELINIDTRKNLTEERAADLNKIDF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m292.pep	ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTVYSEMMPIAGLHPDA					
g292	ASLPLDKAIKEVRGNGKLVAVFSDPDCPFCKRLEHEFEKMTDVTVYSEMMPIAGLHPDA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m292.pep	ARKAQILWCQPDRAKAWTDWMRKGFVPVGGICDNPVAETTSLSGEQFGFNGTPTLVFPNG					
g292	ARKAQILWCQPDRAKAWTDWMRKGFVPVGGICDNPVAETTSLSGEQFGFNGTPTLRPQR					
	190	200	210	220	230	240
	250	260				
m292.pep	RSQSGYSPMPQLEEIIRKNQX					
g292	AHPKRLQPDAPTGGNHPQKPAVNPOX					
	250	260				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1221>:

```

a292.seq
  1 ATGAAAACCA AGTTAATCAA AATCTTGACC CCCTTTACCG TCCTCCCGCT
 51 GCTGGCTTGC GGGCAAACGC CCGTTTCCAA TGCCAACGCC GAACCCGCCG
101 TCAAAGCCGA GTCCGCCGGC AAATCCGTTG CCGCCTCTTT GAAAGCGCGT
151 TTGGAAAAAA CCTATTCCGC CCAAGATTG AAAGTGTGA GCGTCAGCGA
201 AACACCGGTC AAAGGCATTT ACGAAGTCGT CGTCAGCGGC AGGCAGATTA
251 TCTACACCGA TGCCGAAGGC GGCTATATGT TCGTCGGCGA ACTCATCAAC
301 ATCGACACGC GCAAAAACCT GACCGAAGAA CGCGCCGCCG ATTTGAACAA
351 AATCGACTTC GCCTCCCTGC CTTTGGACAA AGCCATCAA GAAGTGCGCG
401 GCAACGCAA GCTGAAAGTC GCCGTCTTCT CCGACCCCGA TTGTCCGTT
451 TGCAAACGCT TGGAACACGA GTTTGAAAAA ATGACCGACG TGACGGTTTA
501 CAGCTTTATG ATGCCCATG CCGGCCGTGA CCCCAGTGCC GCGCGCAAGG
551 CGCAAATCTT ATGGTGTGAG CCCGACCGCG CCAAAGCGTG GACGGATTGG
601 ATGCGTAAAG GCAAATCCG GGTGCGCGGC AGCATCTGCG ACAATCCCGT
651 CGCGGAAACC ACTTCCTTGG GCGAACATT CGGCTCAAC GGCACGCCGA
701 CCCTCGTCTT CCCCACGGG CGCAGCCAAA GCGGCTACAG CCCGATGCCC
751 CAACTGGAGG AAATCATCCG CAAAAATCAA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1222; ORF 292.a>:

```

a292.pep
1  MKTKLIKILT PFTVLPLLAC GQTPVSNANA EPAVKAESAG KSPAASLKAR
51  LEKTYSAQDL KVLVSSETPV KGIYEVVVSQ RQIIYTDAGG GYMFGELIN
101 IDTRKNLTEE RAADLNKIDF ASLPLDKAIK EVRGNGKLK AVFSDPDCPF
151 CKRLEHEFEK MTDVTVYSFM MPIAGLHPDA ARKAQILWCQ PDRAKAWTDW
201 MRKGKFPVGG SICDNPVAET TSLGEQFGFN GTPTLVFPNG RSQSGYSPMP
251 QLEEIIRKNQ *

m292/a292 100.0% identity in 260 aa overlap

m292.pep      10      20      30      40      50      60
MKTCLKIKILT PFTVLPLLACGQTPVSNANAEP AVKAESAGK SVAASLKARLEK TYSAQDL
|||||
a292          10      20      30      40      50      60
MKTCLKIKILT PFTVLPLLACGQTPVSNANAEP AVKAESAGK SVAASLKARLEK TYSAQDL

m292.pep      70      80      90     100     110     120
KVLVSSETPVKGIYEVVVSQ RQIIYTDAGG GYMFGELIN IDTRKNL TEERAADLNKIDF
|||||
a292          70      80      90     100     110     120
KVLVSSETPVKGIYEVVVSQ RQIIYTDAGG GYMFGELIN IDTRKNL TEERAADLNKIDF

m292.pep     130     140     150     160     170     180
ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFM MPIAGLHPDA
|||||
a292         130     140     150     160     170     180
ASLPLDKAIKEVRGNGKLKVAVFSDPDCPFCKRLEHEFEKMTDVTVYSFM MPIAGLHPDA

m292.pep     190     200     210     220     230     240
ARKAQILWCQPDRAKAWTDW MRKGKFPVGG SICDNPVAETTSLGEQFGFN GTPTLVFPNG
|||||
a292         190     200     210     220     230     240
ARKAQILWCQPDRAKAWTDW MRKGKFPVGG SICDNPVAETTSLGEQFGFN GTPTLVFPNG

m292.pep     250     260
RSQSGYSPMPQLEEIIRKNQX
|||||
a292         250     260
RSQSGYSPMPQLEEIIRKNQX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1223>:

```

g294.seq (partial)
1  atgcgtatatta cctgtgcgcc gatgtcgctt ttgtcggcgg cagtctggtc
51  ggttcgggct gtcagaacat catcgaaccg ctttcctgcg gcgttacgac
101 gatattcggc ttttcgacct acaatttttc cgaagcctgc cggcacgcct
151 tggcatcggg tgcggcgggt caagtcgaat cggcggacgc gtggcgtgaa
201 gccgttgaaa aaaccttatac tggcgagggg ggcggaatgc agatgcaggc
251 gcgcgtggac ggctttatcg cacaacatcg cggagcgggc gcgagaatcg
301 ccgaggcggt gcgggaagcg gtatgcggac atcgggggcg atagtatac
351 aatccgtatc cgagttttcc ggttggagca tcgtatgagt atttatgcgc
401 tcgcgcacat catccacctg tattgcgcca ccgcctttgt cggcggcgtg
451 ttttttgaag tgctggtttt gtccgtccctg catacgggac ggggtgcgcg
501 cgaggcgagg cgcaagtgg aaaaggcaat gtcttaccgc gccgtcaggg
551 tgatgccgtt tgcggtcggc ctgctgttcg ccagggggaa tctagagtcg
601 actgcagcag catgccctc...

```

This corresponds to the amino acid sequence <SEQ ID 1224; ORF 294.ng>:

```

g294.pep (partial)
1  MRITCAPMSL LSAAVWSVRA VRTSSNRFPA ALRRYSAFRP TIFPKPAGTP
51  WHRVRRFKSN RRTRGVPLK KPYLARGAEC RCRRRAWTALS HNIAERARES
101 PRCGKRYAD IGDSDTIRI RVFRLEHRMS IYAVAHIIHL YCATAFVGGV
151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMPPAVG LLFARGTLES
201 TAAACP....

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1225>:

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m294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTCGGGTT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
 101 GATATTCGGC TTTTCAACCT ACAATTTTTC CGAAGCCTGC CGACACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGATGC GTGGCGGGAA
 201 GCCGTTGAAA AAACCTTATC GTCCGAGGGG GGGGGGATGC AGATGCAGGC
 251 GCGCGTGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT GCGGGAAGCG GTATGCGGAT ATCGGGGGCG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GTTTGGAGCA TCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTTCATCTG TATTGCGCTA TTGCCTTTGT CGGCGGCGTG
 451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTA TTGGCGCACT
 701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC GGTGCGTTGG
 751 TCGAAATACA TACACGCCGT CGTCTTACC CATATGcTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1226; ORF 294>:

m294.pep
 1 MRITCAPMSL LSAAVWSIRV VRTSSNRFP AFRRYSAFQP TIFPKPADTP
 51 WHRVRRFKSN RMRGGKPLK KPYRPRGGC RCRRRAWTALS HNIAERARES
 101 PRRCGRYAD IGGDSDTIRI RVFRLEHRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSREAR REVEKAMSYR AVRVMFVVG LFFASGIVMA
 201 ANRYSILGE PFATSFGTML TLKILLAFSV LAHFIAVVK MARSTLTGVG
 251 SKYIHAVVFT HMLLIVFLAK AMFYISW*

g294/m294 92.3% identity in 196 aa overlap

	10	20	30	40	50	60
g294.pep	MRITCAPMSLLSAAVWSVRAVRTSSNRFPALRRYSAFRPTIFPKPAGTPWHRVRRFKSN					
m294	: : : : :					
	10	20	30	40	50	60
g294.pep	RRTRGVKPLKKPYLARGAECRCRRRAWTALSHNIAERARESPRRCGRYADIGGDSDTIRI					
m294	RRMRGGKPLKKPYRPRGGCRRRAWTALSHNIAERARESPRRCGRYADIGGDSDTIRI					
	70	80	90	100	110	120
g294.pep	RVFRLEHRMSIYAVAHIIHLYCATAFVGGVFFEVLVLSVLHTGRVSREARREVEKAMSYR					
m294	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFFEVLVLSVLHTGRVSREARREVEKAMSYR					
	130	140	150	160	170	180
g294.pep	AVRVMFVAVGLLFARGTLESTAAACP					
m294	AVRVMFVVGGLLFASGIVMAANRYSILGEPFATSFGTMLTLKILLAFSVLAHFIAVVK					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1227>:

a294.seq
 1 ATGCGTATTA CCTGTGCGCC GATGTCGCTT TTGTCGGCGG CAGTCTGGTC
 51 GATTCGGGCT GTCAGAACAT CATCGAACCG CTTTCCTGCG GCGTTCCGAC
 101 GATATTCGGC TTTTCGACCT ACAATTTTTC CGAAGCCTGC CGGACACGCCT
 151 TGGCATCGGG TCGGCGGGT CAAGTCGAAT CGGCGGACGC GTGGCGGGAA
 201 GCCGTTGAAA AAAACTTATC GTCCGAGGAG GCGGGAATGC AGATGCAGGC
 251 GCGCGCGGAC GGCTTTATCG CACAACATCG CGGAGCGGGC GCGAGAATCG
 301 CCGAGGCGGT ACGGGAAGCG GTATGCGGAC ATCGGGGACG ATAGTGATAC
 351 AATCCGTATC CGAGTTTTC GGTGAGTA CCGTATGAGT ATTTATGCCG
 401 TCGCGCACAT CGTCCACCTG TATTGCGCCA TCGCCTTTGT CGGCGGCGTG
 451 TTTTTTGAAG TGCTGGTTTT GTCCGTCCTG CATACGGGAC GGGTGTCGCG
 501 CGAGGCGCGG CGCGAAGTGG AAAAGGCAAT GTCTTACCGC GCCGTCAGGG
 551 TGATGCCGTT TGTGGTCGGA CTGCTGTTCG CCAGCGGCAT CGTGATGGCG
 601 GCAAACCGCT ATCTTTCTAT ATTGGGCGAA CCGTTTGCCA CTTCTTCGG
 651 TACGATGCTG ACGCTGAAAA TCCTGTTGGC GTTCAGCGTG TTGGCGCACT

683

701 TCGCCATCGC CGTCGTCAAA ATGGCGCGTT CCACACTGAC CGTCGGCTGG
 751 TCGAAATACA TACACACCGT CGTCTTACC CATATGCTGC TGATTGTCTT
 801 TTTGGCAAAA GCGATGTTTT ATATCAGCTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1228; ORF 294.a>:

a294.pep
 1 MRITCAPMSL LSAAVWSIRA VRTSSNRFP AFRYSAPFR TIFPKPAGTP
 51 WHRVRFRKSN RTRGGKPLK KTYRPRRAEC RCRRARTALS HNIAERARES
 101 PRRYGKRYAD IGDDSDTIRI RVFRLEYRMS IYAVAHIVHL YCAIAFVGGV
 151 FFEVLVLSVL HTGRVSCEAR REVEKAMSYR AVRVMFVVG LLFASGIVMA
 201 ANRYLSILGE PFATSFGTML TLKILLAFSV LAHFAIAVVK MARSTLTVGW
 251 SKYIHTVVFT HMLLIVFLAK AMFYISW*

m294/a294 94.9% identity in 277 aa overlap

	10	20	30	40	50	60
m294.pep	MRITCAPMSLLSAAVWSIRVVRTSSNRFPAAFRYSAPFQPTIFPKPADTPWHRVRRFKSN					
a294	MRITCAPMSLLSAAVWSIRAVRTSSNRFPAAFRYSAPFRPTIFPKPAGTPWHRVRRFKSN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m294.pep	RRMRGGKPLKKPYRPRGGGCRRAWTALSHNIAERARESPRRCGKRYADIGGDSDTIRI					
a294	RRTRGGKPLKKTYRPRRAECRCRRARTALSHNIAERARESPRRYGKRYADIGGDSDTIRI					
	70	80	90	100	110	120
	130	140	150	160	170	180
m294.pep	RVFRLEHRMSIYAVAHIVHLYCAIAFVGGVFEVLVLSVLHTGRVSREARREVEKAMSYR					
a294	RVFRLEYRMSIYAVAHIVHLYCAIAFVGGVFEVLVLSVLHTGRVSCEARREVEKAMSYR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m294.pep	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
a294	AVRVMFVVGLLFASGIVMAANRYLSILGEPFATSFGTMLTLKILLAFSVLAHFAIAVVK					
	190	200	210	220	230	240
	250	260	270			
m294.pep	MARSTLTVGWSKYIHAVVFTHMLLIVFLAKAMFYISWX					
a294	MARSTLTVGWSKYIHTVVFTHMLLIVFLAKAMFYISWX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1229>:

g295.seq
 1 atgctcggga tggcgcggca cgacggccag cagggcatcg ccgcgatatt
 51 gttgccacgc cgccagcagt ttttcgcct cgtcttcgcc ccgataaacg
 101 cgcgtgctgc cgacacggc aaccggccgg cctccgatgc gtttttcaa
 151 ctgccccgcc agcgttttca tgtcttcaga cggcatcagg tcgtatttgg
 201 tattgccgca cacctgcacg gatgccgcgc ccaatttcgc caaccgcgcc
 251 gcatccgcct ccgtctgcgc cagacagccc gtcagcgaag cggtctgcgg
 301 acggatcagg cggcggactt tcagataacc gttcagcgat ttttcgaca
 351 gccgcgcatt cgccaaaaac agcggcacac ccgtctgcgc gcattccttc
 401 atcagattgg gccagatttc ggtttccatc aaaatgccga acatcggcg
 451 gtgttcgcgc aaaaactgcc gtaccacgt tttttgtca tacggaagat
 501 agcggcattg cgcacggga aacagaactt gcgggtttc ccgtcccgtc
 551 ggggtcatct gcgtcatcag cagcggcgca tcgggaaaac gccgccgcaa
 601 ctgcggtatc aagggtggg cggcacgcgt ttctccgacc gaaacggcgt
 651 gtatccaaac cgcgccggta acgggattcg gatgcggctt gccgaaacgc
 701 tcgtccctat gcgcccggtg tgccggggca cttccggagc gtttgtccaa
 751 ataacgccgt atccatatcg gcgcaagcag ccacaatata tcataaagcc
 801 attggaacat ctttctattt cctgcaaaac aaatgccgtc cgaacgggtc
 851 ggacggcatt tcggcaacgg aatcaaatat cgtag

This corresponds to the amino acid sequence <SEQ ID 1230; ORF 295.ng>:

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1231>:

m295.seq

This corresponds to the amino acid sequence <SEQ ID 1232; ORF 295>:

m295 . pep

m295/q295 93.9% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMA	RHDDQ	QRIAA	ILLPR	RQQFF	RLVFT
g295	MLGMA	RHDDQ	QQGI	AAILL	PRRQ	FFRLV
	10	20	30	40	50	60
m295.pep	70	80	90	100	110	120
g295	70	80	90	100	110	120
m295.pep	130	140	150	160	170	180
g295	130	140	150	160	170	180
m295.pep	190	200	210	220	230	240
g295	190	200	210	220	230	240
m295.pep	250	260	270	280	290	
g295	250	260	270	280	290	

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1233>:

```
a295.seq
1  ATGCTCGGGA TGGCGCGGCA CGACGACCAG CAGGGCATCG CCGCGATATT
51  GTTGCCACGC CGCCAGCAGT TTTTCCGCCT CGTCTTCACC CCGATAAACG
101 CGCGTGCTGC CGCACACGGC AACCTGCCGG TCTCCGATGC GTTTTTCAAA
151 CTGCCCCGCC AGCGTTTTCA TCTGTTCCGA CGGCATCAGG TCGTATTTGG
201 TATTGCCGCA CACCTGCACG GATGCCGCGC CCAATTTTCG CAACCCGCGC
251 GCATCCGCCT CCGTCTGTGC CAGACAGCCC GTCAGCGAAG CGGCGGCAGG
301 ACGGATCAGG CTGCGGACTT TCAGATAACC GTTTAGCGAT TTTTCCGACA
351 GCCGCGCATT CGCCAAAAAC AGCGGCACAC CCGTGCGCCG GCATTCTTTC
401 ATCAGATTGG GCCAGATTTC GGTTCCTATC AAAATGCCGA ACATCGGGCG
451 GTGTTTCGCG AAAAAGTCCG GTACCCACGT TTTTGTGTC TACGGAAGAT
501 AGCGGCATTG TGCATCAGGA AACAGAACTT GCGCGGTTTC CCGTCCCGTC
551 GGGGTCATCT GCGTCATCAG CAGCGGCGCA TCGGGAAGAA GCTGCCGCAA
601 CTCGCGTATC AAAGGTTGGG CGGCACGCGT TCCCCGACC GAAACGGCGT
651 GTATCCAAAC CGCGCCGGTA ACGGGATTCG GATACGGCTT GCCGAAACGC
701 TCGCCCCGAT GCGCCCGATA TGCAGGGGCA CTTCCGGAGC GTTTGTCCAA
751 ATAACGCCGT ATCCATATCG GCGCAAGCAG CCACAATACA TCATAAAGCC
801 ATTGGAACAT CTTTCTATTT CCTGCAAAAC AAATGCCGTC CGAACGGTTC
851 GGACGGCATT TCGGCAACGG AATCAAATAT CGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1234; ORF 295.a>:

```
a295.pep
1  MLGMARHDDQ QGIAAILLPR RQOFFRLVFT PINARAAAHG NLPVSDAFFK
51  LPRQRFHLFR RHQVVFGLIA HLHGCRAQFR QPRRIRLRLC QTARQSGGR
101 TDQAADFQIT V*FFRQPRI RQQRHTRAP AFLHQIGPDF GFHQNAEHRA
151 VFAQKLPYPR FVIRKIAAL CIRKQNLRGF PSRRGHLRHQ QRRIGKTLPLQ
201 LAYQRLGGTR FPDNRGVYPN RAGNGIRIRL AETLAPMRPI CRGTSGAFVQ
251 ITPYPYRRKQ PQYIIKPLEH LSISCKTNAV RTVRTAFRQR NQIS*
```

m295/a295 93.2% identity in 294 aa overlap

	10	20	30	40	50	60
m295.pep	MLGMARHDDQ	RIAAILLPR	RQOFFRLVFT	PINARAAAHG	NRNPASDAFFK	LPRQRFHLFR
a295	MLGMARHDDQ	QGIAAILLPR	RQOFFRLVFT	PINARAAAHG	NLPVSDAFFK	LPRQRFHLFR
	70	80	90	100	110	120
m295.pep	RYDVVFGLIA	HLHGCRAQFR	QPRRIRLRLC	QTPRQSGGR	TDQAADFQIT	VQRFRRQPRI
a295	RHQVVFGLIA	HLHGCRAQFR	QPRRIRLRLC	QTARQSGGR	TDQAADFQIT	VXRFFRQPRI
	130	140	150	160	170	180
m295.pep	RQQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQK	LPYPRFFV	IRKIAALRIGKQNLRGF
a295	RQQRHTRAP	AFPHQVGP	DFGFHQNAE	HRAVFAQK	LPYPRFFV	IRKIAALRIGKQNLRGF
	190	200	210	220	230	240
m295.pep	PSRRGHLRH	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETLVPMRPI
a295	PSRRGHLRH	QRRIGKTP	PQLAYQGL	GGTRFSDR	NGVYPNR	RAGNGIRIRLAETLVPMRPI
	250	260	270	280	290	
m295.pep	CRGTSGAFV	QITPYPY	RRKQPQY	IIKPLEH	LSISCKT	NAVXTVQTAFRQRNQISX
a295	CRGTSGAFV	QITPYPY	RRKQPQY	IIKPLEH	LSISCKT	NAVXTVQTAFRQRNQISX

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1235>:

```
g297.seq
1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
```

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51  GCTTGCCGTT TCGATTATTC TGGTgtcgGC GGCATACATT Gcttcgacag
101 aggggaccga ggcggtcaga ccgcAGCGCG TggaacaaAA ACTGCCGCCG
151 CTGTCTtTGGg gcggaacagg CGTtcagacg gcaTATTGGG TGCAGGAGGC
201 GGTGCagccg ggggactcgC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGgacga gattgCCcga ATcacGGAAA aataTgcgG CGAAGCCGAT
301 TTGCGgcatt tGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGCGGCGCA
351 CGGCAGTGCG CGCGAAGTGC AGTTTTttaC CGACGAAGAC GGCAGCGCA
401 aTctGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GATGCGGATA TGAAGGTTTT GCCGACACTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCCGC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTT GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GCTTTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC GGAAGTTGTC AAGGGCGGCA
701 CAACCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAG CGGAGGGGCG
751 GGCAATTATT ACGATGAAGA CGGCAGGTG TGCAGGAAA AAGGCGGCTT
801 CAACATCgaG CCGCTGGTCT ATACGCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGcAGGCA
1051 CAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACAGG
1101 CGGTTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1236; ORF 297.ng>:

g297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTEGTERVR PORVEQKLPP
51  LSWGGNGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGSA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151 DADMKVLPPL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK
201 EGDVRLLYD SLYFHGQOVA AGDILAAEVV KGGTTHQAFY YRSDKEGGGG
251 GNYDEEDGRV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTpVRA SADGVITFKG RKGGYGNAMV IRHANGVETL YAHLSAFSQA
351 QGNVRGGEVI GFVGSSTGRST GPHLHYEARI NGQPVNPVSV ALPTPELTQA
401 DKAAFAAQKQ KADALLARLR GIPVTVSQSD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1237>:

m297.seq

```

1  ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGTGC
51  GCTTGCCGTT TCGATTATTT TGGTGTcGGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAAACAAA TCTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG CGTTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCGG GCGACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA GATTGCCCCG ATCACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGCGGCGCA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTTAC CGACGAAGAC GGCAGAGCGCA
401 ATCTGGTTCG TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCCGC GAAATCCGCG
551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA CGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATGTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTTTGGCGGC TGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGCTTCTAT TACCGTTCGG ACAAGGAAGG CGGAGGGGGC
751 GGCAATTATT ATGATGAAGA CGGCAAGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCGCTGGTCT ATACGCGCAT TTCTTCGCGG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACATGGCGGC TGCACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTcAGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGCG GATACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAACGCTG TACGCGCACT TGAGCGCGTT TTCGcAGGCG
1051 GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTTGTG GTTCGACCGG
1101 GCGTTTCGACC GGGCCGCACC TGCATTACGA GGCGCGCATC AACGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1238; ORF 297>:

m297.pep

```

1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV PORVEQNLPP
51  LSWGGSGVQT AYWVQEAQVP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGDGGA REVQFFTDDE GERNLVALEK KGGIWRRSAS
151 EADMKVLPPL RSVVVKTSAR GSLARAEVPV EIRESLSGIF AGRFSLDGLK

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201 EGDVRLMYD SLYFHGQOVA AGDILAAEVV KGGTRHQAFY YRSDKEGGGG
251 GNYDEDEGKV LQEKGGFNIE PLVYTRISSP FGyRMHPILH TWRLHTGIDY
301 AAPQGTPVRA SADGVITFKG RKGGYGNAVM IRHANGVETL YAHLSAFSQA
351 EGNVRGGEVI GFVGSTGRST GPHLHYEARI NGQPNPVS SV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/g297 97.9% identity in 430 aa overlap

	10	20	30	40	50	60
m297.pep	MAVFPLSAKHKYALRALAVSIILVSAAYIASTERTERVRPQORVEQNLPPLSWGGSGVQT					
g297	MAVFPLSAKHKYALRALAVSIILVSAAYIASTEGTERVRPQORVEQKLPPLSWGGNGVQT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m297.pep	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGGA					
g297	AYWVQEAQPGDSLADVLARSGMARDEIARITEKYGGEADLRHLRADQSVHVLVGGDGSA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m297.pep	REVQFFTTDEDGERNLVALEKKGGIWRRSASEADMKVLPTLRSVVVKTSARGSLARAEVPV					
g297	REVQFFTTDEDGERNLVALEKKGGIWRRSASDADMKVLPTLRSVVVKTSARGSLARAEVPV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m297.pep	EIRELSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQOVAAGDILAAEVVKGGTRHQAFY					
g297	EIRELSGIFAGRFSLDGLKEGDAVRLLYDSLYFHGQOVAAGDILAAEVVKGGTTHQAFY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m297.pep	YRSDKEGGGGGNYDEDEGKVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
g297	YRSDKEGGGGGNYDEDEGRVLQEKGGFNIEPLVYTRISSPFGYRMHPILHTWRLHTGIDY					
	250	260	270	280	290	300
	310	320	330	340	350	360
m297.pep	AAPQGTPVRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAEGNVRGGEVI					
g297	AAPQGTPVRASADGVITFKGRKGGYGNAMIRHANGVETLYAHLSAFSQAQGNVRGGEVI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m297.pep	GFVGSTGRSTGPHLHYEARINGQPNPVSVALPTPELTQADKAFAAQKQKADALLARLR					
g297	GFVGSTGRSTGPHLHYEARINGQPNPVSVALPTPELTQADKAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297.pep	GIPVTVSQSDX					
g297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1239>:

```

a297.seq
1   ATGGCTGTCT TCCCACTTTC GGCAAAACAT CGGAAATACG CGCTGCGCGC
51  GCTTGCCGTT TCGATTATTT TGGTGTCCGC GGCATACATT GCTTCGACAG
101 AGAGGACGGA GCGCGTCAGA CCGCAGCGCG TGGAACAAAA ACTGCCGCCG
151 CTGTCTTGGG GCGGCAGCGG TGTCAGACG GCATATTGGG TGCAGGAGGC
201 GGTGCAGCCA GCGCACTCGC TGGCGGACGT GCTGGCGCGT TCGGGTATGG
251 CGCGGGACGA AATTGCCCGA ATAACGGAAA AATATGGCGG CGAAGCCGAT
301 TTGCGGCATT TGCGTGCCGA CCAGTCGGTT CATGTTTTGG TCGGCGGCGA
351 CGGCGGCGCG CGCGAAGTGC AGTTTTTTAC CGACGAAGAC GGCGAGCGCA
401 ATCTGGTCGC TTTGGAAAAA AAAGGCGGCA TATGGCGGCG GTCGGCTTCT
451 GAGGCGGATA TGAAGGTTTT GCCGACGCTG CGTTCGGTCG TGGTCAAAC
501 GTCGGCGCGC GGTTCGCTGG CGCGGGCGGA AGTGCCCGTC GAAATTCGCG

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688

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551 AATCCTTAAG CGGGATTTTC GCCGGCCGCT TCAGCCTTGA TGGTTTGAAG
601 GAAGGCGATG CCGTGCGCCT GATTACGAC AGCCTGTATT TCCACGGGCA
651 GCAGGTGGCG GCGGGCGATA TTCTGGCGGC GGAAGTCGTT AAGGGCGGCA
701 CAAGGCATCA GCGTTTCTAT TACCGTTCGG ACAAGGAAGG AGGAGGGGGC
751 GGCAATTATT ACGATGAAGA CGGCAGGGTG TTGCAGGAAA AAGGCGGCTT
801 CAACATCGAG CCACTGGTCT ATACGCGCAT TTCTTCGCCG TTCGGCTACC
851 GTATGCACCC CATCCTGCAC ACTTGGCGGC TGACACGGG CATCGATTAT
901 GCCGCACCGC AGGGAACGCC GGTACGGGCT TCCGCCGACG GCGTGATTAC
951 CTTTAAAGGC CGGAAGGGTG GCTACGGCAA CGCGGTGATG ATACGCCACG
1001 CCAACGGTGT GGAAACGCTG TATGCGCACT TGAGCGCGTT TTCTCAGGCA
1051 GAAGGCAATG TGCGCGGCGG CGAGGTCATC GGTTTGTGCG GTTCGACCGG
1101 GCGTTCGACG GGGCCGCACC TGCATTACGA GGCGCGCATC AATGGGCAGC
1151 CCGTCAATCC TGTTTCGGTC GCATTGCCGA CACCCGAATT GACGCAGGCG
1201 GACAAGGCGG CGTTTGCCGC GCAGAAACAG AAGGCGGACG CGCTGCTTGC
1251 GCGCTTGCGC GGCATACCGG TTACCGTGTC GCAATCGGAT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1240; ORF 297.a>:

```

a297.pep
1  MAVFPLSAKH RKYALRALAV SIILVSAAYI ASTERTERV R PQRVEQKLPP
51  LSWGGSGVQT AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEAD
101 LRHLRADQSV HVLVGGD GGA REVQFFTD DED GERNLVALEK KGGIWRRSAS
151 EADMKVLP TL RSVVVKTSAR GSLARAEV PV EIRESLSGIF AGRFSLDGLK
201 EGDVRLIYD SLYFHGQ QVA AGDILAAEV V KGGTRHQAFY YRSDKEGGGG
251 GNYDDE DGRV LQEKGGFNIE PLVYTRISSP FG YRMHPILH TWRLHTGIDY
301 AAPQGT PVR A SADGVITFKG RKG YGNVAVM IRHANGVETL YAHLSAFSQA
351 EGNVRG GEVI GFV GSTGRST GPHLHYEAR I NGQPVNPVSV ALPTPELTQA
401 DKAFAAQKQ KADALLARLR GIPVTVSQSD *

```

m297/a297 99.3% identity in 430 aa overlap

```

              10      20      30      40      50      60
m297.pep      MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV R PQRVEQNL PPLSWGGSGVQT
              |||
a297           MAVFPLSAKHKRYALRALAVSIILVSAAYIASTERTERV R PQRVEQKL PPLSWGGSGVQT
              10      20      30      40      50      60

              70      80      90      100     110     120
m297.pep      AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEADLRHLRADQSVHVLVGGD GGA
              |||
a297           AYWVQEA VQP GDSLADVLAR SGMARDEIAR ITEKYGGEADLRHLRADQSVHVLVGGD GGA
              70      80      90      100     110     120

              130     140     150     160     170     180
m297.pep      REVQFFTD DEDGERNLVALEK KGGIWRRSASEADMKVLP TLRSVVVKTSARGSLARAEV PV
              |||
a297           REVQFFTD DEDGERNLVALEK KGGIWRRSASEADMKVLP TLRSVVVKTSARGSLARAEV PV
              130     140     150     160     170     180

              190     200     210     220     230     240
m297.pep      EIRESLSGIFAGRFSLDGLKEGDAVRLMYDSLYFHGQ QVAAGDILAAEVVKGGTRHQAFY
              |||
a297           EIRESLSGIFAGRFSLDGLKEGDAVRLIYDSLYFHGQ QVAAGDILAAEVVKGGTRHQAFY
              190     200     210     220     230     240

              250     260     270     280     290     300
m297.pep      YRSDKEGGGGGNYDDEGKV LQEKGGFNIEPLVYTRISSPFG YRMHPILHTWRLHTGIDY
              |||
a297           YRSDKEGGGGGNYDDEGKV LQEKGGFNIEPLVYTRISSPFG YRMHPILHTWRLHTGIDY
              250     260     270     280     290     300

              310     320     330     340     350     360
m297.pep      AAPQGT PVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
              |||
a297           AAPQGT PVRASADGVITFKGRKGGYGNVAVMIRHANGVETLYAHLSAFSQAEGNVRGGEVI
              310     320     330     340     350     360

```

689

	370	380	390	400	410	420
m297 . pep	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
a297	GFVVGSTGRSTGPHLHYEARINGQPVNPVSVALPTPELTQADKAAFAAQKQKADALLARLR					
	370	380	390	400	410	420
	430					
m297 . pep	GIPVTVSQSDX					
a297	GIPVTVSQSDX					
	430					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1241>:

g298 . seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGAGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AACCTTCCTG TCCGGCGAAA cgcgcgcac ggCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GCGTGAAGCC GCCGCATCCG AAGCCGCCCC GCGGCCGGGC
301 GGAACAGAAT GGAAACAAGG CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTCGCCGGAG ATTCGCTGAT GCAGGCGGTT GCGCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGC CAACCTCAGC
451 AAACAAAGCA CGGGGCTTTC CTATCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCTTGAAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGCCC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACGCTACCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC GCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGTC AAGCTCGACG GTCAGATGCG CTACCTCGAC
751 AAATGCTTT CGGAACACTT GAAAGGCAAA ATCATCCTGA TTCCACCGC
801 GCAAACTAG AGCGGCGGGA AAGgcccGTA CACCGATTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGTAAG ACGCATACA CTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCGAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1242; ORF 298.ng>:

g298 . pep

```

1  MKNFLSLFAS ILSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51  SGAALQENAY ALSDGIKTFL SGETPPTAQD GGSADMPPEA AASEAAPAG
101 GTEWKQGTGA AAVRSGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESANLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDF WDFPVGKRYL
201 KFASDEWAQE YLKRVDRILE AAHTRVQVV WLGIPLYMKKV KLDGQMRYLD
251 KLLSEHLK GK IILIPTAQL SGGKGRYTDS VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAEKI MEKIVFEPST QPSSTQP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1243>:

m298 . seq

```

1  ATGAAAAACT TTCTTTCCCT TTTCTCCTCC ATACTGATGT CTGCCCTGAT
51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101 ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCTACGG ATGGTGGCGG
151 AGCGGTGCGG CGTTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201 AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GCGGTTTCGG
251 CAGATATGCC GTCTGAAGCC GCCGCATCCG AAGCCGTCCC TCAAACCGGT
301 GAAACAGAAT GGAAACAAGA CACCGAAGCC GCCGCCGTCC GCAGCGGCGA
351 CAAAGTCTTT TTTGTCGGCG ACTCGCTGAT GCAGGGCGTT GCCCTTTCG
401 TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451 AAACAAAGCA CGGGGCTGTC CTACCCCTCA TTCTTCGACT GGCCGAAAAC
501 GATTGAAGAA ACCCTGCAAA AACATCCCGA AATCAGCGTA CTCGCCGTCT
551 TCCTCGGACC GAACGACCCG TGGGATTTCC CCGTCGGCAA ACTCTATCTC
601 AAATTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GTGTCGACCG
651 CATCCTTGAA GCCGCACACA CGCACC GCGT CCAAGTCGTC TGGCTCGGCA
701 TCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC
751 AAATCGCTTT CGGAACATTT GAAAGGCAAA ATCATCCTGA TTCCCAACAC
801 GCACACCTAG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAAAC CGTCCGCTAC CGCAGCAAG ACGCATACA CTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGAAAAATA ATGGAAAAAA TCGTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1244; ORF 298>:

```

m298.pep
  1  MKNFLSLFSS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
 51  SGAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AASEAVPQTG
101  ETEWKQDTEA AAVRSGDKVF FVGDSLMOGV APFVQKSLKQ QYGIESVNLS
151  KQSTGLSYPS FFDWPKTIEE TLQKHPEISV LAVFLGPNDP WDFPVGKLYL
201  KFASDEWAQE YLKRVDRIE AAHTRVQVV WLGIPYMKKA KLDGQMRYLD
251  KLLSEHLKGI ILIPTHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301  EGQKLLAAKI MEKIVFEPST QPSSTQP*

m298/g298  94.8% identity in 327 aa overlap

      10      20      30      40      50      60
m298.pep  MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g298       MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY
          10      20      30      40      50      60

      70      80      90     100     110     120
m298.pep  ALSDGIKAFISGETPPTAQDGGSDMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g298       ALSDGIKTFLSGETPPTAQDGGSDMPPEAAASEAAPPAGGTEWKQDTEAAAVRSGDKVF
          70      80      90     100     110     120

      130     140     150     160     170     180
m298.pep  FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g298       FAGDSLMOGVAPFVQKSLKQQYGIESANLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV
          130     140     150     160     170     180

      190     200     210     220     230     240
m298.pep  LAVFLGPNDPWFDPVVGKLYLKFADEWAQEYLKRVDRILEAAHTRVQVVWLGIPYMKKA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g298       LAVFLGPNDPWFDPVVGKRYLKFADEWAQEYLKRVDRILEAAHTRVQVVWLGIPYMKKV
          190     200     210     220     230     240

      250     260     270     280     290     300
m298.pep  KLDGQMRYLDKLLSEHLKGI ILIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g298       KLDGQMRYLDKLLSEHLKGI ILIPTAQLSGGKGRTDSDNVNGKPVRYRSKDGIHFTA
          250     260     270     280     290     300

      310     320
m298.pep  EGQKLLAAKIMEKIVFEPSTQPSSTQPX
          |||||:|||||:|||||:|||||:|||||:
g298       EGQKLLAEKIMEKIVFEPSTQPSSTQPX
          310     320

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1245>:

```

a298.seq
  1  ATGAAAACT TTCTTCCCT TTTCGCCTCC ATACTGATGT CTGCCCTGAT
 51  TGCCGTGTGG TTCAGCCAAA ACCCCATCAA CGCCTACTGG CAGCAGACCT
101  ACCACCGCAA CAGCCCGCTC GAACCGCTTG CCGCCTACGG ATGGTGGCGG
151  AGCGGTGCGG CATTGCAAGA AAACGCCTAC GCCCTTTCAG ACGGCATCAA
201  AGCCTTCCTG TCCGGCGAAA CGCCGCCGAC GGCTCAAGAC GGCGGTTCGG
251  CAGATATGCC GTCTGAAGCC GCCGCACCCG AAACCGCCCC TCAAACCTGGC
301  GAAACAGAAT GGAACAAAA CACCGAAGCC GCCGCCGTCC GAACAGGGGA
351  CAAAGTCTTT TTCGCCGCG ACTCGCTGAT GCAGGGCGTT GCACCTTCG
401  TGCAAAAAAG CCTGAAACAG CAATACGGCA TCGAATCCGT CAACCTCAGC
451  AAACAAAGCA CGGGGTGTC CTACCCCTCA TTCTTCGACT GGCGAAAAC
501  GATTGAAGAA ACCCTGAAA AACATCCCGA AATCAGCGTG CTCGCCGTCT
551  TCCTCGGTCC GAACGACCCG TGGGATTTC CCGTTGGCAA ACGCTACCTC
601  AAATTTCGCTT CCGACGAATG GCGCAAGAA TACCTGAAAC GCGTCGACCG
651  CATCCTTGAA GCCGCACACA CGCACTACGT CCAAGTCGTC TGGCTCGGCA
701  TCCCCTACAT GAAAAAGCC AAGCTCGACG GACAGATGCG CTACCTAGAC

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691

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751 AAACCTGCTTT CGGAATATTT GAAAGGCAAA ATCATCCTGA TTCCCACCGC
801 GCACACCCTG AGCGGCGGGA AAGACCGCTA CACCGACTCC GTCAACGTCA
851 ACGGCAAACC CGTCCGCTAC CGCAGCAAGG ACGGCATACA CTTTACCGCC
901 GAAGGACAAA AACTGCTGGC GGCAAAAATA ATGGAAAAAA TCGTTTTTTGA
951 ACCAAGTACG CAACCATCAA GTACACAGCC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1246; ORF 298.a>:

```

a298.pep
1 MKNFLSLFAS ILMSALIAVW FSQNPINAYW QQTYHRNSPL EPLAAYGWWR
51 SGAAALQENAY ALSDGIKAFI SGETPPTAQD GGSADMPSEA AAPETAPQTG
101 ETEWKQNTTEA AAVRTGDKVF FAGDSLMOGV APFVQKSLKQ QYGIESVNLS
151 KQSTGLSYPS FFDWPKTIEE TLKKHPEISV LAVFLGPNDP WDFPVGKRYL
201 KFASDEWAQE YLKRVDRIE AAHthyVQVW WLGIPYMKKA KLDGQMRyLD
251 KLLSEYLKGI ILIPTAHTL SGGKDRYTDV VNVNGKPVRY RSKDGIHFTA
301 EGQKLLAAKI MEKIVFEPST QPSSTQP*

```

m298/a298 96.3% identity in 327 aa overlap

	10	20	30	40	50	60
m298.pep	MKNFLSLFSSILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
a298	MKNFLSLFASILMSALIAVWFSQNPINAYWQQTYHRNSPLEPLAAYGWWRSGAALQENAY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m298.pep	ALSDGIKAFISGETPPTAQDGGADMPSEAAASEAVPQTGETEWKQDTEAAAVRSGDKVF					
a298	ALSDGIKAFISGETPPTAQDGGADMPSEAAAPETAPQTGETEWKQNTTEAAAVRTGDKVF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m298.pep	FVGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLQKHPEISV					
a298	FAGDSLMOGVAPFVQKSLKQQYGIESVNLSKQSTGLSYPSFFDWPKTIEETLKKHPEISV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m298.pep	LAVFLGPNDPWDFPVGKLYLKFADEWAQEYLYKRVDRILEAAHthRVQVWVWLGIPYMKKA					
a298	LAVFLGPNDPWDFPVGKRYLKFADEWAQEYLYKRVDRILEAAHthyVQVWVWLGIPYMKKA					
	190	200	210	220	230	240
	250	260	270	280	290	300
m298.pep	KLDGQMRyLDKLLSEHLKGIILIPTHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
a298	KLDGQMRyLDKLLSEYLKGIILIPTAHTLSGGKDRYTDVNVNGKPVRYRSKDGIHFTA					
	250	260	270	280	290	300
	310	320				
m298.pep	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
a298	EGQKLLAAKIMEKIVFEPSTQPSSTQPX					
	310	320				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1247>:

```

g299.seq
1 ATGAACCCCA AACACTTCAT CGCATTTTCC GCCCTGTTCC CCGCCACGCA
51 GGCAGAAGCC CTGCCCCGTC CCTCCGTCAG CCCCGACACC GTTACCGTTT
101 CCCCCTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCCGCG CTCGCTTG GATGAAAAAA CTCCGATCCG TCGCACAAGG
201 CAGCGCGGAG GCCTTCCGCA TCCTGCAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGAGGCC CTGCGCAAAC GCCTGCAAAA AACATGGGGC
301 GACGCGGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGCGGCGGTC CGTCACAGCG GCAACTGGCA AAGCTTCACC AGCAGGAACA
401 ATACCGGAGA TTTCCCGCTC GCGGCATCC TCGCCCAAAC CGGCAGCGGC
451 GGCGGCATGA CCCTGACCGC GTCTGACGGC AAAACCGGCA AACAGCGCGT

```

501	TTCCTGTTT	GCCAAACCGC	TGCTCGCCGA	ACAAACCTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGGCGCT	GGCAGGTACT	GGATACGGGC
601	CGCGCACTGC	CCCTGGCCAT	ACGACCGCAA	ATGCCGTGGG	CGATCGGGTT
651	CATCAACATC	GAAAATCCCG	CCGGCGGCAT	TACCGTTTCC	GCATGGGCCA
701	TCAACGGCGC	ACAATTGACC	CAGTGGTCTG	AATGGCGTGC	CGACCGTATG
751	AACGACCTTG	CCCCAAACCG	CGCCGATTTG	GTATTCTCTT	CCTACGGCAC
801	CAACGAAGCG	TTCAACAACA	ACATCGACAT	TCCGATAC	GAACAAAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCGCGACA	GCCTGCCCGC	CGCCGGCATC
901	CTCATCATCG	GCGCGCCCGA	ATCCCTGAAA	AACACGTCTG	CGGTATGCGG
951	CACGCGCCCC	GTCTTCTTGA	CCGAAGTCCA	ACAGATGTCG	CGGCGCGTCG
1001	CCCGTCAGGG	CGACAGCATG	TTTTGGTCTT	GGCAAAACGC	AATGGGCGGC
1051	ATATGCAGCA	TGAAAAATCG	GCTCAACCAA	GGATGGGCGG	CCAAAGACGG
1101	CGTACACTTC	TCCGCCCAAG	GCTACCGGCG	CGCGGCGGAA	ATGCTTGGCG
1151	ACAGCTCTCGA	AGAACTCGTC	CGCCGCGCGC	CAATCAGGCA	ATAA

g299.pep

1	<u>MNPKHFIAFS</u>	<u>ALFAATQAEA</u>	LPVASVSPDT	VTVSPSAPYT	DTNGLLLTDYG
51	NAAASVPMWK	LRSVQAQSGS	AFRLIQIGDS	HTAGDFFTTA	LRKRLQKXTWG
101	DGGIGWVYPA	NVKGQRMMAV	RHSGNWQSFT	SRNNTGDFPL	GGIGALQVLTG
151	GGMTLTASDG	KTGKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGQWQLTDS
201	AALPLAIQTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NDLAQTGADL	VILSYGTNEA	FNNNIADIAT	EQMQLQVTRQ	IRDSLPAAGI
301	LIIGAPESLK	NTLGVCGRTP	VLLTEVQQGT	RRVARQQTGT	FWSWQNAMGG
351	ICSMKNWLNO	GWAAKDGVHF	SAOQYRRAE	MLADSLEELV	RAAAIRO*

m299.seq

1	ATGAACCCCA	AACACCTCAT	CGCATTTTTC	GCCCTATTTCG	CCGCCACGCA
51	GGCAGAAGCC	CTACCTGTGC	CCTCCGTGCG	CCTCGACACC	GTTACCGTTT
101	CCCCGTCGCG	CCCCTACACC	GATACAAACG	GGCTGTGTGAC	CGCATACGGC
151	AACGCTCTCG	CCTCGCTTTG	GATGAAAAAA	TCCAATTCCG	TCGCACAAGG
201	CAGCGGCGAG	ACCTTCCGTA	TCCTGCAAAT	CGGCGACTCG	CATACCGCCG
251	GCGACTTCTT	TACCGACAGC	CTGCGCAAA	GCCTGCAAAA	AACTTGGGGC
301	GACGGCGGCA	TAGGCTGGGT	TATCCCGGCC	AACGTCAAAG	GGCAGCGCAT
351	GGCGGGCGTC	CGGCACAACG	GTAACGTGCA	AAGCCTCACC	ACGAGGAACA
401	ACACCGGAGA	CTTCCCGCTC	GGCGGCATCC	TCGCCACAC	CGGCAGCGGC
451	GGCAGATCTA	CCCTGACCGC	ATCGGACGGC	ATAGCAAGCA	AGCAGCGCGT
501	TTCCCTGTTT	GCCTAACCCC	TGCTTGCCGA	ACAAACCTTG	ACCGTCAACG
551	GCAACACCGT	CTCCGCCAAC	GGCGGGCGCT	GCAGGTACT	GGATACGGGC
601	GCGGCACTGC	CCCTGACCAT	ACACACCGAA	ATGCCGTGGG	ACATCGGCTT
651	CATCAACATG	GAAAACTCCG	CCGGCGCGAT	TACCGTTTTC	GCGATGGGCA
701	TCAACGGCGC	ACAATTAAAC	CAGTGGTCGA	ATATGGCGTG	CGACCGTATG
751	AACGACCTCG	CCCAAAACCG	CGCCGATTTG	GTTATCCTTT	CCTACGGCAC
801	CAACGAAGCT	TTCAACAACA	ACATCGACAT	TGCCGACACC	GAACAAAAAT
851	GGCTGGATAC	CGTCCGCCAA	ATCCCGGACA	GCCTGCCTCG	CGCCGGCATC
901	CTCATCATCG	GCGCACCCGA	ATCCCTGAAA	AACACGCTCG	GCGTATGCGG
951	CACACGCCCC	GTCGCGCTGA	CCGAAGTCCA	ACAGATGCA	CGCGCGCTCG
1001	CCCGTCAGGG	GCAGACGATG	TTCTGGTCTT	GGCAAAACGC	CATGGGCGGC
1051	ATATGTCAGCA	TGAAAAATCG	GCTCAACCCA	GGATGGGCCG	CCAAAGACGG
1101	CGTACACTTC	TCGCCCAAAG	GCTACCGCGG	CGCGGCGGAA	ATGCTCGCCG
1151	ACAGCCTCGA	AGAATCTCGT	CCTCCGCTG	CAATCAGGCA	ATAA

m299.pep

1	<u>MNP</u> <u>KHLIAF</u>	<u>ALFAATQAEA</u>	LPVASVSLDT	VTVSPSAPYT	DTNGLLLTDYG
51	NASASPWMKK	LQSVAGQSGE	TFRILQIGDS	HTAGDFFTDS	LRKRLQKTFWG
101	DGGIGWVYPA	NVKGQRMASV	RHNGNMQSLT	SRNNTGDFPL	GGGLAHTGSG
151	GSMTLLTASD	IASKQRVSLF	AKPLLAEQTL	TVNGNTVSAN	GGGWQVLDTG
201	AALPLTIHTE	MPWDIGFINI	ENPAGGITVS	AMGINGAQLT	QWSKWRADRM
251	NLIAQPTGADL	VILSYGTNEA	FNNNIIDIADT	EQKVLARQVTQ	IRDSLPAAGI
301	LDLAGAPESLK	NTLGVCCTRP	VRLETVQQQK	RRWRDQGTQ	FWSWQNAMGG
351	ICSMKNWLNQ	GWAAKDGVHF	SAGKYRRAAE	MLADSLEELV	RSAAIRO*

m299/g299 95.5% identity in 397 aa overlap

m299.pep MNPKHLIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDTNGLLTDYGNASASPWMKK

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g299	MNPKHFIAFSALFAATQAEALPVASVSPDTVTVSPSAPYTDNGLLTDYGNAAASPWMKK
	10 20 30 40 50 60
m299.pep	LQSV AQSGSETFRILQIGDSHTAGDFFTD SLRKLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
g299	LRSV AQSGGEAFRILQIGDSHTAGDFFTDALRKLQKTWGDGGIGWVYPANVKGQORMAAV
	70 80 90 100 110 120
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
g299	RHSGNWQSFSTRNNTGDFPLGGILAQTGSGGSMTLTASDGKTGQRVSLFAKPLLAEQTL
	130 140 150 160 170 180
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
g299	TVNGNTVSANGGGWQVLDTGAAALPLAIQTTEMPWDIGFINIENPAGGITVSAMGINGAQLT
	190 200 210 220 230 240
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
g299	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI
	250 260 270 280 290 300
m299.pep	LIIGAPESLKNLTGVCGTRPVRLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
g299	LIIGAPESLKNLTGVCGTRPVLLTEVQQMQRVARQGQTMFWSWQNAMGGICSMKNWLNQ
	310 320 330 340 350 360
m299.pep	GWAAKDGVHFSAKGYRRAEMLADSLEELVRSAAIRQX
	370 380 390
g299	GWAAKDGVHFSAQGYRRAEMLADSLEELVRAAAIRQX
	370 380 390

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1251>:

```

a299.seq
1  ATGAACCCCA AACACCTCAT CGCATTTTCC GCCCTATTTCG CCGCCACGCA
51  GGCAGAAGCC CTACCTGTCG CCTCAGTCAG CCTCGACACC GTTACCGTTT
101 CCCCGTCCGC CCCCTACACC GATACAAACG GGCTGCTGAC CGACTACGGC
151 AACGCCTCCG CCTCGCCTTG GATGAAAAAA CTCCAATCCG TCGCACAAAG
201 CAGCGGCGAG ACCTTCCGTA TCCTGCAAAAT CGGCGACTCG CATACCGCCG
251 GCGACTTCTT TACCGACAGC CTGCGCAAAC GCCTACAAAA AACTTGGGGC
301 GACGGCGGCA TAGGCTGGGT TTACCCCGCC AACGTCAAAG GGCAGCGCAT
351 GGC GGCCGTC CGGCACAACG GTA ACTGGCA AAGCCTCACC AGCAGGAACA
401 ACACCGGAGA CTTC CCGCTC GCGGCATCC TCGCCACAC CCGCAGCGGC
451 GGCAGCATGA CCCTGACCGC ATCGGACGGC ATAGCAAGCA AGCAGCGCGT
501 TTCCCTGTTT GCCAAACCCC TGCTTGCCGA ACAAACCCTG ACCGTCAACG
551 GCAACACCGT CTCCGCCAAC GCGGCGGCT GGCAGGTA CTGGATACGGGC
601 GCGGCACTGC CCCTGACCAT ACACACCGAA ATGCCGTGGG ACATCGGCTT
651 CATCAACATC GAAAATCCCG CCGGCGGCAT TACCGTTTCC GCGATGGGCA
701 TCAACGCGC ACAATTAACC CAGTGGTCGA AATGGCGTGC CGACCGTATG
751 AACGACCTTG CCCAAACCGG CGCCGATCTA GTCATCCTTG CCTACGGTAC
801 CAACGAAGCC TTCGGCGACA ACATCGACAT TGCCGATACC GAACAGAAAT
851 GGCTGGATAC CGTCCGCCAA ATCCGCGACA GCCTACCTGC CGCCGGCATC
901 CTCATCATCG GCGCGCCCGA ATCCCTGAAA AACACGCTCG GCGTATGCGG
951 CACACGCCCC GTCCGCCTGA CCGAAGTCCA ACAGATGCAG CGGCGCATCG
1001 CCCGT CAGGG GCAGACGATG TTCTGGTCTT GGCAAAACGC GATGGGCGGC
1051 GTTTGCAGCA TGAAAACTG GCTCAACCAC GGATGGGCCG CCAAAGACGG
1101 CGTACACTTT TCCGCCAAAG GCTACCAACG GTCGGCGGAA ATGCTCGCCG
1151 ACAGCCTCGA AGA ACTCGTC CGCTCCGCTG CAATCAGGCA ATAA

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This corresponds to the amino acid sequence <SEQ ID 1252; ORF 299.a>:

```
a299.pep
1  MNPKHIAFS ALFAATQAEA LPVASVSLDT VTVSPSAPYT DTNGLLTDYG
51  NASASPWMKK LQVAQGSGE TFRILQIGDS HTAGDFFTD LKRLQKTWG
101 DGGIGWVYPA NVKGQMAAV RHNGNWQSLT SRNNTGDFPL GGILAHTGSG
151 GSMTLTASDG IASKQRVSLF AKPLLAEQTL TVNGNTVSAN GGGWQVLDTG
201 AALPLTIHTE MPWDIGFINI ENPAGGITVS AMGINGAQLT QWSKWRADRM
251 NDLAQTGADL VILAYGTNEA FGDNIDIADT EQKWLDTVRQ IRDSLPAAGI
301 LIIGAPESLK NTLGVCGRP VRLTEVQQMQ RRIARQGQTM FWSWQNAMGG
351 VCSMKNLNLH GWAAKDGVHF SAKGYQRSAE MLADSLEELV RSAAIRQ*
```

m299/a299 98.0% identity in 397 aa overlap

	10	20	30	40	50	60
m299.pep	MNPKHIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
a299	MNPKHIAFSALFAATQAEALPVASVSLDTVTVSPSAPYTDNGLLTDYGNASASPWMKK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m299.pep	LQVAQGSGETFRILOIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQMAAV					
a299	LQVAQGSGETFRILOIGDSHTAGDFFDLSLRKRLQKTWGDGGIGWVYPANVKGQMAAV					
	70	80	90	100	110	120
	130	140	150	160	170	180
m299.pep	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL					
a299	RHNGNWQSLTSRNNTGDFPLGGILAHTGSGGSMTLTASDGIASKQRVSLFAKPLLAEQTL					
	130	140	150	160	170	180
	190	200	210	220	230	240
m299.pep	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
a299	TVNGNTVSANGGGWQVLDTGAAALPLTIHTEMPWDIGFINIENPAGGITVSAMGINGAQLT					
	190	200	210	220	230	240
	250	260	270	280	290	300
m299.pep	QWSKWRADRMNDLAQTGADLVILSYGTNEAFNNNIDIADTEQKWLDTVRQIRDSLPAAGI					
a299	QWSKWRADRMNDLAQTGADLVILAYGTNEAFNGDNIDIADTEQKWLDTVRQIRDSLPAAGI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m299.pep	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRVARQGQTMFWSWQNAMGGICSMKNWLNQ					
a299	LIIGAPESLKNTLGVCGRTPVRLTEVQQMQRRRIARQGQTMFWSWQNAMGGVCSMKNLNLH					
	310	320	330	340	350	360
	370	380	390			
m299.pep	GWAAKDGVHFSAGGYRRAEMLADSLEELVRSAAIRQX					
a299	GWAAKDGVHFSAGGYQRSAEMLADSLEELVRSAAIRQX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1253>:

```
g302.seq
1  ATGCACTCAA TATATTTTT TAAGGAGAAG CAGATGAGTC AAACCGACGC
51  GCGTCGTAGC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGTCC
201 TGTGGGGCG AAAGGACGTG CCGATGACGG TTTGATTCAC GTTGTACGCC
251 TGCTCGATGC CGACGGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGAACGGTG TTGGTTCTT TATTGGGCGT
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351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC CCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCCA ATACGGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCGGTC ATCTTTCATT CGCTCGGCCG CCATCCGCTT GCCGGTTTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAA
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 CAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGGCATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTGGGGC AGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCCGACGG TATTTTGCCT CATCCTGAAA CAGGATTGGT
951 TGCCGGTTCG CCGTTTTTAA AATCGATTGT TGTTTTTATT TTCTTGTGT
1001 TTGCGCTGCC GGCATTGTT TATGGCCGGA TAACCCGAAG TTTGCGCGGC
1051 GAACGGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTTTGGGACT
1101 TTATTGGTTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGGCGGT GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG TGTGTTGTTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCGTCCTT ATGCTGATGT TGGCCGGCTA CGCGCCCCAA
1351 GTCATTCAAG CCGCTTACCG CATCGGTGAT TCCGTTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTTC GGCTGATTAT GGCGACGGTA ATCAAATACA
1451 AAAAAGATGC GGGCGTAGGC ACGCTGATTT CTATGATGTT GCCGTATTCC
1501 GCTTCTTCT TAATTGCATG GATCGCCTTA TCTGCATTT GGGTATTTGT
1551 TTTGGGTCTG CCCGTCGGTC CCGGCACACC CACATTCTAT CCGGTGCCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1254; ORF 302.ng>:

g302.pep

```

1 MHSIYFFKEK QMSQTDARRS GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51 ASAVGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILTHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSLGISALM RLLLTSPRK LTFMVVFTG
151 ILSNTASELG YVVLIPLSAV IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQQAQIIHP DYVVGPEANW FFMAASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVAGS PFLKSIVVFI FLLFALPGIV YGRITRSLRG
351 EREVVNAMAE SMSTLGLYLV IIFFAAQFVA FFWNTNIGQY IAVKGAFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPQ
451 VIQAAYRIGD SVTNITPMM SYFGLIMATV IKYKKDAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGTPTFY PVP*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1255>:

m302.seq

```

1 ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51 GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCATCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG TCGGTGCGTA TTTCGGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTTGGTGCG AAAGGACGTG CCGATGACGG TTTGATTTAC ATTGTCAGCC
251 TGCTCAATGC CGACGGTTTT ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGGCGT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAAATG CGCTTATTGC
401 TCACAAAATC GCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCCGGCGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 AGCACAATCG ATCCGCTCTT GGCATGCATC ACCCATCAGG CGGCGGTCTG
651 AGGCCCTGAA GCCAACTGGT TTTTATGGT AGCCAGTACG TTTGTGATTG
701 CTTTGATTGG TTATTTTGTG ACTGAAAAAA TCGTCGAACC GCAATTGGGC
751 CTTTATCAAT CAGATTTGTC ACAAGAAGAA AAAGACATTC GCATTCCAA
801 TGAAATCACG CCTTTGGAAT ATAAAGGATT AATTTGGGCT GGCGTGGTGT
851 TTGTTGCCTT ATCCGCCCTA TTGGCTTGGA GCATCGTCCC TGCCGACGGT
901 ATTTTGCCTC ATCCTGAAAC AGGATTGGTT TCCGGTTCGC CGTTTTTAA
951 ATCGATTGTT GTTTTTATTT TCTTGTGTT TGCACTGyCG GGCmTTGTTT
1001 ATGmCGGGT AACCCGAAGT TTGCGCGGCG AACAGGAAGT CGTTAATGCG

```

1051	ATGGCCGAAT	CGATGAGTAC	TCTGGsGCTT	TmTTTGswCA	kcATCTTTTT
1101	TGCCGCACAG	TTTGTGCGAT	TTTTTAATTG	GACGAATATT	GGGCAATATA
1151	TTGCCGTAA	AGGGGCGACG	TTCTTAAAAG	AAGTCGGCTT	GGGCGGCAGC
1201	GTGTTGTTTA	TCGGTTTTAT	TTTAATTTGT	GCTTTTATCA	ATCTGATGAT
1251	AGGCTCCGCC	TCCGCGCAAT	GGGCGGTAAC	TGCGCCGATT	TTCGTCCCTA
1301	TGCTGATGTT	GGCCGGCTAC	GCGCCCGAAG	TCATTCAAGC	CGCTTACCGC
1351	ATCGGTGATT	CCGTATACCA	TATTATTACG	CCGATGATGA	GTTATTTTCGG
1401	GCTGATTATG	GCGACGGTGA	TCAAATACAA	AAAAGATGCG	GGCGTGGGTA
1451	CGCTGATTTT	TATGATGTTG	CGTATTCCG	CTTCTCTCTT	GATTGCGTGG
1501	ATTGCCTTAT	TCTGCATTTG	GGTATTTGTT	TTGGGCCTGC	CCGTGCGTCC
1551	CGGCGCGCCC	ACATTCTATC	CCGCACCTTA	A	

m302.ppt

1	MHSIYFFKEK	QMSQTDTRD	GRFLRTVEWL	GNMLPHPVTL	FIIFIVLLLI
51	<u>ASAVGAYFGL</u>	SVPDRPVGA	KGRADDGLIY	IVSLLNADGF	IKILTHTVKN
101	<u>FTGFAPLGTV</u>	<u>LVSLLGVGIA</u>	EKSGLISALM	RLLLTSPRK	LTTFMVFTG
151	<u>ILSNTASELG</u>	<u>YVVLIPLSAI</u>	<u>IFHSLGRHPL</u>	AGLAAAFAGV	SGGYSANLFL
201	STIDPELLACI	THQAAVVGPE	ANWFFMVAST	FVIALIGYFV	TEKIVEPQLG
251	PYQSDLSQEE	KDIRHSNEIT	PLEYKGLIWA	GVVFVALSAL	LAWSIVPADG
301	ILRHPETGLV	SGSPFLKSIV	VFIFLLFALX	GXVYGRVTRS	LRGEQEVVNA
351	MAESMSTLXL	<u>XLXXIFFAAQ</u>	<u>FVAFFWNWTNI</u>	GOYIAVKGAT	FLKEVGLGGS
401	<u>VLFIGILICL</u>	<u>AFINLMIGSA</u>	<u>SAQAVWTAPI</u>	FVPMLMLAGY	APEVIOAAYR
451	IGDSVTNIIT	PMSYFGLMI	ATVIKYKDA	GVGTLISMML	<u>PYSAFFLIAW</u>
501	IALFCIWVVFV	LGLPVGPGAP	TFYPAP*		

Homology with a predicted ORF from *N. gonorrhoeae*

m302/g302

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	TQRDGRFLRTVEWL	GNMLPHPVTLF	IIFIVLLLIASAV	GAYFGL	
g302	MHSIYFFKEKQMSQTD	ARRSGRFLRTVEWL	GNMLPHPVTLF	IIFIVLLLIASAV	GAYFGL	
	10	20	30	40	50	60
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADGFI	KILTHTVKNFTGFAP	LGTVLVSL	LGVGIA	
g302	SVPDPRPVGAKGRADD	GLIHVVSLLDADGLI	KILTHTVKNFTGFAP	LGTVLVSL	LGVGIA	
	70	80	90	100	110	120
	130	140	150	160	170	180
m302.pep	EKSGLISALMRL	LLTKSPRKL	TTFMVFTGIL	SNTASELGYV	VLIPLSAI	I FHS
g302	EKSGLISALMRL	LLTKSPRKL	TTFMVFTGIL	SNTASELGYV	VLIPLSAVI	FHS
	130	140	150	160	170	180
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGY	SANLFLSTID	PLLACITHQAA	-----	VVGPEANWFF	MVASTFVI
g302	AGLAAAFAGVSGGY	SANLFLGTID	PLLAGITQQA	QAIHPDPYV	VVGPEANWFF	MAASTFVI
	190	200	210	220	230	240
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVE	PQLGPYQSDLS	QEEKDIRHSNEI	TPLEYKGLIWAG	VVVFVALS	ALLAW
g302	ALIGYFVTEKIVE	PQLGPYQSDLS	QEEKDIRHSNEI	TPLEYKGLIWAG	VVVFVALS	ALLAW
	250	260	270	280	290	300
	300	310	320	330	340	350

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m302.pep	SIVPADGILRHPETGLVSGSPFLKSI	VVFIFLLFALXGXVYGRVTRSLRGEQEVVNAMAE
g302	SIVPADGILRHPETGLVAGSPFLKSI	VVFIFLLFALPGIVYGRITRSLRGEREVVNAMAE
	310 320 330 340 350 360	
m302.pep	SMSTLXLXLXIIFFAAQFVAFFNWTNIGQYIAVKGATFLKEVGLGGSVLFIFIGILICAFI	
g302	SMSTLGLYLVIIFFAAQFVAFFNWTNIGQYIAVKGAVFLKEVGLGGSVLFIFIGILICAFI	
	360 370 380 390 400 410	
m302.pep	NLMIGSASAQWAVTAPIFVPMMLLAGYAPEVIQAAYRIGDSVTNIIITPMMSYFGLIMATV	
g302	NLMIGSASAQWAVTAPIFVPMMLLAGYAPQVIQAAYRIGDSVTNIIITPMMSYFGLIMATV	
	420 430 440 450 460 470	
m302.pep	IKYKKDAGVGTLSMMLPYSAFFLIWIALFCIWVFLGLPVGPGAPTFFYPAPX	
g302	IKYKKDAGVGTLSMMLPYSAFFLIWIALFCIWVFLGLPVGPGTPTFFYPVPX	
	480 490 500 510 520	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1257>:

```

a302.seq
1  ATGCACTCAA TATATTTTTT TAAGGAGAAG CAGATGAGTC AAACCGATAC
51  GCAACGGGAC GGACGATTTT TACGCACAGT CGAATGGCTG GGCAATATGT
101 TGCCGCACCC GGTACGCTT TTTATTATTT TCATTGTGTT ATTGCTGATT
151 GCCTCTGCCG CCGGTGCGTA TTTTCGACTA TCCGTCCCCG ATCCGCGCCC
201 TGTGTGTGCG AAAGGACGTG CCGATGACGG TTTGATTAC GTTGTCAGCC
251 TGCTCGATGC TGACGTTTG ATCAAAATCC TGACGCATAC CGTTAAAAAT
301 TTCACCGGTT TCGCGCCGTT GGGAACGGTG TTGGTTTCTT TATTGGCGCT
351 GGGGATTGCG GAAAAATCGG GCTTGATTTC CGCATTAATG CGCTTATTGC
401 TCACAAAATC TCCACGCAAA CTCACTACTT TTATGGTTGT TTTTACAGGG
451 ATTTTATCTA ATACCGCTTC TGAATTGGGC TATGTCGTCC TAATCCCTTT
501 GTCCGCCATC ATCTTTCATT CCCTCGGCCG CCATCCGCTT GCCGGTCTGG
551 CTGCGGCTTT CGCGGCGGTT TCGGGCGGTT ATTCGGCCAA TCTGTTCTTA
601 GGCACAATCG ATCCGCTCTT GGCAGGCATC ACCCAACAGG CGGCGCAAT
651 CATCCATCCC GACTACGTCG TAGGCCCTGA AGCCAACTGG TTTTATATGG
701 TAGCCAGTAC GTTTGTGATT GCTTTGATTG GTTATTTTGT TACTGAAAAA
751 ATCGTCGAAC CGCAATTGGG CCCTTATCAA TCAGATTGTG CACAAGAAGA
801 AAAAGACATT CGACATTCCA ATGAAATCAC GCCTTTGGAA TATAAAGGAT
851 TAATTTGGGC TGGCGTGGTG TTTGTTGCCT TATCCGCCCT ATTGGCTTGG
901 AGCATCGTCC CTGCGCAGCG TATTTTGCCT CATCTGAAA CAGGATTGGT
951 TTCCGGTTCT CCGTTTTTAA AATCAATTGT TGTTTTATT TTCTTGTGT
1001 TTGCACTGCC GGGCATTGTT TATGGCCGGG TAACCGAAG TTTGCGCGGC
1051 GAACAGGAAG TCGTTAATGC GATGGCCGAA TCGATGAGTA CTCTGGGGCT
1101 TTATTTGGTC ATCATCTTTT TTGCCGCACA GTTTGTCGCA TTTTAAATT
1151 GGACGAATAT TGGGCAATAT ATTGCCGTTA AAGGGCGGAC GTTCTTAAAA
1201 GAAGTCGGCT TGGGCGGCAG CGTGTGTGTT ATCGGTTTTA TTTTAATTTG
1251 TGCTTTTATC AATCTGATGA TAGGCTCCGC CTCCGCGCAA TGGGCGGTAA
1301 CTGCGCCGAT TTTCTGCCCT ATGCTGATGT TGGCCGGCTA CGCGCCCGAA
1351 GTCATTCAAG CCGTTACCG CATCGGTGAT TCCGTACCA ATATTATTAC
1401 GCCGATGATG AGTTATTTCT GGCTGATTAT GGCGACGGTG ATCAAATACA
1451 AAAAAGATGC GGGCGTGGGT ACGCTGATTT CTATGATGTT GCCGTATTC
1501 GCTTTCTTCT TGATTGCGTG GATTGCCTTA TTCTGCATT GGGTATTTGT
1551 TTTGGGCCTG CCCGTCGGTC CCGGCGCGCC CACATTCTAT CCCGCACCTT
1601 AA

```

This corresponds to the amino acid sequence <SEQ ID 1258; ORF 302.a>:

```

a302.pep
1  MHSIYFFKEK QMSQTDTORQ GRFLRTVEWL GNMLPHPVTL FIIFIVLLLI
51  ASAAGAYFGL SVPDPRPVGA KGRADDGLIH VVSLLDADGL IKILHTVKN
101 FTGFAPLGTV LVSLLGVGIA EKSGLISALM RLLLTSPRK LTTFMVFTG

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151 ILSNTASELG YVVLIPLSAI IFHSLGRHPL AGLAAAFAGV SGGYSANLFL
201 GTIDPLLAGI TQAAQIIHP DYVVGPEANW FFMVASTFVI ALIGYFVTEK
251 IVEPQLGPYQ SDLSQEEKDI RHSNEITPLE YKGLIWAGVV FVALSALLAW
301 SIVPADGILR HPETGLVSGS PFLKSIVVFI FLLFALPGIV YGRVTRSLRG
351 EQEVVNAMAE SMSTLGLYLV IIFFAAQFVA FFNWTNIGQY IAVKGATFLK
401 EVGLGGSVLF IGFILICAFI NLMIGSASAQ WAVTAPIFVP MLMLAGYAPE
451 VIQAAYRIGD SVTNIITPMM SYFGLIMATV IKYKKGAGVG TLISMMLPYS
501 AFFLIAWIAL FCIWVFLGL PVGPGAPTFY PAP*

```

m302/a302 96.1% identity in 533 aa overlap

	10	20	30	40	50	60
m302.pep	MHSIYFFKEKQMSQTD	QDRGRFLRTVEWLG	NMLPHPVTLFII	FIVLLLIASAV	GAYFGL	
a302	MHSIYFFKEKQMSQTD	QDRGRFLRTVEWLG	NMLPHPVTLFII	FIVLLLIASA	AAGAYFGL	
	70	80	90	100	110	120
m302.pep	SVPDPRPVGAKGRADD	GLIYIVSLLNADG	FIKILHTVKNFT	GFAPLGTVLVS	LLGVGIA	
a302	SVPDPRPVGAKGRADD	GLIHVVSLLDADG	LILHTVKNFT	GFAPLGTVLVS	LLGVGIA	
	130	140	150	160	170	180
m302.pep	EKSGLISALMRLLLT	TKSPRKLTFMVVFT	GILSNTASELG	YVVLIPLSAI	IFHSLGRHPL	
a302	EKSGLISALMRLLLT	TKSPRKLTFMVVFT	GILSNTASELG	YVVLIPLSAI	IFHSLGRHPL	
	190	200	210	220	230	
m302.pep	AGLAAAFAGVSGGYS	ANLFLSTIDPL	LACITHQAA-----	VVGPEANW	FFMVASTFVI	
a302	AGLAAAFAGVSGGYS	ANLFLGTIDPL	LAGITQAAQIIHP	DYVVGPEANW	FFMVASTFVI	
	240	250	260	270	280	290
m302.pep	ALIGYFVTEKIVEP	QLGPYQSDLSQ	EEDIRHSNEIT	PLEYKGLIWAG	VVFVALSALLAW	
a302	ALIGYFVTEKIVEP	QLGPYQSDLSQ	EEDIRHSNEIT	PLEYKGLIWAG	VVFVALSALLAW	
	300	310	320	330	340	350
m302.pep	SIVPADGILRHPET	GLVSGSPFLKS	IVVFI FLLFAL	GXVYGRVTR	SLRGEQEVVNAMAE	
a302	SIVPADGILRHPET	GLVSGSPFLKS	IVVFI FLLFAL	PGIVYGRVTR	SLRGEQEVVNAMAE	
	360	370	380	390	400	410
m302.pep	SMSTLXLXLXII	FFAAQFVAFFN	WTNIGQYIAV	KGATFLKEV	GLGGSVLF	IGFILICAFI
a302	SMSTLGLYLVII	FFAAQFVAFFN	WTNIGQYIAV	KGATFLKEV	GLGGSVLF	IGFILICAFI
	420	430	440	450	460	470
m302.pep	NLMIGSASAQWAV	TAPIFVPM	LMLAGYAPEVI	QAAYRIGD	SVTNIITP	MMSYFGLIMATV
a302	NLMIGSASAQWAV	TAPIFVPM	LMLAGYAPEVI	QAAYRIGD	SVTNIITP	MMSYFGLIMATV
	480	490	500	510	520	
m302.pep	IKYKKGAGVGT	LISMMLPYSA	FFLIAWIAL	FCIWVFLGL	PVGP	GAPTFYPAPX
a302	IKYKKGAGVGT	LISMMLPYSA	FFLIAWIAL	FCIWVFLGL	PVGP	GAPTFYPAPX
	490	500	510	520	530	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1259>:

699

g305.seq

```

1 ATGGATTTTT TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CGGTTTGGC GGTAGTGTG GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTTCGTCC
251 TCAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GACAAACAAA TCAAAGAGTA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GTGTGCCCCA AGTGTGTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGGTTATGG GCGGGATGCT TTGGGGAAATC GAGCGGAAAA
551 CGGCAACGGA GTTTCATTT TTCTTGCCCG TTCCGATGAT GGTTGCAGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATAGGCT TTATTGCCGC TTTTGTTCCT GGTTTGGTAG
701 CGGTTAAAGC ACTGCTGAAG TTTGTTTCCA AGAAAACTA TATCCCGTTT
751 GCCTATTACC GCATTGTTTT CGGCATTGTC ATCATAATAT TGTGGTTGTC
801 GGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1260; ORF 305.ng>:

g305.pep

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFSNVL HGVGKDRKAN RFVLNLIAIF IPAAVMGLLF
101 DKQIKEYLFN PLSVAVMLVL GGFILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TVMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLK FVSKKNYIPF
251 AYYRIVFGIV IILWLSGWI SWE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1261>:

m305.seq (partial)

```

1 AtGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51 TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTCCG
101 GCAATCTGAT TGGTTTTCAC AGCAATCACA AGGTTTTTGA AATTGCCATC
151 CAGCTCGGTG CAGTTTGGC GGTAGTGTG GAATACCGGC AACGTTTCAG
201 CAATGTGTTG CACGGCTTGG GAAAAGACCG GAAAGCCAAC CGCTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAWACAAA TCAAAGAGyA TCTGTTTAAAC CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTyTG GrCGGTTTTT yTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGCC GATGTTGATG CATTGCGTCC GATTGATGCC
451 TTGATGATCG GCGTTGCCCA AGTGTGTGCA CTGGTTCCGG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGCATC GAACGGAAAA
551 CTGCGACAGA ATTCTCGTTT TTCTTGCTG TGCCGATGAT GGTTGCCGCA
601 ACGGCTTATG ATGTCCTGAA ACATTACCGA TTTTTCACCC TGCATGATGT
651 CGGTTTGATT CTGATAGGCT TTATTGCTGC CTTTGTTCCTA GGCTTGGTAG
701 CGGTAAGAGC GTTGCTGAGG TTTGTTTCGG GTAC...

```

This corresponds to the amino acid sequence <SEQ ID 1262; ORF 305>:

m305.pep (partial)

```

1 MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIGFH SNHKVFEIAI
51 QLGAVLAVVF EYRQRFSNVL HGLGKDRKAN RFVLNLIAIF IPAAVMGLLF
101 GXQIKEXLFN PLSVAVMLVL XGFXILWVEK RQSRAPKIA DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHYR FFTLHDVGLI LIGFIAAFVS GLVAVKALLR FVSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 305 shows 96.7% identity over a 243 aa overlap with a predicted ORF (ORF 305.ng) from *N. gonorrhoeae*:

g305/m305

```

          10      20      30      40      50      60
g305.pep  MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          |||||
m305      MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEIAIQLGAVLAVVF
          10      20      30      40      50      60

```

700

	70	80	90	100	110	120
g305.pep	EYRQRFNSVLHGVGKDRKANRFVNLNLAIAFIPAAVMGLLFDKQIKEYLFNPLSVAVMLVL					
	:					
m305	EYRQRFNSVLHGLGKDRKANRFVNLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	70	80	90	100	110	120
	130	140	150	160	170	180
g305.pep	GGFFILWVEKQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTVMGGMLWGI					
	:					
m305	XGFXILWVEKQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMLWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
g305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLK					
	:					
m305	ERKTATEFSFFLAVPMMVAATAYDVLKHRYFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
	190	200	210	220	230	240
	250	260	270			
g305.pep	FVSKKNYIPFAYYRIVFGIVIIILWLSGWISWEX					
m305	FVSG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1263>:

```

a305.seq
1  ATGGATTTTC TGATTGTCCT GAAAGCCCTG ATGATGGGCT TGGTAGAAGG
51  TTTTACCGAA TTTTACCGA TTTCCAGCAC CGGACATTG ATTGTGTTTCG
101 GCAATCTGAT TGATTTTCAC AGCAATCACA AGGTTTTTGA AATTACCATC
151 CAGCTCGGTG CGGTTTTGGC GGTAGTGTTC GAATACCGGC AGCGTTTCAG
201 CAATGTGTTG CATGGCGTGG GAAAAGACCG GAAAGCCAAC CGTTCGTCC
251 TTAATCTTGC CATTGCTTTT ATACCTGCCG CCGTGATGGG GCTGTTGTTC
301 GGCAACAAA TCAAAGAGTA TCTGTTTAA CCCTTGAGTG TTGCAGTCAT
351 GCTGGTTTG GCGGTTTTT TTATTTTGTG GGTGGAGAAA CGCCAAAGCC
401 GAGCAGAGCC TAAAATTGTC GATGTTGATG CATTGCGTCC GATTGATGCG
451 TTGATGATCG GCGTTGCCA AGTGTGTTGCA CTGGTTCCAG GTACGTCCCG
501 TTCGGGCAGT ACGATTATGG GCGGGATGCT TTGGGGAATC GAGCGGAAAA
551 CGGCAACGGA GTTTTCATTT TTCTTGSCCG TTCCGATGAT GGTGACAGCA
601 ACGGCTTATG ATGCTCTGAA GCATTACCGG TTTTTCACCC TGCATGATGT
651 CGGTTTGATT TTGATTGGCT TTGTTGCTGC CTTTGTTCCTA GGCTTGGTGG
701 CGGTCAAAGC GTTGCTGAGG TTTGTTTCCA AGAAAAATTA TATTCCTTTT
751 GCCTATTACC GCATTGTTTT TGGTATTGCC ATCATTATAT TGTGGCTGTC
801 AGGCTGGATA AGTTGGGAAT GA

```

This corresponds to the amino acid sequence <SEQ ID 1264; ORF 305.a>:

```

a305.pep
1  MDFLIVLKAL MMGLVEGFTE FLPISSSTGHL IVFGNLIDFH SNHKVFEITI
51  QLGAVLAVVF EYRQRFNSVL HGVGKDRKAN RFVNLNLAIAF IPAAVMGLLF
101 GKQIKEYLFN PLSVAVMLVL GGFILWVEK QSRAPKIV DVDALRPIDA
151 LMIGVAQVFA LVPGTSRSGS TIMGGMLWGI ERKTATEFSF FLAVPMMVAA
201 TAYDVLKHRY FFTLHDVGLI LIGFVAAFVS GLVAVKALLR FVSKKNYIPF
251 AYYRIVFGIA IILWLSGWI SWE*

```

m305/a305 96.3% identity in 243 aa overlap

	10	20	30	40	50	60
m305.pep	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIGFHSNHKVFEITAIQLGAVLAVVF					
	:					
a305	MDFLIVLKALMMGLVEGFTEFLPISSSTGHLIVFGNLIDFHSNHKVFEITAIQLGAVLAVVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m305.pep	EYRQRFNSVLHGLGKDRKANRFVNLNLAIAFIPAAVMGLLFGXQIKEXLFNPLSVAVMLVL					
	:					
a305	EYRQRFNSVLHGVGKDRKANRFVNLNLAIAFIPAAVMGLLFGXQIKEYLFNPLSVAVMLVL					

701

	70	80	90	100	110	120
	130	140	150	160	170	180
m305.pep	XGFXILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMWGI					
a305	GGFFILWVEKRQSRAPKIDVDALRPIDALMIGVAQVFALVPGTSRSGSTIMGGMWGI					
	130	140	150	160	170	180
	190	200	210	220	230	240
m305.pep	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFIAAFVSGLVAVKALLR					
a305	ERKTATEFSFFLAVPMMVAATAYDVLKHYRFFTLHDVGLILIGFVAAAFVSGLVAVKALLR					
	190	200	210	220	230	240
m305.pep	FVSG					
a305	FVSKKNYIPFAYYRIVFGIAIILWLSGWISWEX					
	250	260	270			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1265>:

```

g306.seq
1   ATGTTTATGA  ACAAATTTTC  CCAATCCGGA  AAAGGTCTGT  CCGGTTTCTT
51  CTTCGGTTTG  ATACTGGCAA  CGGTCATTAT  TGCCGGTATT  TTGCTTTATC
101 TGAACCAGGG  CGGTCAAAAT  GCGTTCAAAA  TCCCGGCTCC  GTCGAAGCAG
151 CCTGCAGAAA  CGGAAATCCT  GAAACTGAAA  AACCAGCCTA  AGGAAGACAT
201 CCAACCTGAA  CCGGCCGATC  AAAACGCCTT  GTCCGAACCG  GATGTTGCGA
251 AAGAGGCAGA  GCAGTCGGAT  GCGGAAAAAG  CTGCCGACAA  GCAGCCCGTT
301 GCCGACAAAG  CCGACGAGGT  TGAAGAAAAG  GCGGCGGAGC  CGGAACGGGA
351 AGAGCCGGAC  GGACAGGCAG  TGCGCAAGAA  AGCACTGACT  GAAGAGCGTG
401 AACAAACCGT  CAGGGAAAAA  GCGCAGAAGA  AAGATGCCGA  AACGGTTAAA
451 AAAAAAGCGG  TAAAACCGTC  TAAAGAAACA  GAGAAAAAAG  CTTCAAAAAG
501 AGAGAAAAAG  GCGGCGAAAG  AAAAAGTTGC  ACCCAAACCG  ACCCCGGAAC
551 AAATCCTCAA  CAGCCGCAGT  ATCGAAAAAG  CGCGTAGTGC  CGCTGCCAAA
601 GAAGTGCAGA  AAATGAAAAA  CTTTGGGCAA  GGCGGAAGCC  AACGCATTAT
651 CTGCAAATGG  GCGCGTATGC  CGAACCCCGG  AGCGCGGAAG  GGCAGCGTGC
701 CAAACTGGCA  ATCTTGGGCA  TATCTTCCGA  AGTGGTCGGC  TATCAGGCGG
751 GACATAAAAC  GCTTTACCGC  GTGCAAAGCG  GCAATATGTC  CGCCGATGCG
801 GTGA

```

This corresponds to the amino acid sequence <SEQ ID 1266; ORF 306.ng>:

```

g306.pep
1   MFMNKFQSG  KGLSGFFFGL  ILATVIIAGI  LLYLNQGGQN  AFKIPAPSKQ
51  PAETEILKLK  NQPKEDIQPE  PADQNALSEP  DVAKEAEQSD  AEKAADKQPV
101 ADKADEVEEK  AGEPEREEDP  GQAVRKKALT  EEREQTVREK  AQKKDAETVK
151 KKAVKPSKET  EKKASKEEKK  AAKEKVAPKP  TPEQILNSRS  IEKARSAAAK
201 EVQKMNFGQ  GGSQRIICKW  ARMPNPGARK  GSVPNWQSWA  YLPKWSAIRR
251 DIKRFTACKA  AICPPMR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1267>:

```

m306.seq (partial)
1   ..GGTTTGTCT  TCGGTTTGAT  ACTGGCGACG  GTCATTATTG  CCGGTATTTT
51  GTTTTATCTG  AACCAGAGCG  GTCAAAATGC  GTCAAAATC  CCGGCTTCGT
101 CGAAGCAGCC  TGCAGAAACG  GAAATCCTGA  AACCGmAawA  CCAGCyTAAG
151 GAAGACATCC  AACCTGawCC  GGCCGATCAA  AACGCCTTGT  CCGAACCGGA
201 TGCTGCGACA  GAGGCAGAGC  AGTCGGATGC  GGAAAawGCT  GCCGACAAGC
251 AGCCCGTTGC  CGATAAAGCC  GACGAGGTTG  AAGAAAAGGC  GGGCGAGCCG
301 GAACGGGAAG  AGCCGGACGG  ACAGGCAGTG  CGTAAGAAAG  CGCTGACGGA
351 AGAGCGTGAA  CAAACCGTCA  GGGAAAAAGC  GCAGAAGAAA  GATGCCGAAA
401 CGGTTAAAaw  ACAAGCGGTA  AAACCGTCTA  AAGAAACAGA  GAAAAAAGCT
451 TCAAAAGAAG  AGAAAAAGGC  GGCGAAGGAA  AAAGTTGCAC  CCAAACCAAC
501 CCCGGAACAA  ATCCTCAACA  GCGGCAGCAT  CGAAAAAGCG  CGCAGTGCCG
551 CCGCCAAAGA  AGTGCAGAAA  ATGAAAACGC  CGACAAGGCG  GAAGCAACGC

```

702

```

601   ATTATCTGCA AATGGGCGCG TATGCCGACC GTCAGAGCGC GGAAGGGCAG
651   CGTGCCAAAC TGGCAATCTT GGGCATATCT TCCAAGGTGG TCGGTTATCA
701   GGCGGGACAT AAAACGCTTT ACCGGGTGCA AAGCGGCAAT ATGTCTGCCG
751   ATGCGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1268; ORF 306>:

```

m306.pep (partial)
  1   ..GLFFGLILAT VVIAGILFYLNQSGQNAFKI PASSKQPAET EILKPXNQXK
 51   EDIQXPADQ NALSEPDAAT EAEQSDAEXA ADKQPVADKA DEVEEKAGEP
101   EREEPDGQAV RKKALTEERE QTVREKAQKK DAETVKXQAV KPSKETEKKA
151   SKEEKKAAKE KVAPKPTPEQ ILNSGSIEKA RSAAAKEVQK MKTPTRRKQR
201   IICKWARMPT VRARKGSVPN WQSWAYLPRW SVIRRDIKRF TGCKAAICLP
251   MR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 306 shows 88.9% identity over a 253 aa overlap with a predicted ORF (ORF 306.ng) from *N. gonorrhoeae*:

```

m306/g306

          10      20      30      40
m306.pep      GLFFGLILATVVIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306      MFMNKFSQSGKLSGFFFLILATVVIAGILLYLNQGGQNAFKIPAPSKQPAETEILKLK
          10      20      30      40      50      60

          50      60      70      80      90      100
m306.pep      NQXKEDIQXPADQNALSEPDAATEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306      NQPKEDIQPEPADQNALSEPDAEAEQSDAEKAADKQPVADKADEVEEKAGEPEREEDP
          70      80      90      100      110      120

          110     120     130     140     150     160
m306.pep      GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306      GQAVRKKALTEEREQTVREKAQKKDAETVKKAVKPSKETEKKASKEEKKAAKEKVAPKP
          130     140     150     160     170     180

          170     180     190     200     210     220
m306.pep      TPEQILNSGSIEKARSAAAKEVQKMKTPTRR-KQRIICKWARMPTVRARKGSVPNWQSWA
                |||:|||:|||:|||:|||:|||:|||:|||:|||:|||:|||
g306      TPEQILNSRSIEKARSAAAKEVQKMKNFQGGGSRQRIICKWARMPNPGARKGSVPNWQSWA
          190     200     210     220     230     240

          230     240     250
m306.pep      YLPRWSVIRRDIKRFTGCKAAICLPMRX
                |||:|||:|||:|||:|||:|||
g306      YLPKWSAIRRDIKRFTACKAAICPPMRX
          250     260

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1269>:

```

a306.seq
  1   ATGTTTATGA ACAATTTTC CCAATCCGGA AAAGGTCTGT CCGGTTTTTTT
 51   CTTCGGTTTG ATACTGGCGA CGGTCATTAT TGCCGGTATT TTGTTTTATC
101   TGAACCAGAG CGGTCAAAT GCGTTCAAAA TCCCGGTTCC GTCGAAGCAG
151   CCTGCAGAAA CGGAAATCCT GAAACCGAAA AACCAGCCTA AGGAAGACAT
201   CCAACCTGAA CCGGCCGATC AAAACGCCTT GTCCGAACCG GATGCTGCGA
251   AAGAGGCAGA GCAGTCGGAT GCGGAAAAAG CTGCCGACAA GCAGCCCGTT
301   GCCGACAAAG CCGACGAGGT TGAGGAAAAG GCGGACGAGC CGGAGCGGGA
351   AAAGTCGGAC GGACAGGCAG TGCGCAAGAA AGCACTGACG GAAGAGCGTG
401   AACAAACCGT CGGGGAAAAA GCGCAGAAGA AAGATGCCGA AACGGTTAAA
451   AAACAAGCGG TAAACCATC TAAAGAAACA GAGAAAAAAG CTTCAAAAGA
501   AGAGAAAAAG GCGGAGAAGG AAAAAGTTGC ACCCAAACCG ACCCCGGAAC
551   AAATCCTCAA CAGCGGCAGC ATCGAAAAAG CGCGCAGTGC CGCTGCCAAA

```


703

```

601 GAAGTGCAGA AAATGAAAAC GCCGACAAGG CGGAAGCAAC GCATTATCTG
651 CAAATGGGCG CGTATGCCGA CCGCCGGAGC GCGGAAGGGC AGCGTGCCAA
701 ACTGGCAATC TTGGGCATAT CTTCCAAGGT GGTGGTTAT CAGGCGGGAC
751 ATAAACGCT TTACCGGTG CAAAGCGGCA ATATGTCTGC CGATGCGGTG
801 A

```

This corresponds to the amino acid sequence <SEQ ID 1270; ORF 306.a>:

```

a306.pep
  1 MFMNKFSQSG KGLSGFFFFL ILATVIIAGI LFYLNQSGQN AFKIPVPSKQ
 51 PAETEILKPK NQPKEDIQPE PADQNALSEP DAAKEAEQSD AEKAADKQPV
101 ADKADEVEEK ADEPEREKSD QQAVRKKALT EEREQTVGEK AQKKDAETVK
151 KQAVKPSKET EKKASKEEEK AEKEKVAPKP TPEQILNSGS IEKARSAAAK
201 EVQKMKTPTR RKQRIICKWA RMPTAGARKG SVPNWQSWAY LPRWSVIRRD
251 IKRFTGCKAA ICLPMR*

```

m306/a306 93.7% identity in 252 aa overlap

```

                                10      20      30      40
m306.pep                      GLFFGLILATVIIAGILFYLNQSGQNAFKIPASSKQPAETEILKPX
                                |:|||||||||||||||||||||||||:|||||||||
a306                          MFMNKFSQSGKGLSGFFFFLILATVIIAGILFYLNQSGQNAFKIPVPSKQPAETEILKPK
                                10      20      30      40      50      60

                                50      60      70      80      90      100
m306.pep                      NQXKEDIQXPADQNALSEPDAAEAEQSDAEXAADKQPVADKADEVEEKAGEPEREEDP
                                ||||||| ||||||||||||||||||| ||||||| ||||||| ||||||| |||||||
a306                          NQPKEDIQPEPADQNALSEPDAAEAEQSDAEXAADKQPVADKADEVEEKADEPEREKSD
                                70      80      90      100     110     120

                                110     120     130     140     150     160
m306.pep                      GQAVRKKALTEEREQTVREKAQKKDAETVKXQAVKPSKETEKKASKEEKKAAKEKVAPKP
                                ||||||| ||||||||||||||||||| ||||||| ||||||| ||||||| |||||||
a306                          GQAVRKKALTEEREQTVGEKAQKKDAETVKKQAVKPSKETEKKASKEEKKAEKEKVAPKP
                                130     140     150     160     170     180

                                170     180     190     200     210     220
m306.pep                      TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTVRARKGSVPNWQSWAY
                                ||||||| ||||||||||||||||||| ||||||| ||||||| ||||||| |||||||
a306                          TPEQILNSGSIEKARSAAAEVQKMKTPTRRKQRIICKWARMPTAGARKGSVPNWQSWAY
                                190     200     210     220     230     240

                                230     240     250
m306.pep                      LPRWSVIRRDIKRFTGCKAAICLPMRX
                                ||||||| ||||||| |||||||
a306                          LPRWSVIRRDIKRFTGCKAAICLPMRX
                                250     260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1271>:

```

g307.seq
  1 atgaaaacct tcttcaaaac cctttcgacc gcgtcactcg cgctcatcct
 51 cgcagcctgc ggcggtcaaa aagacagcgc gcccgagcc tctgccgccg
101 ccccttctgc cgataacggc gcggcgaaaa aagaaatcgt cttcggcacg
151 accgtgggcg acttcggcga tatggtcaaa gaacaaatcc aagccgagct
201 ggagaaaaaa ggctacaccg tcaaattggt cgaatttacc gactatgtgc
251 gcccgaaatc ggcatcggcg gagggcgagt tggacatcaa cgtcttccaa
301 cacaaaccct atcttgacga tttcaaaaaa gaacacaacc tggacatcac
351 cgaagccttc caagtgccga ccgcgccttt gggactgtat ccggggcaaac
401 tgaaatcgct ggaagaagtc aaagacggca gcaccgtatc cgcgccaac
451 gaccgcgtcca acttcgcacg cgccttggtg atgctgaacg aactggggtg
501 gatcaaactc aaagacggca tcaatccgct gaccgcatcc aaagccgaca
551 tcgcggaaaa cctgaaaaac atcaaatcgc tcgagcttga agccgcacaa
601 ctgccgcgca gccgcgccga cgtggatttt gccgtcgtca acggcaacta
651 cgccataagc agcggcatga agctgaccga agccctgttc caagagccga

```

704

```

701 gctttgccta tgtcaactgg tctgccgtca aaaccgccga caaagacagc
751 caatggccta aagacgtaac cgaggcctat aactccgacg cgttcaaagc
801 ctacgcgcac aaacgcttcg agggctacaa ataccctgcc gcatggaatg
851 aaggcgcagc caaataa

```

This corresponds to the amino acid sequence <SEQ ID 1272; ORF 307.ng>:

```

g307.pep
  1 MKTFFKTLST ASLALILAAC GGQKDSAPAA SAAAPSadNG AAKKEIVFGT
 51 TVGDFGDMVK EQIQAELEKK GYTVKLVEFT DYVRPNLALA EGELDINVFO
101 HKPYLDDFKK EHNLDITEAF QVPTAPLGLY PGKLKSLLEV KDGSTVSAPN
151 DPSNFARALV MLNELGWIKL KGINPLTAS KADIAENLKN IKIVELEAAQ
201 LPRSRADVDF AVVNGNYAIS SGMKLTEALF QEPSFAYVNW SAVKTADKDS
251 QWLKDVTEAY NSDAFKAYAH KRFEGYKYP A WNEGAAK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1273>:

```

m307.seq (partial)
  1 ..CAATGGCTTA AAGACGTAAC CGAGGCCTAT AACTCCGACG CGTTCAAAGC
 51 CTACGCGCAC AAACGCTTCG AGGGCTACAA ATCCCCTGCC GCATGGAATG
101 AAGGCGCAGC CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1274; ORF 307>:

```

m307.pep (partial)
  1 ..QWLKDVTEAY NSDAFKAYAH KRFEGYKSPA A WNEGAAK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 307 shows 97.4% identity over a 38 aa overlap with a predicted ORF (ORF 307.ng) from *N. gonorrhoeae*:

```

m307/g307

                                10      20      30
m307.pep                                QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
g307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKYP
              230      240      250      260      270      280

              39
m307.pep      A WNEGAAKX
              |||||
g307      A WNEGAAKX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1275>:

```

a307.seq
  1 ATGAAAACCT TCTTCAAAAC CCTTTCGCC GCCGCACTCG CGCTCATCCT
 51 CGCCGCCTGC GCGGGTCAAA AAGATAGCGC GCCCGCCGCA TCCGCTTCTG
101 CCGCCGCCGA CAACGGCGCG GCGAAAAAAG NAATCGTCTT CGGCACGACC
151 GTCGGCGACT TCGGCGATAT GGTCAAAGAA CAAATCCAAC CCGAGCTGGA
201 GAAAAAAGGC TACACCGTCA AACTGGTCTG GTTTACCGAC TATGTGCGCC
251 CGAATCTGGC ATTGGCTGAG GCGGAGTNGG ACATCAACGT CTTCCAACAC
301 AAACCCTATC TTGACGACTT CAAAAAAGAA CACAATCTGG ACATCACCGA
351 AGTCTTCCAA GTGCCGACCG CGCCTTTGGG ACTGTACCCG GGCAAGCTGA
401 AATCGCTGGA AGAAGTCAAA GACGGCAGCA CCGTATCCGC GCCCAACGAC
451 CCGTCCAAC TCGCCCGCGT CTGGGTGATG CTCGACGAAC TGGGTGGGAT
501 CAAACTCAAA GANGGCATCA ATCCGCTGAC CGCATCCAAA GCGGACATTG
551 CCGAAAACCT GAAAAACATC AAAATCGTCG AGCTTGAAGC CGCGCAACTG
601 CCGCGTAGCC GCGCCGACGT GGATTTTGNC GTCGTCAACG GCAANTACGC
651 CATAAGCAGC GGCATGAAGC TGACCGAAGC CCTGTTCCAA GAACCGAGCT
701 TTGCCTATGT CAACTGGTCT GCCGTCAAAA CCGCCGACAA AGACAGCCAA
751 TGGCTTAAAG ACGTAACCGA GGCCTATAAC TCCGACGCGT TCAAAGCCTA
801 CGGCACAAA CGCTTCGAGG GCTACAAATC CCCTGCCGCA TGAATGAAG
851 GCGCAGCCAA ATAA

```

This corresponds to the amino acid sequence <SEQ ID 1276; ORF 307.a>:

```

a307.pep
  1 MKTFFKTL SA AALALILAAC GGQKDSAPAA SASAADNGA AKKXIVFGTT

```

705

```

51  VGDFGDMVKE  QIQPELEKKG  YTVKLVEFTD  YVRPNLALAE  GEXDINVFQH
101 KPYLDDFKKE  HNLDITEVFQ  VPTAPLGLYP  GKLSLEEVK  DGSTVSAPND
151 PSNFARVLVM  LDELGWIKLK  XGINPLTASK  ADIAENLKN  KIVELEAAQL
201 PRSRADVDFX  VVNGXYAISS  GMKLTEALFQ  EPSFAYVNWS  AVKTADKDSQ
251 WLKDVTEAYN  SDAFKAYAHK  RFEGYKSPAA  WNEGAAK*

```

m307/a307 100.0% identity in 38 aa overlap

```

                                10      20      30
m307.pep                      QWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
                                |||||
a307      SGMKLTEALFQEPSFAYVNWSAVKTADKDSQWLKDVTEAYNSDAFKAYAHKRFEGYKSPA
          220      230      240      250      260      270

                                39
m307.pep      AWNEGAAXX
                                |||||
a307      AWNEGAAXX
          280

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1277>:

```

g308.seq
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTGTTTA  TCGGATTTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGCGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGATTATA  CGAAAGACGA  AGTATATGCC
301 TTGGCTGATT  TCGTCCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCACCTGT  TCGATGCGGA
401 CGCTTGCTCT  TGTCGCGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCT  CGATGTACCG  CAAGCCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTATC  GCACACACGC  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGATT  TGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1278; ORF 308.ng>:

```

g308.pep
1  MLNRVYRIL  GVADNLYPCL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TDYTKDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLNMRK  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSI  AHTLSLFGID  TPDLAEWQGM  AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1279>:

```

m308.seq (partial)
1  ATGTTAAATC  GGGTATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGCGTTTA  TCGGATTTCT  GTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGCG  GGGCGAGCGG  TTTCCAATAC  GCGGTGAAGG  CTTTGGAACT
201 TTTGCGCGCG  CAAGATGTCT  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGCTTATG  CGAGAGACGA  GGTATATGCC
301 TTGGCGGACT  TCGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGATG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTCT  TGTCGCGCAC  GGCTTCGGCG  ACAATCTGcT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAAGCGG  GwAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCT  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGcT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGATT  CGGCGGAATG  GCArGGAATG  gcG...

```

This corresponds to the amino acid sequence <SEQ ID 1280; ORF 308>:

```

m308.pep (partial)

```

706

```

1  MLNRVFYRIL  GVADNLYPRL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMKR  XTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  A..

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 308 shows 96.5% identity over a 231 aa overlap with a predicted ORF (ORF 308.ng) from *N. gonorrhoeae*:

m308/g308

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
g308	MLNRVFYRILGVADNLYPCLSDFCFFFTIIAGLPLQAVLWERRMMVRRLLIIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADFVHPIGNIGACIASGTF					
g308	GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADFVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
g308	KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKPOQTADDIVAHSAHALSLFGIDTPDSAEOQGM					
g308	VTEMGGVVFPVPAMYRKPOQTADDIVAHSAHTLSLFGIDTPDLAEWQGMAD					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1281>:

a308.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTGTTGCCG
101 TGCAGGCGGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCCTGAAGG  CTTTGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGGCGCG  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCCCT  GGTCGTGCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCCTG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1282; ORF 308.a>:

a308.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTIIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLVRETPL  NLAHLDNMXR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHASLFGID  TPDSAEOQGM  AD*

```

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m308/a308 95.7% identity in 231 aa overlap

	10	20	30	40	50	60
m308.pep	MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	: : : : : : : : : : :					
a308	MLNRIFYRILGVADNLYPYLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY					
	10	20	30	40	50	60
	70	80	90	100	110	120
m308.pep	GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF					
	: : : : : : : : : :					
a308	GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m308.pep	KTDGMLVAPCSMRTLASVAHGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	: : : : : : : : : :					
a308	KTDGMLVAPCSMRTLASVVHFGFGDNLLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR					
	130	140	150	160	170	180
	190	200	210	220	230	
m308.pep	XTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGM A					
	: : : : : : : : : :					
a308	VTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSA EWQGM ADX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1283>:

g308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTGCGC ACAATTTGTA
51  TCCGTGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGCGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGATTATA CGAAAGACGA AGTATATGCC
301 TTGGCTGATT TCGTCCATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGACG GGATGCTGGT CGCACCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAACCTCTT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CTTGTTCCCTG CGATGTACCG CAAGCCGCG
601 ACGGCGGACG ACATAGTGGC GCACAGTATC GCACACACGC TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT TGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1284; ORF 308-1.ng>:

g308-1.pep

```

1  MLNRVFYRIL GVADNLYPCL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI
51  GISGASGFQY GVKALELLRA QDVETHLVVS KGAEMARASE TDYTKDEVYA
101 LADVFVHPIGN IGACIASGTF KTDGMLVAPC SMRTLASVAH GFGDNLLTRA
151 ADVVLKERRR LVMVRETPL NLAHLDNMKR VTEMGGVVFP PVPAMYRKPO
201 TADDIVAHSI AHTLSLFGID TPDLA EWQGM AD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1285>:

m308-1.seq

```

1  ATGTTAAATC GGGTATTTTA TCGGATATTG GGTGTGCGC ACAATTTGTA
51  TCCGCGTTTA TCGGATTTCT GTTTTTTCAC TATAATAGCC GGTTTGCCGT
101 TGCAGGCGGT TTTATGGGAA AGGCGGATGA TGGTACGGCG TTTGATAATC
151 GGCATCAGCG GGGCGAGCGG TTTCCAATAC GGCGTGAAGG CTTTGGAAC
201 TTTGCGCGCG CAAGATGTCG AAACGCACCT TGTGGTATCG AAAGGTGCGG
251 AGATGGCGCG CGCTTCGGAA ACGGCTTATG CGAGAGACGA GGTATATGCC
301 TTGGCGGACT TCGTGATCC GATCGGCAAT ATCGGGGCGT GCATTGCCAG
351 CGGTACGTTT AAAACGGATG GGATGCTGGT CGCCCCCTGT TCGATGCGGA
401 CGCTTGCCTC TGTCGCGCAC GGCTTCGGCG ACAATCTGCT GACGCGTGCG
451 GCGGATGTGG TTTTGAAGGA AAGGCGGCGG CTGGTGCTGA TGGTGCGCGA
501 AACGCCGCTG AACCTTGCCC ATTTGGACAA TATGAAGCGG GTAACGGAAA
551 TGGGCGGCGT GGTGTTTCCC CTTGTTCCCTG CGATGTACCG CAAACGCGAG
601 ACGGCGGACG ACATAGTGGC GCACAGTGTG GCACACGCTT TGTCGCTGTT
651 CGGAATCGAT ACGCCGGATT CGGCGGAATG GCAGGGAATG GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1286; ORF 308-1>:

m308-1.pep

```

1  MLNRVFYRIL GVADNLYPRL SDFCFFTTIA GLPLQAVLWE RRMVRRLLI

```

708

```

51  GISGASGFQY  GVKALELLRA  QDVETHLVVS  KGAEMARASE  TAYARDEVYA
101 LADVFVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVAH  GFGDNLTRA
151 ADVVLKERRR  LVLMVRETPL  NLAHLDNMKR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  AD*

```

m308-1/g308-1 97.0% identity in 232 aa overlap

```

              10      20      30      40      50      60
m308-1.pep  MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              |||||:|||||:|||||:|||||:|||||:|||||
g308-1      MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              10      20      30      40      50      60

              70      80      90     100     110     120
m308-1.pep  GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF
              |||||:|||||:|||||:|||||:|||||:|||||
g308-1      GVKALELLRAQDVETHLVVSKGAEMARASETDYTKDEVYALADVFVHPIGNIGACIASGTF
              70      80      90     100     110     120

              130     140     150     160     170     180
m308-1.pep  KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              |||||:|||||:|||||:|||||:|||||:|||||
g308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMKR
              130     140     150     160     170     180

              190     200     210     220     230
m308-1.pep  VTEMGGVVFPVPAMYRKPOQTADDIVAHSVAHALSFLGIDTPDSA EWQGMADX
              |||||:|||||:|||||:|||||:|||||
g308-1      VTEMGGVVFPVPAMYRKPOQTADDIVAHSLAHTLSLFGIDTPDLA EWQGMADX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1287>:

a308-1.seq

```

1  ATGTTAAATC  GGATATTTTA  TCGGATATTG  GGTGTTGCCG  ACAATTTGTA
51  TCCGTATTTA  TCGGATTTCT  GTTTTTTCAC  TATAATAGCC  GGTTTGCCGT
101 TGCAGCGCGT  TTTATGGGAA  AGGCGGATGA  TGGTACGGCG  TTTGATAATC
151 GGCATCAGTG  GGGCGAGCGG  TTTCCAATAC  GGCGTGAAGG  CTTGGANCT
201 TTTACGCGCG  CAAGATATCG  AAACGCACCT  TGTGGTATCG  AAAGGTGCGG
251 AGATGCGCGC  CGCTTCGGAA  ACGGNTTATG  CGAGAGACGA  NGTATATGCC
301 TTGGCGGACT  TNGTGCATCC  GATCGGCAAT  ATCGGGGCGT  GCATTGCCAG
351 CGGTACGTTT  AAAACGGACG  GGATGCTGGT  CGCCCCCTGT  TCGATGCGGA
401 CGCTTGCTC  GGTCTGTCAC  GGCTTCGGCG  ACAACCTCTT  GACGCGTGCG
451 GCGGATGTGG  TTTTGAAGGA  AAGGCGGCGG  CTGGTGCTGA  TGGTGCGCGA
501 AACGCCGCTG  AACCTTGCCC  ATTTGGACAA  TATGAANCGG  GTAACGGAAA
551 TGGGCGGCGT  GGTGTTTCCC  CCTGTTCTCG  CGATGTACCG  CAAACCGCAG
601 ACGGCGGACG  ACATAGTGGC  GCACAGTGTT  GCACACGCTT  TGTCGCTGTT
651 CGGAATCGAT  ACGCCGGATT  CGGCGGAATG  GCAGGGAATG  GCGGATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1288; ORF 308-1.a>:

a308-1.pep

```

1  MLNRIFYRIL  GVADNLYPYL  SDFCFFTTIA  GLPLQAVLWE  RRMVRRLLII
51  GISGASGFQY  GVKALXLLRA  QDIETHLVVS  KGAEMARASE  TXYARDXVYA
101 LADXVHPIGN  IGACIASGTF  KTDGMLVAPC  SMRTLASVVH  GFGDNLTRA
151 ADVVLKERRR  LVLMVRETPL  NLAHLDNMXR  VTEMGGVVFP  PVPAMYRKPO
201 TADDIVAHSV  AHALSFLGID  TPDSA EWQGM  AD*

```

a308-1/m308-1 96.1% identity in 232 aa overlap

```

              10      20      30      40      50      60
a308-1      MLNRIFYRILGVADNLYPYLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              |||||:|||||:|||||:|||||:|||||:|||||
m308-1      MLNRVFYRILGVADNLYPRLSDFCFFTTIAGLPLQAVLWERRMMVRRLLIIGISGASGFQY
              10      20      30      40      50      60

              70      80      90     100     110     120
a308-1      GVKALXLLRAQDIETHLVVSKGAEMARASETXYARDXVYALADXVHPIGNIGACIASGTF
              |||||:|||||:|||||:|||||:|||||:|||||
m308-1      GVKALELLRAQDVETHLVVSKGAEMARASETAYARDEVYALADVFVHPIGNIGACIASGTF
              70      80      90     100     110     120

              130     140     150     160     170     180
a308-1      KTDGMLVAPCSMRTLASVVHFGFGDNLTRAADVVLKERRRLVLMVRETPLNLAHLDNMXR
              |||||:|||||:|||||:|||||:|||||:|||||

```

709

```

m308-1      KTDGMLVAPCSMRTLASVAHGFGDNLTRAADVVLKERRRRLVLMVRETPLNLAHLDNMKR
              130      140      150      160      170      180

              190      200      210      220      230
a308-1      VTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSEWQGMADX
              |||||
m308-1      VTEMGGVVFPVPAMYRKQPQTADDIVAHSAHALSLFGIDTPDSEWQGMADX
              190      200      210      220      230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1289>:

g311.seq

```

1   atgttcagtt tcggctgggc gtttgaccgc ccgcagtatg agttgggttc
51  gctgtgcgct gttgcggcac ttgcgtgccg gcgcgctttg ggggtgtttg
101 gtttggaac gcaaatcaag tggccaaacg atttggtcgt cggacgcgac
151 aaattgggcg gcattctgat tgaaacagtc agggcgggcg gtaaaacggg
201 tgccgtggtc ggtatcggca tcaatttcgt gctgcccaag gaagtggaaa
251 acgccgcttc cgtgcagtcg ctgtttcaga cggcatcgcg gcggggcaat
301 gccgatgccg ccgtattgct ggaaacattg cttgcggaac tggcgcggt
351 gttggaacaa tatgcggaag aagggttcgc gccattttta aatgagtatg
401 aaacggccaa ccgcgaccac ggcaaggcgg tattgctgtt gcgcgacggc
451 gaaaccgtgt gcgaaggcac ggttaaaggc gtggacggac gaggcgttct
501 gcacttgga acggcagaag gcgaacagac ggtcgtcagc ggcgaatca
551 gcctgcggcc cgacaacagg tcggtttccg tgccgaagcg gccggattcg
601 gaacgttttt tgctgttgga aggcgggaac agccggctca agtggcggtg
651 ggtggaaaac ggcacgttcg caaccgtggg cagcgcgccg taccgcgatt
701 tgtcgccttt gggcgcgag tggcggaaa aggcggatgg aaatgtccgc
751 atcgtcggtt gcgccgtgtg cggagaatcc aaaaaggcac aagtgaagga
801 acagctcgcc cgaaaaatcg agtggctgcc gtcttcgca caggctttgg
851 gcatacgcaa ccactaccgc caccccaag aacacggttc cgaccgttgg
901 ttcaacgcct tgggcagccg ccgcttcagc cgcaacgcct gcgtcgtcgt
951 cagttgcggc acggcggtaa cggttgacgc gctcaccgat gacggcatt
1001 atctcgccg aaccatcatg cccggcttcc acctgatgaa agaatcgctc
1051 gccgtccgaa ccgccaacct caaccgcccc gccggcaaac gttacccttt
1101 cccgaccaca acgggcaacg ccgtcgcaag cggcatgatg gacgcggttt
1151 gcggctcgat aatgatgatg cacggccggt tgaaagaaaa aaacggcgcg
1201 ggcaagcctg tcgatgtcat cattaccggc ggcggcgcgg cgaaagtcgc
1251 cgaagccctg ccgcctgcat ttttggcgga aaataccgtg cgctggcg
1301 acaacctcgt catccacggg ctgctgaacc tgattgccgc cgaagcggg
1351 gaatcggaac acgcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1290; ORF 311.ng>:

g311.pep

```

1   MFSFGWAFDR PQYELGSLSP VAALACRRAL GCLGLETQIK WPNDLVVGRD
51  KLGILLETIV RAGGKTVAVV GIGINFLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLETI LAELGAVLEQ YAEFGFAPFL NEYETANRDH GKAVLLLRDG
151 ETVCEGTVKG VDGRGVLHLE TAEGEQTVVS GEISLRPDNR SVSVPKRPDS
201 ERFLILLEGN SRLKAWVEN GTFATVGSAP YRDLSPGAE WAEKADGNVR
251 IVGCAVCGES KKAQVKEQLA RKIEWLPSSA QALGIRNHYR HPPEHGS DRW
301 FNALGSRRFS RNACVVVSCG TAVTVDALTD DGHYLG GTIM PGFHLMKESL
351 AVRTANLNRP AGKRYPFPTT TGNVAVSGMM DAVCGSIMMM HGRLKEKNGA
401 GKPVDVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1291>:

m311.seq (partial)

```

1   ATGTTTCAAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGTG GCGCGCCTTG TCGCGTTTAG
101 GTTTGGATGT GCArATTAAG TGGCCCAATG ATTTGGTTGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTTGT CCTGCCCAAn GAAGTAGAAA
251 ATGCCGCTTC CGTGCAATCG CTGTTTCAGA CGGCATCGCG GCGGGGCAAT
301 GCCGATGCCG CCGTGCTGCT nnnnnnnnnn nnnnnnnnnn nnnnGGAAAT
351 CAGCTGCGG TCCGACnACA GGCCGGTTTC CGTGnCGAAG CGGCGGATT

```

710

```

401 CGGAACGTTT TCTGCTGTTG GACGGCGGCA ACAGCCGGCT CAAGTGGgCG
451 TGGGTGGAAG ACGGCACGTT CGCAACCGTC GGTAGCGCGC CGTACCgCGA
501 TTTGTGCCTT TTGGGCGCGG AGTGGGCGGA AAAGGCGGAT GGAAATGTCC
551 GCATCGTCGG TTGCGCTGTG TCGGAGAAT TCAAAAAGGC ACAAGTGCAG
601 GAACAGCTCG CCCGAAAAAT CGAGTGGCTG CCGTCTTCCG CACAGGCTTT
651 GTTTGGCATA CGCAACCACT ACCGCCACCC CGAAGAACAC GGTTCGACC
701 GCTGGTTCAA CGCCTTGGGC AGCCGCCGCT TCAGCCGCAA CGCyTGCCTC
751 GTCGTCAGTT GCGGCACGGC GGTAACGGT GACGCGCTCA CCGATGACGG
801 ACATTATCTC GGrgGAACCA TCATGCCCGG TTCCACCTG ATGAAAGAAT
851 CGCTCGCCGT CCGAACCGCC AACCTCAACC GGCACGCCGG TAAGCGTTAT
901 CCTTTCCCGA CCACAACGGG CAATGCCGTC GCCAGCGGCA TGATGGATGC
951 GGTTTGCCTG TCGGTTATGA TGATGCACGG GCGTTTGAAG GAAAAAACCG
1001 GGGCGGGCAA GCCTGTCTGAT GTCATCATT CCGGCGGGCG CGCGGCAAAA
1051 GTTGCCGAAG CCCTGCCGCC TGCATTTTGT GCGGAAAATA CCGTGCGCGT
1101 GGCGGACAA CTGCTCATT ACGGGTTGTT GAACATGATT GCCGCCGAAG
1151 GCAGGGAATA TGAACAT...

```

This corresponds to the amino acid sequence <SEQ ID 1292; ORF 311>:

```

m311.pep (partial)
  1 MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLDVQIK WPNDLVVGRD
 51 KLGILITV RTGGKTAVAV GIGINFVLPX EVENAASVQS LFQTASRRGN
101 ADAAVLLXXX XXXXXEISLR SDXRPVSVXK RRDSEFLLL DGGNSRLKWA
151 WVENGTATV GSAPYRDLSP LGAEWAEEKAD GNVIRVGCAG CGEFKKAQVQ
201 EQLARKIEWL PSSAQALFGI RNHYRHPEEH GSDRWFNALG SRRFSRNACV
251 VVSCGTAVTV DALTDDGHYL GGTIMPGFHL MKESLAVRTA NLNRHAGKRY
301 PFPTTGNNAV ASGMMDAVCG SVMMMHGRLE EKTGAGKPDV VIITGGGAAG
351 VAEALPPAFL AENTVRVADN LVIYGLLNMI AAEGREYEH....

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 311 shows 78.5% identity over a 455 aa overlap with a predicted ORF (ORF 311.ng) from *N. gonorrhoeae*:

```

m311/g311

      10      20      30      40      50      60
m311.pep MFSFGWVFDRPQYELGSLSPVAAVACRRALSRLGLDVQIKWPNDLVVGRDKLGILITV
          |||||:|||||||||||||||:|||||: |||::|||||||||||||||||||
g311      MFSFGWAFDRPQYELGSLSPVAALACRRALGCLGLETQIKWPNDLVVGRDKLGILITV
          10      20      30      40      50      60

      70      80      90      100     110
m311.pep RTGGKTAVAVGIGINFVLPXEVENAASVQSLFQTASRRGNADA AVLLXXX-----
          |:||||||||||||||| ||||||||||||||||||||| :
g311      RAGGKTAVAVGIGINFVLPKEVENAASVQSLFQTASRRGNADA AVLLLETLAELGAVLEQ
          70      80      90      100     110     120

m311.pep -----XXXXXXXX
          :
g311      YAEEGFAPFLNEYETANRDHGKAVLLLLRDGETVCEGTVKGV DGRGV LHLETAEGEQTVVS
          130     140     150     160     170     180

      120     130     140     150     160     170
m311.pep XEISLRSDXRPVSVXKRRDSEFLLLDGGNSRLKWA WVENGTATVGSAPYRDLSP LGAE
          ||||| | ||| | |||||||:|||||||||||||||||||||
g311      GEISLRPDNRSVSVKRPDSEFLLLEGGNSRLKWA WVENGTATVGSAPYRDLSP LGAE
          190     200     210     220     230     240

      180     190     200     210     220     230
m311.pep WAEKADGNVRIVGCAVCGEFKKAQVQEQLARKIEWLPSSAQALFGIRNHYRHPEEHGSDR
          ||||||| |||||:||||||||||||||||| |||||||
g311      WAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL-GIRNHYRHPEEHGSDR
          250     260     270     280     290

```


711

	240	250	260	270	280	290
m311.pep	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
g311	WFNALGSRFRSRNACVVVSCGTAVTVDALTDGHYLGGTIMPGFHLMKESLAVRTANLNR					
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYFPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKPVDVIIITGGGAAKVAEA					
g311	PAGKRYFPFPTTTGNAVASGMMDAVCGSIMMHGRLEKKNAGKPVDVIIITGGGAAKVAEA					
	360	370	380	390	400	410
	360	370	380	390	400	410
m311.pep	LPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEH					
g311	LPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX					
	420	430	440	450		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1293>:

```

a311.seq
1   ATGTTTCAGTT TTGGCTGGGT GTTTGACCGG CCGCAGTATG AGTTGGGTTC
51  GCTGTCGCCT GTTGCGGCAG TGGCGTGCCG GCGCGCCTTG TCGCGTTTGG
101 GTTTGAAAAC GCAATCAAG TGGCCAAACG ATTTGGTCGT CGGACGCGAC
151 AAATTGGGCG GCATTCTGAT TGAAACGGTC AGGACGGGCG GCAAAACGGT
201 TGCCGTGGTC GGTATCGGCA TCAATTTCGT GCTGCCCAAG GAAGTGGAAA
251 ACGCCGCTTC CGTGCATCG CTGTTTCAGA CGGCATCGCG GCGGGGAAAT
301 GCCGATGCCG CCGTGTGCT GGAAACGCTG TTGGCGGAAC TTGATGCGGT
351 GTTGTTGCAA TATGCGCGGG ACGGATTTGC GCCTTTTGTG GCGGAATATC
401 AGGCTGCCAA CCGCGACCAC GGCAAGCGCG TATTGCTGTT GCGCGACGGC
451 GAAACCGTGT TCGAAGGCAC GGTAAAGGC GTGGACGGAC AAGGCGTTCT
501 GCACTTGGA ACGGCAGAGG GCAAACAGAC GGTGCTCAGC GCGGAAATCA
551 GCCTGCGGTC CGACGACAGG CCGGTTTCG TGCCGAAGCG GCGGGATTTCG
601 GAACGTTTTT TGCTGTTGGA CGGCGGCAAC AGCCGGCTCA AGTGGGCGTG
651 GGTGGAAAAC GGCACGTTTC CAACCGTCGG TAGCGCGCCG TACCGCGATT
701 TGTCGCCTTT GGGCGCGGAG TGGGCGGAAA AGGTGGATGG AAATGTCCGC
751 ATCGTCGGTT GCGCCGTGTG CGGAGAATT CAAAAGGCAC AAGTGCAGGA
801 ACAGCTCGCC CGAAAAATCG AGTGGCTGCC GTCTTCCGCA CAGGCTTTGG
851 GCATACGCAA CCACTACCGC CACCCGAAG AACACGGTTC CGACCGCTGG
901 TTCAACGCCT TGGGCGGCCG CCGCTTCAGC CGCAACGCCT GCGTCGTCGT
951 CAGTTGCGGC ACGGCGGTAA CGGTTGACGC GCTCACCGAT GACGGACATT
1001 ATCTCGGGG AACCATCATG CCCGTTTCC ACCTGATGAA AGAATCGCTC
1051 GCCGTCCGAA CCGCCAACCT CAACCGGCAC GCCGTAAGC GTTATCCTTT
1101 CCCGACCACA ACGGCAATG CCGTCGCCAG CGGCATGATG GATGCGGTTT
1151 GCGGCTCGGT TATGATGATG CACGGGCGTT TGAAAGAAAA AACCAGGGCG
1201 GGCAAGCCTG TCGATGTCAT CATTACCGGC GGCGGCGCGG CAAAAGTTGC
1251 CGAAGCCCTG CCGCTGCAT TTTTGGCGGA AAATACCGTG CCGTGGCGG
1301 ACAACCTCGT CATTACGGG CTGCTGAACC TGATTGCCGC CGAAGCGGG
1351 GAATCGGAAC ATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1294; ORF 311.a>:

```

a311.pep
1   MFSFGWVFDR PQYELGSLSP VAAVACRRAL SRLGLKTQIK WPNDLVVGRD
51  KLGGILIETV RTGGKTVAVV GIGINFVLPK EVENAASVQS LFQTASRRGN
101 ADAAVLLET L LAELDAVLLQ YARDGFAPFV AEYQAANRDH GKAVLLLRDG
151 ETVFEGTVKG VDGQGVHLLE TAEGKQTVVS GEISLRSDDR PVSVPKRDS
201 ERFLLDGGN SRLKWAVVEN GTFATVGSAP YRDLSPLGAE WAEKVDGNVR
251 IVGCAVCEGF KKAQVQEQLA RKIEWLPSSA QALGIRNHYR HPEEHGSDRW
301 FNALGSRFRS RNACVVVSCG TAVTVDALTD DGHYLGGTIM PGFHLMKESL
351 AVRTANLNRH AGKRYFPFPTT TGNASGMM DAVCGSVMM HGRLEKKTGA
401 GKPDVVIITG GGAAKVAEAL PPAFLAENTV RVADNLVIHG LLNLIAAEGG
451 ESEHT*

```

m311/a311 81.3% identity in 455 aa overlap

712

	10	20	30	40	50	60
m311.pep	MFSFGWVFD	RQYELGSL	SPVAACRR	ALSRLGLD	VQIKWPND	LVVGRDKLGGIL
a311	MFSFGWVFD	RQYELGSL	SPVAACRR	ALSRLGLK	TQIKWPND	LVVGRDKLGGIL
	10	20	30	40	50	60
	70	80	90	100	110	
m311.pep	RTGGKTVAV	VGIGINFV	LPXEVENA	ASVQSLFQ	TASRRGNAD	AAVLLXXXXXX
a311	RTGGKTVAV	VGIGINFV	LPXEVENA	ASVQSLFQ	TASRRGNAD	AAVLLLETLAELDAVLLQ
	70	80	90	100	110	120
m311.pep	-----					
a311	YARDGFAPF	VAEYQAAN	RDHGKAVL	LLLRDGET	VFEGTVKG	VDGQGV LHLETAEGKQTVVS
	130	140	150	160	170	180
	120	130	140	150	160	170
m311.pep	-EISLRSDX	RPVSVXKR	RDSERFLL	LDGGNSRL	KWAWVENGT	FATVGSAPYRDLSP
a311	GEISLRSD	RPVSVPKR	RDSERFLL	LDGGNSRL	KWAWVENGT	FATVGSAPYRDLSP
	190	200	210	220	230	240
	180	190	200	210	220	230
m311.pep	WAEKADGN	VRIVGCA	VCGEFKKA	QVQEQ LAR	KIEWLPSSA	QALFGIRNHYP
a311	WAEKVDGN	VRIVGCA	VCGEFKKA	QVQEQ LAR	KIEWLPSSA	QAL-GIRNHYP
	250	260	270	280	290	
	240	250	260	270	280	290
m311.pep	WFNALGSR	RFSRNAC	VVVSCGT	AVTVDALT	DDGHYLG	GTIMPGFHLMKESLAVRTANLNR
a311	WFNALGSR	RFSRNAC	VVVSCGT	AVTVDALT	DDGHYLG	GTIMPGFHLMKESLAVRTANLNR
	300	310	320	330	340	350
	300	310	320	330	340	350
m311.pep	HAGKRYPF	PPTTGN	AVASGMM	DAVCGSV	MMMHGRL	KEKTGAGKPV
a311	HAGKRYPF	PPTTGN	AVASGMM	DAVCGSV	MMMHGRL	KEKTGAGKPV
	360	370	380	390	400	410
	360	370	380	389		
m311.pep	LPPAFLA	ENTVRV	ADNLVI	YGLLNMI	AAEGREY	EH
a311	LPPAFLA	ENTVRV	ADNLVI	HGLNLIA	AEEGSEH	TX
	420	430	440	450		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1295>:

g311-1.seq

```

1  ATGACGGTTT TGAAGCCTTC GCATTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTAT CGCAATTGGC GCGTGAGGCG GACATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA TATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CCTTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGATCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGGC GAAAGTGGTC CACCGTTTGG
401 GCGAGTGCCT GATGTTCACT TTCGGCTGGG CGTTTGACCG GCCGCAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTGCGGCA CTTGCGTGCC GGC GCGCTTT
501 GGGGTGTTTG GGTTTGGAAG CGCAAATCAA GTGGCCAAAC GATTGGTTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACAGT CAGGGCGGGC
601 GGTAACACGG TTGCCGTGGT CGGTATCGGC ATCAATTTCC TGCTGCCCAA
651 GGAAAGTGGA AACGCCGCTT CCGTGCAGTC GCTGTTTCAG ACGGCATCGC
701 GGCGGGGCAA TGCCGATGCC GCCGTATTGC TGGAACATT GCTTGCGGAA
751 CTGGGCGCGG TGTGGAACA ATATGCGGAA GAAGGTTTCG CGCCATTTT

```

```

801 AAATGAGTAT GAAACGGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGGACGG CGAAACCGTG TGC GAAGGCA CGGTTAAAGG CGTGGACGGA
901 CGAGGCGTTC TGCACTTGGA AACGCGAGaa ggCGAACAGA cggctGtcag
951 cggcGaaaTC AGccTGCGGc CCGacaacag gtcggtttcc GTgccgaagc
1001 gGccggatTC GgaacgttTT tTGCTgttgg aagcgggaa cagccggctc
1051 aAGTGGgctt gGGTggAAAA Cggcacgttc gcaaccgtgg gcAGCGcCC
1101 gtaCCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGC GCGGTGT GCGGAGAATC CAAAAGGCA
1201 CAAGTGAAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGTTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGCG GAACCATCAT GCCCGGCTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGCCC CGCCGGCAAA
1501 CGTTACCCCT TCCCGACCAC AACGGGCAAC GCCGTCGCAA CCGGCATGAT
1551 GGACGCGGTT TCGGCTCGA TAATGATGAT GCACGGCCGT TTGAAAGAAA
1601 AAAACGGCGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGCGGCGCGC
1651 GCGAAAGTCG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATCCACGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CACGCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1296; ORF 311-1.ng>:

g311-1.pep

```

1 MTVLKPSHWR VLAELADGLP QHVSQ LAREA DMKPQQLNGF WQOMPAHIRG
51 LLRQHDGYWR LVRPLAVFDA EGLRDLGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWAFDRPQY
151 ELGSLSPVAA LACRRALGCL GLETQIKWPN DLVVGRDKLG GILIETVRAG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LGAVLEQYAE EGFAPFLNEY ETANRDHGKA VLLLRDGETV CEGTVKGVDG
301 RGVHLHLETA GEQTVVSGEI SLRPDNRVS VPKRPDSERF LLEGGNSRL
351 KWAVVENGTG ATVGSAPYRD LSP LGAEWAE KADGNVRIVG CAVCGESKKA
401 QVKEQLARKI EWLPSAQAL GIRNHYRHE EHGSDRWFNA LGSRRFSRNA
451 CVVVSCGTAV TVDALTDGHH YLGGTIMGPF HLMKESLAVR TANLNRPAKG
501 RYFPPTTTGN AVASGMDAV CGSIMMMHGR LKEKNGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1297>:

m311-1.seq

```

1 ATGACGGTTT TGAAGCTTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51 CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTTT TGGCAGCAGA TGCCGGCGCA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GCGGCACAAA ACCATATGCG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTCACT TTTGGCTGGG TGTTTGACCG GCCGAGTAT
451 GAGTTGGGTT CGCTGTGCGC TGTTGCGGCA GTGGCGTGTC GGCGCGCCTT
501 GTCGCGGTTA GGTTTGGATG TGCAGATTAA GTGGCCCAAT GATTGTGTTG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTTG TCCTGCCCAA
651 GAAAGTAGAA AATGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGGCAA TGCCGATGCC GCCGTGCTGC TGGAAACGCT GTTGGTGGAA
751 CTGGACGCGG TGTTGTTGCA ATATGCGCGG GACGGATTTC CGCCTTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TGCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTT TGCACTTGGA AACGGCAGAG GGCAACAGA CGGTCGTCAG
951 CGGCGAAATC AGCCTCGCGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGGGGATTG GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGGTGAAAAA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGCGGATG
1151 GAAATGTCCG CATCGTCGGT TGC GCTGTGT GCGGAGAATT CAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAAATC GAGTGGCTGC CGTCTTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCAGCC GCCGCTTCAG CCGCAACGCC
1351 TCGCTCGTCCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTCACC GA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAATCGCT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCA CCGGCATGAT
1551 GGATGCGGTT TGCGGCTCGG TTATGATGAT GCACGGCGCT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GTTGTGAAC ATGATTGCCG

```

1751 CCGAAGGCAG GGAATATGAA CATATTTAA

This corresponds to the amino acid sequence <SEQ ID 1298; ORF 311-1>:

m311-1.pep

```

1  MTVLKLSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELGERS GFQTALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFDROPY
151 ELGSLSPVAA VACRRALSRL GLDVQIKWPN DLVVGRDKLG GILLETVRTG
201 GKTVAUVGIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLVE
251 LDAVLLQYAR DGFAPFVAEY QAANRDHGKA VLLLRDGETV FEGTVKGVGDG
301 QGVHLHLETAE GKQTVVSGEI SLRSDDRPVS VPKRRDSERF LLLDGGNSRL
351 KWAVVENGTF ATVGSAPYRD LSPLGAEWAE KADGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSSAQAL GIRNHYRHPE EHGSDFWFNA LGSRRFSRNA
451 CUVVSCGTAV TVDALTDGHL YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYPPFTTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIYGLLN MIAAEGREYE HI*

```

m311-1/g311-1 93.9% identity in 591 aa overlap

	10	20	30	40	50	60
m311-1.pep	MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
g311-1	MTVLKPSHWRVLAELADGLPQHVSQALAREADMKPQQLNGFWQOMPAHIRG	LLRQHDGYWR				
	70	80	90	100	110	120
m311-1.pep	LVRPLAVFDAEGLRELGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
g311-1	LVRPLAVFDAEGLRDLGERSGFQTALKHECASSNDEILELARIAPDKAHKTICVTHLQSK					
	130	140	150	160	170	180
m311-1.pep	GRGRQGRKWSHRLGECLMFSFGWVFDROPYELGSLSPVAAVACRRALSRLGLDVQIKWPN					
g311-1	GRGRQGRKWSHRLGECLMFSFGWAFDRPQYELGSLSPVAAALACRRALGCLGLETQIKWPN					
	190	200	210	220	230	240
m311-1.pep	DLVVGRDKLGGILLETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
g311-1	DLVVGRDKLGGILLETVRTAGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
	250	260	270	280	290	300
m311-1.pep	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVGDG					
g311-1	AVLLETLLAELGAVLEQYAEEGFAPFLNEYETANRDHGKAVLLLRDGETVCEGTVKGVGDG					
	310	320	330	340	350	360
m311-1.pep	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSERFLLLDGGNSRLKWAVVENGTF					
g311-1	RGVLHLETAEGEQTVVSGEISLRPDNRVSVPKRPDSERFLLLEGNSRLKWAVVENGTF					
	370	380	390	400	410	420
m311-1.pep	ATVGSAPYRDLSPPLGAEWAEKADGNVRIVGCAVCGEFKKAQVQEQALARKIEWLPSSAQAL					
g311-1	ATVGSAPYRDLSPPLGAEWAEKADGNVRIVGCAVCGESKKAQVKEQLARKIEWLPSSAQAL					
	430	440	450	460	470	480
m311-1.pep	GIRNHYRHPEEHGSDFWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHLGGTIMPGF					
g311-1	GIRNHYRHPEEHGSDFWFNALGSRRFSRNACVVVSCGTAVTVDALTDGHLGGTIMPGF					
	490	500	510	520	530	540
m311-1.pep	HLMKESLAVRTANLNRHAGKRYPPFTTTGNASGMMDAVCGSVMMHGRLEKKTGAGKP					
g311-1	HLMKESLAVRTANLNRHAGKRYPPFTTTGNASGMMDAVCGSIMMHGRLEKKNAGKP					
	550	560	570	580	590	

715

```

m311-1.pep  VDVIITGGGAAKVAELPPAFLAENTVRVADNLVIYGLLNLMIAAEGREYEHIX
|||||
g311-1      VDVIITGGGAAKVAELPPAFLAENTVRVADNLVIHGLLNLMIAAEGGESEHAX
          550      560      570      580      590

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1299>:

```

a311-1.seq
1  ATGACGGTTT TGAAGCCTTC GCACTGGCGG GTGTTGGCGG AGCTTGCCGA
51  CGGTTTGCCG CAACACGTCT CGCAACTGGC GCGTATGGCG GATATGAAGC
101 CGCAGCAGCT CAACGGTTT TGGCAGCAGA TGCCGCGCGA CATACGCGGG
151 CTGTTGCGCC AACACGACGG CTATTGGCGG CTGGTGCGCC CATTGGCGGT
201 TTTCGATGCC GAAGGTTTGC GCGAGCTGGG GGAAAGGTCG GGTTTTCAGA
251 CGGCATTGAA GCACGAGTGC GCGTCCAGCA ACGACGAGAT ACTGGAATTG
301 GCGCGGATTG CGCCGGACAA GGCGCACAAA ACCATATGTG TGACCCACCT
351 GCAAAGTAAG GGCAGGGGGC GGCAGGGGCG GAAAGTGGTCG CACCGTTTGG
401 GCGAGTGTCT GATGTTTCACT TTTGGCTGGG TGTTTGACCG GCCGCGAGTAT
451 GAGTTGGGTT CGCTGTCGCC TGTTGCGGCA GTGGCGTGCC GCGCGCCTT
501 GTCGCGTTTG GGTGTTGAAA CGCAAATCAA GTGGCCAAAC GATTTGGTCG
551 TCGGACGCGA CAAATTGGGC GGCATTCTGA TTGAAACGGT CAGGACGGGC
601 GGCAAAACGG TTGCCGTGGT CCGTATCGGC ATCAATTTCG TGCTGCCCAA
651 GGAAGTGGAA AACGCCGCTT CCGTGCAATC GCTGTTTCAG ACGGCATCGC
701 GCGGGGAAA TGCCGATGCC GCCGTGTGCG TGGAACGCGT GTTGCGGAA
751 CTTGATGCGG TGTGTTGCA ATATGCGCGG GACGGATTG CGCCTTTGT
801 GCGGGAATAT CAGGCTGCCA ACCGCGACCA CGGCAAGGCG GTATTGCTGT
851 TCGCGACGG CGAAACCGTG TTCGAAGGCA CGGTTAAAGG CGTGGACGGA
901 CAAGGCGTTC TGCACTTGGG AACGGCAGAG GGCAAACAGA CGGTCGTCAG
951 CGCGGAAATC AGCCTGCGGT CCGACGACAG GCCGGTTTCC GTGCCGAAGC
1001 GCGGGGATTC GGAACGTTTT CTGCTGTTGG ACGGCGGCAA CAGCCGGCTC
1051 AAGTGGGCGT GGTGGAATA CGGCACGTTT GCAACCGTCG GTAGCGCGCC
1101 GTACCGCGAT TTGTCGCCTT TGGGCGCGGA GTGGGCGGAA AAGGTGGATG
1151 GAAATGTCCG CATCGTCGGT TCGCGCGTGT GCGGAGAATT CAAAAAGGCA
1201 CAAGTGCAGG AACAGCTCGC CCGAAAATC GAGTGGCTGC CGTCTCCGC
1251 ACAGGCTTTG GGCATACGCA ACCACTACCG CCACCCCGAA GAACACGGTT
1301 CCGACCGCTG GTTCAACGCC TTGGGCGAGC GCCGCTTACG CCGCAACGCC
1351 TGCGTCGTCG TCAGTTGCGG CACGGCGGTA ACGGTTGACG CGCTACCGA
1401 TGACGGACAT TATCTCGGGG GAACCATCAT GCCCGGTTTC CACCTGATGA
1451 AAGAAATCGT CGCCGTCCGA ACCGCCAACC TCAACCGGCA CGCCGGTAAG
1501 CGTTATCCTT TCCCGACCAC AACGGGCAAT GCCGTCGCCA GCGGCATGAT
1551 GGATGCGGTT TCGGCTCTCG TTATGATGAT GCACGGGCGT TTGAAAGAAA
1601 AAACCGGGGC GGGCAAGCCT GTCGATGTCA TCATTACCGG CGGCGGCGCG
1651 GCAAAAGTTG CCGAAGCCCT GCCGCTGCA TTTTGGCGG AAAATACCGT
1701 GCGCGTGGCG GACAACCTCG TCATTACCGG GCTGCTGAAC CTGATTGCCG
1751 CCGAAGGCGG GGAATCGGAA CATACTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1300; ORF 311-1.a>:

```

a311-1.pep
1  MTVLKPSHWR VLAELADGLP QHVSQALARMA DMKPQQLNGF WQOMPAHIRG
51  LLRQHDGYWR LVRPLAVFDA EGLRELTERS GFQALKHEC ASSNDEILEL
101 ARIAPDKAHK TICVTHLQSK GRGRQGRKWS HRLGECLMFS FGWVFD RPQY
151 ELGSLSPVAA VACRRALSRL GLKTQIKWPN DLVVGRDKLG GILIEVVRTG
201 GKTVAUVVIG INFVLPKEVE NAASVQSLFQ TASRRGNADA AVLLETLLE
251 LDAVLLQYAR DGFAPFVAEY QANRDHGKA VLLLRDGETV FEGTVKGVDG
301 QGVHLHLETA GKQTVVSGEI SLRSDRPPVS VPKRRDSERF LLLDGGNSRL
351 KWAUVENGTF ATVGSAFYRD LSPLGAEWAE KVDGNVRIVG CAVCGEFKKA
401 QVQEQALARKI EWLPSAQAL GIRNHYRHEP EHGSDRWFNA LGSRRFSRNA
451 CVVVSCTAV TVDALTDGHH YLGGTIMPGF HLMKESLAVR TANLNRHAGK
501 RYFPFTTGN AVASGMMDAV CGSVMMHGR LKEKTGAGKP VDVITGGGA
551 AKVAEALPPA FLAENTVRVA DNLVIHGLLN LIAAEGGESE HT*

```

a311-1/m311-1 98.5% identity in 591 aa overlap

```

a311-1.pep      10      20      30      40      50      60
MTVLKPSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR
|||||
m311-1          10      20      30      40      50      60
MTVLKLSHWRVLAELADGLPQHVSQALARMADMKPQQLNGFWQOMPAHIRGLLRQHDGYWR

a311-1.pep      70      80      90      100     110     120
LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK
|||||
m311-1          70      80      90      100     110     120
LVRPLAVFDAEGLRELTERS GFQALKHECASSNDEILELARIAPDKAHKTICVTHLQSK

```

a311-1.pep	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVFDPRQYELGSLSPVAAVACRRALSRLGLKTQIKWPN					
m311-1	130	140	150	160	170	180
	GRGRQGRKWSHRLGECIMFSFGWVFDPRQYELGSLSPVAAVACRRALSRLGLDVQIKWPN					
a311-1.pep	190	200	210	220	230	240
	DLVVGRDKLGGILIIETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
m311-1	190	200	210	220	230	240
	DLVVGRDKLGGILIIETVRTGGKTVAVVGIGINFVLPKEVENAASVQSLFQTASRRGNADA					
a311-1.pep	250	260	270	280	290	300
	AVLLETLLAELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVDG					
m311-1	250	260	270	280	290	300
	AVLLETLLVELDAVLLQYARDGFAPFVAEYQAANRDHGKAVLLLRDGETVFEGTVKGVVDG					
a311-1.pep	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAVVENGTFF					
m311-1	310	320	330	340	350	360
	QGVHLHLETAEGKQTVVSGEISLRSDDRPVSVPKRRDSEFLLLDGGNSRLKWAVVENGTFF					
a311-1.pep	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKVDGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
m311-1	370	380	390	400	410	420
	ATVGSAPYRDLSPGAEWAEEKADGNVRIVGCAVCGEFKKAQVQEQQLARKIEWLPSSAQAL					
a311-1.pep	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
m311-1	430	440	450	460	470	480
	GIRNHYRHPEEHGSDRWFNALGSRFRSRNACVVVSCGTAVTVDALTDGHHYLGGTIMPGF					
a311-1.pep	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
m311-1	490	500	510	520	530	540
	HLMKESLAVRTANLNRHAGKRYPFPTTTGNAVASGMMDAVCGSVMMHGRLEKKTGAGKP					
a311-1.pep	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIHGLLNLI AEGGESEHTX					
m311-1	550	560	570	580	590	
	VDVIITGGGAAKVAEALPPAFLAENTVRVADNLVIYGLNMI AEGGREYEHIX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1301>:

g312.seq

```

1  atgaGtatCc aatCcGgcga AATTTtagaa accgtCAAAA TGGTTGCCGA
51  ccggaATttt gAtgtccgCA CCATTAccat cggcaTTgaT ttgcacgact
101 gcatcagcac cgacatcgac gtgttaAACC AAAACATtta caaCAaaaTc
151 accacggtcg gcaaagactT GGTGGCAacg Gcgaaacacc tTTccgcCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGAttgccc
251 AaatcGCGGC GGcgaccaAa gccgaCAGTT AtgtcAGCgt ggcgCAGact
301 tTGGACAAGG CAGCCAAAGC CATCGGCGTG TCCTTTATCG GcggCTTTTC
351 CGCGCTGGTG CAAAAAGGTA TGTGCGCTTC GGATGAGGTG TTGATCCGTT
401 CCGTTCCCGA AGCGATGAAA ACTACCGATA TCGTGTGCAG CTCCATCAAT
451 ATCGGCAGCA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCAGG
501 CGAAACCATC AAACGCACGG CTGAAATCAC ACCCGAAGGT TTCGCTGCG
551 CCAAAATCGT CGTGTTCTGC AACCGGTGG AAGACAATCC GTTTATGGCG
601 GGTGCGTTCT ACGGCTCGGG CGAAGCGGAT GCTGTGATTA ATGTCGGCGT
651 ATCCGGTCCA GGCGTGGTCA AAGCCGCGCT GGAAAATTCG GACGCGGTCA
701 GCCTGACCGA GGTGCGCGAA GTCGTGAAGA AAACCGCTTT CAAAATCACC
751 CGCGTGGGCG AACTCATCGG TCGCGAAGCC TCAAAAATGC TGAATATCCC
801 GTTCGGCATT CTCGATTGTG CGCTGGCACC GACCCCGGCC GTCGGCGACT
851 CCGTGGCGCG CATTCTTGAA GAAATGGGCT TGAGCGTCTG CCGTACGCAC

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717

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901 GGCACAACAG CAGCTTTGGC ATTGCTGAAC GATGCCGTGA AAAAGGGCGG
951 CATGATGGCT TCCAGCGCGG TCGGCGGTTT GAGCGGCGCG TTTATCCCCG
1001 TTTCCGAAGA CGAAGGTATG ATTGCCGCCG CCGAGGCAGG CGTGTTGACG
1051 CTGGACAAAC TCGAAGCCAT GACCGCCGTC TGCTCCGTTG GTTTGGACAT
1101 GATTGCCGTT CCCGGCGACA CGCCCGCGCA CACCATTTCG GGCATCATCG
1151 CCGACGAAGC CGCCATCGGC ATGATCAACA GCAAAACCAC CGCCGTGCGC
1201 ATTATTCGGG TAACGGGCAA AACCGTCGGC GACAGCGTCG AGTTCGGCGG
1251 TCTGTTGGGC TACGCGCCTG TAATGCCGGC AAAAGAAGGT TCGTGCGAAG
1301 TGTTCTGCAA CCGGGGCGGC AGGATTCCTG CACCGGTTCA ATCGATGAAA
1351 AACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1302; ORF 312.ng>:

g312.pep

```

1  MSIQSGEILE TVKMVADRNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT AKHLSAKYGV PIVNQRISVT PIAQIAAATK ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSVPEAMK TTDIVCSSIN
151 IGSTRAGINM DAVKLAGETI KRTAEITPEG FGC AKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP GVVKAALENS DAVSLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALLN DAVKKGGMMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV CSVGLDMIAV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPAKEG SCEVFNRRGG RIPAPVQSMK
451 N*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1303>:

m312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGTTGCCGGA
51  CCAGAATTTT GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAG CGATATCAAT GTGTTGAACC AAAATATTTA CAATAAAATT
151 ACCACAGTCG GCAAAGACTT GGTCACACG GCAAAATATC TGTCTGCCAA
201 ATACGGCGTA CCGATTGTGA ATCAGCGCAT TTCCGTTACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAC
301 TTGGATAAAG CTGCCAAAGC CATCGGTGTG TCTTTTATCG GCGGTTTTTC
351 CGCGTTGGTG CAAAAGGGA TGTGCGCTTC GGATGAGGTG TTAATCCGCT
401 CCATTCCCGA AGCGATGAAG ACTACCGATA TTGTGTGCwG CTCCATCAAT
451 ATCGGCAGTA CGCGTGCCGG TATCAATATG GATGCGGTCA AGCTGGCGGG
501 CGAAACCGTc AAACGCACGG CGGAAATCAC GCCGAAGGT TTCGGTGCGG
551 CTAAAATTGT CGTGTCTGCG AACGCGGTGG AAGACAACCC GTTTWTGCGG
601 GGCGCGTTTC ATGGTTCGGG CGATGCCGTT ATCAATGTGCG GCGTATCCGG
651 CCCAGGTGTC GTAAAAGCCG CGTTGGAAAA TTCAGATGCA ACGACATTGA
701 CCGAAGTTGC GGAAGTAGTG AAGAAAAC TGCTTCAAAT TACCCGCGTG
751 GGCGAACTCA TCGGCCGCGA AGCCTCAAAA ATGCTGAATA TCCCGTTTGG
801 TATTCTCGAC TTGTGCGCGA CCCGCGCGT CGGCGACTCA GTGCGACGCA
851 TTCTTGAAGA AATGGGCTTG AGCGTCTGCG GTACGCACGG CACAACAGCA
901 GCTTTGGCAT TGCTGAACGA TGCCGTGAAA AAAGGCGGCA TGATGGCTTC
951 CAGCGCGGTC GGGGTTTGA GTGGCGCGTT TATCCCCGT TCCGAAGACG
1001 AAGGTATGAT yGmCgCcGCC GAAGCAGGCG TGCTGACGCT GGACAAACTC
1051 GAAGCCATGA CCGCGGTTTG TTCGGTCGGC TTGGATATGA TTGCCGTTCC
1101 CGGCGACACG CCCGCGCACA CCATTTCGG CATCATTGCC GACGAAGCCG
1151 CCATCGGCAt GATCAACAGC AAAACCACTG CCGTGCGCAT TATTCCGGTA
1201 ACCGGTAAAA CCGTCGGCGA CACGGTCGAG TTCGGCGGCT TGTGGGCTA
1251 CGCGCTGTG ATGCCGGTCA AAGAAGGTTG GTGCGAAGTA TTCGTCAACC
1301 GAGGCGGCAG AATTCCGGCT CCGGTTCAAT CGATGAAAAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1304; ORF 312>:

m312.pep

```

1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISSDIN VLNQNIYNKI
51  TTVGKDLVTT AKYLSAKYGV PIVNQRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCX SIN
151 IGSTRAGINM DAVKLAGETV KRTAEITPEG FGC AKIVVFC NAVEDNPFXA
201 GAFHGS GDAV INVGVS GPV VKAALENS DA TTLTEVAEVV KKTAFKITRV
251 GELIGREASK MLNIPFGILD LSPTPPV GDS VARILEEMGL SVCGTHGTTA
301 EALALLNDAVK KGGMMASSAV GGLSGAFIPV SEDEGMIXAA EAGVLTLDKL
351 AMTAVCSVG LDMIAVPGDT PAHTISGIIA DEAAIGMINS KTTAVRIIPV
401 TGKTVGDTVE FGGLLGYPV MPVKEGSCEV FVNRGGRI PA PVQSMKN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 312 shows 95.6% identity over a 451 aa overlap with a predicted ORF (ORF 312.ng) from *N. gonorrhoeae*:

m312/g312

m312.pep	10	20	30	40	50	60
	MSIQSGEILETVKMVADQNFVDTITIGIDLHDCISSDINVLNQNIYNKITTGVKDLVTT					
g312	MSIQSGEILETVKMVADRNFVDTITIGIDLHDCISTDIDVLNQNIYNKITTGVKDLVAT					
	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
	AKYLSAKYGVPIVNQRISVTPIAQIAAATHADSYVSVSAQTLDKAAKAIGVSFIGGFSALV					
g312	AKHLSAKYGVPIVNQRISVTPIAQIAAATKADSYVSVSAQTLDKAAKAIGVSFIGGFSALV					
	70	80	90	100	110	120
m312.pep	130	140	150	160	170	180
	QKGMSPSDEVLIRSIPEAMKTTDIVCXSNIGSTRAGINMDAVKLAGETVKRTAEITPEG					
g312	QKGMSPSDEVLIRSVPEAMKTTDIVCSSINIGSTRAGINMDAVKLAGETIKRTAEITPEG					
	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
	FGCAKIVVFCNAVEDNPFKAGAFHGSG--DAVINVGVS GPGVVKAALENS DATTLTEVAE					
g312	FGCAKIVVFCNAVEDNPFMAGAFHGSGEADAVINVGVS GPGVVKAALENS DAVSLTEVAE					
	190	200	210	220	230	240
m312.pep	240	250	260	270	280	290
	VVKKTAFKITRVGELIGREASKMLNIPFGILDLS--PTPPVGDSVARILEEMGLSVCGTH					
g312	VVKKTAFKITRVGELIGREASKMLNIPFGILDLSLAPTAVGDSVARILEEMGLSVCGTH					
	250	260	270	280	290	300
m312.pep	300	310	320	330	340	350
	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
g312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
m312.pep	360	370	380	390	400	410
	CSVGLDMI AVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
g312	CSVGLDMI AVPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
m312.pep	420	430	440			
	YAPVMPVKEGSCEVFVNRGGRI PAPVQSMKNX					
g312	YAPVMPAKEGSCEVFVNRGGRI PAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1305>:

a312.seq

```

1  ATGAGTATCC AATCCGGCGA AATTTTAGAA ACCGTCAAAA TGGTTGCCGA
51  CCAGAATTTC GATGTCCGCA CCATTACCAT CGGCATTGAT TTGCACGACT
101 GCATCAGCAC CGACATCGAC GTGTGAACC AAAATATTTA CAACAAAATT
151 ACCACGGTCG GCAAAGACTT GGTGGCGACA GCAAATATC TGTCTGCCAA
201 ATACGGCGTG CCGATTGTGA ATCAGCGCAT TTCTGTCACG CCGATTGCCC
251 AAATCGCGGC GGCCACCCAT GCTGATTCTT ACGTCAGCGT GGCGCAAAT

```



```
a312.pep
1  MSIQSGEILE TVKMVADQNF DVRTITIGID LHDCISTDID VLNQNIYNKI
51  TTVGKDLVAT  AKYLSAKYGV PIVNQIRISVT PIAQIAAATH ADSYVSVAQT
101 LDKAAKAIGV  SFIGGFSALV QKGMSPSDEV LIRSIPEAMK TTDIVCSSMA
151 IGSTRAGINM DAVRLAGETI KRTAEITLEG FGCAKIVVFC NAVEDNPFMA
201 GAFHGSGEAD AVINVGVS GP GVVKAALENS DATTLTEVAE VVKKTAFKIT
251 RVGELIGREA SKMLNIPFGI LDLSLAPTPA VGDSVARILE EMGLSVCGTH
301 GTTAALALN  DAVKKGGNMA SSAVGGLSGA FIPVSEDEGM IAAAEAGVLT
351 LDKLEAMTAV  CSVGLDMIIV PGDTPAHTIS GIIADEAAIG MINSKTTAVR
401 IIPVTGKTVG DSVEFGGLLG YAPVMPVKEG SCEVFVNRGG RIPAPVQSMK
451 N*
```

	10	20	30	40	50	60
m312.pep	MSIQSGEILETVKMQVADQNF	DVRTITIGIDLHDCISSDINVL	NQNIYNKITT	VGKDLVTT		
a312	MSIQSGEILETVKMQVADQNF	DVRTITIGIDLHDCISTDIDVL	NQNIYNKITT	VGKDLVAT		
	10	20	30	40	50	60
m312.pep	70	80	90	100	110	120
a312	70	80	90	100	110	120
	130	140	150	160	170	180
m312.pep	QKGMSPSDEVLIRSIPEAMKTT	DIVCX	SINIGSTRAGINMDAVK	LAGETVKRTAEIT	PEG	
a312	QKGMSPSDEVLIRSIPEAMKTT	DIVCSSINIGSTRAGINMDAV	RLAGETIKRTAEIT	LEG		
	130	140	150	160	170	180
m312.pep	190	200	210	220	230	
a312	190	200	210	220	230	
	240	250	260	270	280	290
m312.pep	VVKKTAFKITRVGELIGREASKMLN	IPFGILDLS--PTPPVGDSVARILEEMGLS	VCGTH			
a312	VVKKTAFKITRVGELIGREASKMLN	IPFGILDLSLAPTAVGDSVARILEEMGLS	VCGTH			

720

	250	260	270	280	290	300
	300	310	320	330	340	350
m312.pep	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIXAAEAGVLTLDKLEAMTAV					
a312	GTTAALALLNDAVKKGGMMASSAVGGLSGAFIPVSEDEGMIAAAEAGVLTLDKLEAMTAV					
	310	320	330	340	350	360
	360	370	380	390	400	410
m312.pep	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDTVEFGGLLG					
a312	CSVGLDMIAPGDTPAHTISGIIADEAAIGMINSKTTAVRIIPVTGKTVGDSVEFGGLLG					
	370	380	390	400	410	420
	420	430	440			
m312.pep	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
a312	YAPVMPVKEGSCEVFVNRGGRIAPVQSMKNX					
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1307>:

g313.seq

```

1  atggacgacc cgcgcaccta cggatcgggc aatcccgggc cgaccaatgt
51  tttagcgagc ggcaaaaaaa aggcggccgc gctgacgctc ttgggcgatg
101 cgcgcaaagg tttggttgcc gttttgcttg cacgcgtgct tcaagaaccg
151 ctccggttat ccgacagcgc aatcgccgcc gtcgcactcg ccgcgctggt
201 cgggcatatg tggccggtgt ttttcggatt taaggcgggc aaaggcggtg
251 caacggcatt gggcgtgctt ctggcactct ctctgcaac tgccttggtc
301 tgcgcgttga tttgcttgt gatggcattc ggcttcaaag taccctccct
351 tgccgcgctg gtcgccacaa ccgcgcgcc ccttgccgca ctgtttttta
401 tgccgcatac ttcttggtt ttcgcaaccc tcgcaatcgc catattggtg
451 ttgctccgcc ataagagcaa catcctcaac ctgattaaag gcaaagaaag
501 caaaatcggc gaaaaacgct ga

```

This corresponds to the amino acid sequence <SEQ ID 1308; ORF 313.ng>:

g313.pep

```

1  MDDPRTYSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL VATTAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNILN LIKGESKIG EKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1309>:

m313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTAGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCCACAAC TGCCTTGCTC
301 TGCGCGTTGA TTTGGCTTGT TATGGCATTG GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCACC GGTGCGCGCA TCCTTCTTAA
401 TGCCGCACGT CTCGTGGGTT TGGGCGACCG TCGCCATTGC TTTGCTGGTG
451 TTGTTCCGCC ACAAAGTAA TATCGTCAAG CTGCTCGAAG GCAGAGAAAG
501 CAAAATCGGC GGCAGCCGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1310; ORF 313>:

m313.pep

```

1  MDDPRTYSG NPGATNVLRS GKKKAAALTL LGDAAKGLVA VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKGG KGVATALGLV LALSPATALV
101 CALIWLVMFA GFKVSSLAAL TATIAAPVAA SFFMPHVSWS WATVAIALLV
151 LFRHKSNIVK LLEGRESKIG GSR*

```

Computer analysis of this amino acid sequence gave the following results:

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Homology with a predicted ORF from *N. gonorrhoeae*

ORF 313 shows 90.2% identity over a 173 aa overlap with a predicted ORF (ORF 313.ng) from *N. gonorrhoeae*:

m313/g313

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
g313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
g313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLLEGRESKIGGSRX					
g313	VATTAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNIKGKESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1311>:

a313.seq

```

1  ATGGACGACC CGCGCACCTA CGGATCGGGC AATCCGGGGG CAACCAATGT
51  TTTACGCAGC GGCAAAAAAA AGGCGGCCGC GCTGACGCTC TTGGGCGATG
101 CCGCCAAAGG TTTGGTTGCC GTTTTGCTTG CACGCGTGCT TCAAGAACCG
151 CTCGGTTTAT CCGACAGCGC AATCGCGGCC GTCGCACTCG CCGCGCTGGT
201 CGGGCATATG TGGCCGGTGT TTTTCGGATT TAAAGGCGGC AAAGGCGTGG
251 CAACGGCATT GGGCGTGCTT CTGGCACTCT CTCCACAAC TGCCTTGGTC
301 TCGCGTGA TTTGGCTTGT GATGGCATTC GGCTTCAAGG TGTCTCCCT
351 TGCCGCATTA ACCGCCACAA TCGCCGCCCC CCTTGCCGCA CTGTTTTTTA
401 TGCCGCATAC TTCTTGGATT TTCGCAACCC TCGCAATCGC CATATTGGTG
451 TTGCTCCGCC ATAAGAGCAA CATCTCAAC CTGATTAAAG GCAAAGAAAG
501 CAAAATCGGC GAAAAACGCT GA

```

This corresponds to the amino acid sequence <SEQ ID 1312; ORF 313.a>:

a313.pep

```

1  MDDPRTYGS NPGATNVLR S GKKKAAAL TL LGDAAKGL V VLLARVLQEP
51  LGLSDSAIAA VALAALVGHM WPVFFGFKG G KGVATALGV L LALSPTTALV
101 CALIWLVMF GFKVSSLAAL TATIAAPLAA LFFMPHTSWI FATLAIAILV
151 LLRHKSNI LN LIKGKESKIG EKR*

```

m313/a313 90.8% identity in 173 aa overlap

	10	20	30	40	50	60
m313.pep	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
a313	MDDPRTYGSNPGATNVLRSGKKKAAALTLLGDAAKGLVAVLLARVLQEPGLGLSDSAIAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m313.pep	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPATALVCALIWLVMFAGFKVSSLAAL					
a313	VALAALVGHMWPVFFGFKGGKVATALGVLLALSPPTALVCALIWLVMFAGFKVSSLAAL					
	70	80	90	100	110	120
	130	140	150	160	170	
m313.pep	TATIAAPVAASFFMPHVSWWATVAIALLVLRHKSNIIVKLLLEGRESKIGGSRX					
a313	TATIAAPLAALFFMPHTSWIFATLAIAILVLLRHKSNIILNIKGKESKIGEKRX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1313>:

```
g401.seq
  1  atgaaattac aacaattggc tgaagaaaaa atcggcggttc tgattgtgtt
 51  cacgctgctt gtagtcagtg tcggtctgtt gattgaagtt gtgcccttgg
101  cctttaccaa ggcggaaca cagccggcgc cggcggtgaa gccttacaat
151  gccctgcagg ttgccggacg cgatatttac atccgtgagg gctgttacaa
201  ctgccactct caaatgattc gtccgttccg tgcggaaacc gagcggtacg
251  gtcattactc tgttgccgga gagtcggttt acgaccatcc gttccaatgg
301  ggttccaaac gtaccggtcc tgatttggca cgtgtgggag gccgctattc
351  cgacgaatgg caccgcatcc acctgctgaa tccccgtgat gtcgtgcctg
401  agtccaatat gccggcattc ccgtggcttg cacgcaataa agtcgatgtc
451  gatgcaaccg ttgccaacat gaaggctttg cgtaaagtag gtactcctta
501  cagtgatgag gaaattgcca aagcgcttga ggctttggca aacaaatccg
551  agctggatgc ttagtcgcc tatctgcaag gattgggtct ggctttgaaa
601  aacgtaagggt aa
```

This corresponds to the amino acid sequence <SEQ ID 1314; ORF 401.ng>:

```
g401.pep
  1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1315>:

```
m401.seq
  1  ATGAAATTAC AaCAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
 51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101  CCTTTACCAA GGCGGCAACA CAGCCGGCGC CGGGCGTGAA GCCTTACAAT
151  GCCCTGCAGG TTGCCGGACG CGATATTTAC ATCCGTGAGG GCTGTACAA
201  CTGCCACTCG CAAATGATTG GTCCGTTCCG TGCGGAAACC GAGCGTTACG
251  GTCACTACTC TGTGCGGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301  GGTTCCAAAC GTACCGGTCC TGATTGGGCA CGTGTGGGCG GTCGCTATTC
351  CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCCGTGAT GTCGTGCCTG
401  AGTCCAATAT GCCGGCATTG CCGTGGCTTG CACGCAATAA AGTCGATGTC
451  GATGCAACCG TTGCCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501  CAGTGATGAG GAAATTGCGA AAGCACCTGA GGCTTTGGCA AACAAATCCG
551  AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601  AACGTAAGGT AA
```

This corresponds to the amino acid sequence <SEQ ID 1316; ORF 401>:

```
m401.pep
  1  MKLQQLAEEK IGV LIVFTLL VSVGLLIEV VPLAFTKAAT QPAPGVKPYN
 51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101  GSKRTGPDLA RVGGRYSEW HRIHLLNPRD VVPESNMPAF PWLARNKVDV
151  DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDVVA YLQGLGLALK
201  NVR*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 401 shows 100.0% identity over a 203 aa overlap with a predicted ORF (ORF 401.ng) from *N. gonorrhoeae*:

```
m401/g401
      10      20      30      40      50      60
m401.pep  MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
          |||||
g401      MKLQQLAEEKIGVLIVFTLLVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90     100     110     120
m401.pep  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQW GSKRTGPDLARVGGRYSEW
```

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```

      |||
g401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIKAPEALA
      |||
g401  HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDAVVAYLQGLGLALKNVRX
      |||
g401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1317>:

```

a401.seq
1  ATGAAATTAC AACAAATTGGC TGAAGAAAAA ATCGGCGTTC TGATTGTGTT
51  CACGCTGCTT GTAGTCAGTG TCGGTCTGTT GATTGAAGTT GTGCCCTTGG
101 CCTTTACCAA GCGCGCAACA CAGCCGGCGT CGGGCGTGAA GCCTTACAAT
151 GCCCTGCAGG TTGCCGGACG CGATATTAC ATCCGTGAGG GCTGTTACAA
201 CTGCCACTCG CAAATGATTC GTCCGTTCCG TCGGGAACC GAGCGTTACG
251 GTCATTACTC TGTGCGCGGA GAGTCGGTTT ACGACCATCC GTTCCAATGG
301 GGTTCCAAAC GTACCGGTCC TGATTGGGCA CGTGTGGGCG GTCGCTATTC
351 CGACGAATGG CACCGTATCC ACCTGCTGAA TCCCGTGAT GTCGTGCCTG
401 AGTCCAATAT GCCGGCATTC CCGTGGCTTG CACGCAATAA AGTCGATGTC
451 GATGCAACCG TTGCAACAT GAAGGCTTTG CGTAAAGTAG GTACTCCTTA
501 CAGTGATGAG GAAATTGCGA AAGCGCCTGA GGCTTTGGCA AACAAATCCG
551 AGCTGGATGC TGTAGTCGCC TATCTGCAAG GATTGGGTCT GGCTTTGAAA
601 AACGTAAGGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1318; ORF 401.a>:

```

a401.pep
1  MKLQQLAEEK IGV LIVFTLL VVSVGLLIEV VPLAFTKAAT QPASGVKPYN
51  ALQVAGRDIY IREGCYNCHS QMIRPFRAET ERYGHYSVAG ESVYDHPFQW
101 GSKRTGPDLA RVGGGRYSDEW HRIHLLNPRD VVPESNMPAF PLARNKVDV
151 DATVANMKAL RKVGTPYSDE EIAKAPEALA NKSELDAVVA YLQGLGLALK
201 NVR*

```

m401/a401 99.5% identity in 203 aa overlap

```

      10      20      30      40      50      60
m401.pep MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPAPGVKPYNALQVAGRDIY
      |||
a401  MKLQQLAEEKIGVLIVFTLLVVSVGLLIEVVPLAFTKAATQPASGVKPYNALQVAGRDIY
      10      20      30      40      50      60

      70      80      90      100     110     120
m401.pep IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      |||
a401  IREGCYNCHSQMIRPFRAETERYGHYSVAGESVYDHPFQWGSKRTGPDLARVGGGRYSDEW
      70      80      90      100     110     120

      130     140     150     160     170     180
m401.pep HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIKAPEALA
      |||
a401  HRIHLLNPRDVPESNMPAFPLARNKVDVDATVANMKALRKVGTPYSDEEIIKAPEALA
      130     140     150     160     170     180

      190     200
m401.pep NKSELDAVVAYLQGLGLALKNVRX
      |||
a401  NKSELDAVVAYLQGLGLALKNVRX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1319>:

g402.seq

```

1  ATGGATATGG TGAACACTAA Accgaatact agtgtgatta atatgctttc
51  tttccttacc ggattATTTGA GCTTGGGTat agaagtCtTg tGGGTAAGGA
101 TGttttcgtT CGCagcAcag tccgtgcctc aggcATTtTC atttattcct
151 gcctGttttc tgACCGtat cgccgtcggc gCgTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCctT TATCGGGCAG TgcttcttgT
251 GGGCGGGTAT TgccgaTttt ttgatTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTTccg gtttcGTCCA CCACGCCGGT AtttTCATTA CCCTgtctgc
351 CGtcGTCAGG GGGTTGATT TCCCACTGT ACACCATgtg GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATttggt
501 gTCCACCCAA CAGATTtacc tgctcatCTG TTTGATTtCT GCTGctgtcc
551 cTTTGTtTg tacaCTGtTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTTAC TGCCGGATTTC
651 TGTCTTTCAA AATATTGCTG GCCGTCCGGA TAGGTGATT GAAAAAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTtTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATATATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCC GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGAcg agccgcAAAT CGCACCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATTCGACTT GGTACTGGCG
1101 TGCCTATTCC ACTAACCTGT TGAGTGCGGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATgctTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTACGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCctt AATAAAGAAC
1301 TGCTCaagca aCGCCTTtcc cgGTTGATTT GGCCGAAAAG CGGCAGgcac
1351 gtATTtGACA GCAGCACCGT GGATGTGCA GCACAAAAGG TTGctctcCG
1401 TATGCTGATT CGGATGACGG AAcctTCGGC TGGGGCGGAA GTCATTACTG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1320; ORF 402.ng>:

g402.pep

```

1  MDMVNTKPNT SVINMLSFLT GLLSLGIEVL WVRMFSFAAQ SVPQAFSFLI
51  ACFLTGIavg AYFGKRICRS RFVDIPFIGQ CFLWAGIADf LILGAawLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDLLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIAGRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DIFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSwARVLS
301 AIPeMSMIV AEINPAYRSL IADepQIAPL LQDKRVEIVL DDGRKwLRRH
351 PDEKFDLILM NSTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVVSRLI RMTEPSAGAE VITDDNMIVE YKYGRGI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1321>:

m402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGChTTC
51  TTTCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGTCTTG TGGGTGAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTtTC ATTTACCCTT
151 GCCTGTTTTc TGACCGGTAT CGCCGTGCGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTG ATATTCCCTT TATCGGGCAG TGCTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTTCCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAsA sGGTTGATT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTCGC CamCGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTtCTT
501 GTCCACCCAA CAGATTtACC TGCTCATCTG TwTGATTtCT GCTGCTGTCC
551 CTTTGTtTgT TACACTGTTC CAAAAAAGTC TCCGACTGAA TGCAGTGTCCG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTcyTAC TGCCGGATTTC

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651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAgGCTGATT GAAAACAAAC
701 ACGGCATTGT TGCGGTTTAC CATAGAGATG GTGATAAGGT TGTTTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTTCGT CGTTGGACTG AGTACAGGTT CGTGGGCGCG CGTCTTGCTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAATAGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGC GGA ATTTTAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTTCCTT AATAAGAAG
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTT GGCCGGAAG CCGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG aAcCTTCGGC TGGGGCGGAA GTTATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1322; ORF 402>:

m402.pep

```

1 MDIVNTKPNT SLIYMXSFLS GLLSLGIEVL WVRMFSFAAQ SVPQAFSFTL
51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAWLLT
101 GFSGFVHHAG IFITLSAVVX XLIFPLVHHV GTDGNKSGRQ VSNVYFAXVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICXIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLKQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 402 shows 97.0% identity over a 497 aa overlap with a predicted ORF (ORF 402.ng) from *N. gonorrhoeae*:

m402/g402

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLLSLGIEVLWVRMFSFAAQSVPAFSTLACFLTGIAVG					
	: : :					
g402	MDMVNTKPNTSVINMLSFLTGLLSLGIEVLWVRMFSFAAQSVPAFSTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVX					
g402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
g402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDLLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
g402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIAGRDRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					

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      |||
g402  HRDGDKVYVGANVYDGYNTDIFNSVNGIERAYLLPSLKS GIRRIFVVGLSTG SWARVLS
      250      260      270      280      290      300

      310      320      330      340      350      360
m402.ppep AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLR RHPDEKFDLILM
      |||
g402  AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLR RHPDEKFDLILM
      310      320      330      340      350      360

      370      380      390      400      410      420
m402.ppep NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGI VMFNTTHSPHAFATAVHSIPYAYRYGHMV
      |||
g402  NSTWYWRAYSTNLLSAEFLKQVQSHLTPDGI VMFNTTHSPHAFATAVHSIPYAYRYGHMV
      370      380      390      400      410      420

      430      440      450      460      470      480
m402.ppep VGSATPVVFPNKELLKQRLSRLIWPESGRHV FDSSTVDAAAQKVVSRLIQMTEPSAGAE
      |||
g402  VGSATPVVFPNKELLKQRLSRLIWPESGRHV FDSSTVDAAAQKVVSRLI RMTEPSAGAE
      430      440      450      460      470      480

      490
m402.ppep VITDDNMIVEYKYGRGIX
      |||
g402  VITDDNMIVEYKYGRGI
      490

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1323>:

a402.seq

```

1  ATGGATATAG TGAACACTAA ACCGAATACT AGTTTGATT ATATGCTTTC
51  TTTCCTTAGC GGCTTATTGA GCTTGGGTAT AGAAGCTTG TGGGTAAGGA
101 TGTTTTCGTT CGCAGCACAG TCCGTGCCTC AGGCATTTTC ATTTACTCTT
151 GCCTGTTTTT TGACCGGTAT CGCCGTCGGC GCGTATTTTG GCAAACGGAT
201 TTGCCGCAGC CGCTTTGTTG ATATTCCCTT TATCGGGCAG TGCTTCTTGT
251 GGGCGGGTAT TGCCGACTTT TTGATTTTGG GTGCTGCGTG GTTGTGACG
301 GGTTTTTCG GCTTCGTCCA CCACGCCGGT ATCTTCATTA CCCTGTCTGC
351 CGTCGTCAGA GGGTTGATTT TCCCGCTCGT ACACCATGTG GGTACGGATG
401 GCAACAAATC CGGACGACAG GTTTCCAATG TTTATTTTCG CAACGTTGCC
451 GGCAGTGCAT TGGGTCCGGT CCTTATCGGC TTTGTGATAC TTGATTTCTT
501 GTCCACCCAA CAGATTTACC TGCTCATCTG TTTGATTTCT GCTGCTGTCC
551 CTTTGTTTTG TACACTGTTT CAAAAAAGTC TCCGACTGAA TGCAGTGTCTG
601 GTAGCAGTTT CCCTAATGTT CGGCATCCTC ATGTTCTCTAC TGCCGGATTTC
651 TGTCTTTCAA AATATTGCTG ACCGTCCGGA TAGGCTGATT GAAAAACAAC
701 ACGGCATTGT TCGGTTTAC CATAGAGATG GTGATAAGGT TGTATTATGGG
751 GCGAATGTAT ACGACGGCGC ATACAATACC GATGTATTCA ATAGTGTCAA
801 CGGCATCGAA CGTGCCTATC TGCTACCCTC CCTGAAGTCT GGCATACGCC
851 GCATTTTCGT CGTTGGATTG AGTACAGGTT CGTGGGCGCG CGTCTTGTCT
901 GCCATTCCGG AAATGCAGTC GATGATCGTT GCGGAAATCA ATCCGGCATA
951 CCGTAGCCTT ATCGCGGACG AGCCGCAAAT CGCCCCGCTT TTGCAGGACA
1001 AACGTGTTGA AATTGTATTG GATGACGGTA GGAAATGGCT GCGTCGCCAT
1051 CCTGATGAAA AATTCGACCT GATTTTGATG AATACGACTT GGTACTGGCG
1101 TGCCTATTCC ACCAACCTGT TGAGTGCGGA ATTTTAAAAA CAGGTGCAAA
1151 GCCACCTTAC CCCGGATGGT ATTGTAATGT TTAATACCAC GCACAGCCCG
1201 CATGCTTTTG CTACCGCCGT ACACAGTATT CCCTATGCAT ACCGCTATGG
1251 GCATATGGTA GTCGGCTCGG CAACCCCGGT AGTTTCCCTT AATAAAGAAC
1301 TGCTCAAGCA ACGTCTCTCC CGGTTGATTG GGCCGGAAG CCGCAGGCAC
1351 GTATTTGACA GCAGCACCGT GGATGCTGCA GCACAAAAGG TTGTCTCTCG
1401 TATGCTGATT CAGATGACGG AACCTTCGGC TGGTGCGGAA GTCATTACCG
1451 ACGATAATAT GATTGTAGAA TACAAATACG GCAGAGGGAT TTAA

```

This corresponds to the amino acid sequence <SEQ ID 1324; ORF 402.a>:

a402.ppep

```

1  MDIVNTKPNT SLIYMLSFLS GLLSLGIEVL WVRMFSAFAQ SVPQAFSFTL

```



```

51 ACFLTGIAVG AYFGKRICRS RFVDIPFIGQ CFLWAGIADF LILGAAWLLT
101 GFSGFVHHAG IFITLSAVVR GLIFPLVHHV GTDGNKSGRQ VSNVYFANVA
151 GSALGPVLIG FVILDFLSTQ QIYLLICLIS AAVPLFCTLF QKSLRLNAVS
201 VAVSLMFGIL MFLLPDSVFQ NIADRPDRLI ENKHGIVAVY HRDGDKVYVG
251 ANVYDGAYNT DVFNSVNGIE RAYLLPSLKS GIRRIFFVGL STGSWARVLS
301 AIPEMQSMIV AEINPAYRSL IADEPQIAPL LQDKRVEIVL DDGRKWLRH
351 PDEKFDLILM NTTWYWRAYS TNLLSAEFLK QVQSHLTPDG IVMFNTTHSP
401 HAFATAVHSI PYAYRYGHMV VGSATPVVFP NKELLQRLS RLIWPESGRH
451 VFDSSTVDAA AQKVSRMLI QMTEPSAGAE VITDDNMIVE YKYGRGI*

```

m402/a402 99.0% identity in 497 aa overlap

	10	20	30	40	50	60
m402.pep	MDIVNTKPNTSLIYMXSFLSGLSLGIEVLWVRMFSFAAQSVPAQAFSFTLACFLTGIAVG					
a402	MDIVNTKPNTSLIYMLSFLSGLSLGIEVLWVRMFSFAAQSVPAQAFSFTLACFLTGIAVG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m402.pep	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVX					
a402	AYFGKRICRSRFVDIPFIGQCFLWAGIADFLILGAAWLLTGFSGFVHHAGIFITLSAVVR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m402.pep	XLIFPLVHHVGTGDNKSGRQVSNVYFAXVAGSALGPVLIGFVILDFLSTQQIYLLICXIS					
a402	GLIFPLVHHVGTGDNKSGRQVSNVYFANVAGSALGPVLIGFVILDFLSTQQIYLLICLIS					
	130	140	150	160	170	180
	190	200	210	220	230	240
m402.pep	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
a402	AAVPLFCTLFQKSLRLNAVSVAVSLMFGILMFLLPDSVFQNIADRPDRLIENKHGIVAVY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m402.pep	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
a402	HRDGDKVYVGANVYDGAYNTDVFNSVNGIERAYLLPSLKS GIRRIFFVGLSTGSWARVLS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m402.pep	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHHPDEKFDLILM					
a402	AIPEMQSMIVAEINPAYRSLIADEPQIAPLLQDKRVEIVLDDGRKWLRHHPDEKFDLILM					
	310	320	330	340	350	360
	370	380	390	400	410	420
m402.pep	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
a402	NTTWYWRAYSTNLLSAEFLKQVQSHLTPDGIVMFNTTHSPHAFATAVHSIPYAYRYGHMV					
	370	380	390	400	410	420
	430	440	450	460	470	480
m402.pep	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSTVDAAAQKVSRMLIQMTEPSAGAE					
a402	VGSATPVVFPNKELLQRLSRLIWPESGRHVFDSSTVDAAAQKVSRMLIQMTEPSAGAE					
	430	440	450	460	470	480
	490					
m402.pep	VITDDNMIVEYKYGRGIX					
a402	VITDDNMIVEYKYGRGIX					
	490					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1325>:

g406.seq

```

1   ATGCGGGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACGCTGACAG GTATTCCATC GCATGGCGGA GGCAAACGCT
101 TCGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCGGCG GAATACATAA ACAGCCCTGC CGTCCGCACC
301 GATTACACCT ATCCGCGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACGGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA GGAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CCAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTGCA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCCA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATCAAA CCGACGGAAG GATTGATGGT CGATTTCTCC GATATCCAAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCGAC AACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1326; ORF 406>:

g406.pep

```

1   MRARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK
51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRIYET AETTSGLTGT LTTSLSTLNA PALSRQSDG SGSRSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSQGIK PTEGLMVDPS DIQPYGNHTG NSAPSVEADN
301 SHEGYGYSDE AVRQHRQGP *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1327>:

m406.seq

```

1   ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG ACGCTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TTGCGGTCTGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 CACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTGCTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTTGACAGGT TTAACCACTT CTTTATCTAC ACTTAATGCC CCTGCACTCT
401 CTGCGACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG
501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACAGATGT GTTTATTAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTT GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGGCCGTATA AAGTAAGCAA
801 AGGAATTAAG CCGACGGAAG GATTAATGGT CGATTTCTCC GATATCCGAC
851 CATACGGCAA TCATACGGGT AACTCCGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GTAGTGCGAC AACATAGACA
951 AGGACAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1328; ORF 406>:

m406.pep

```

1   MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFAVEQEL VAASARAANK

```

```

51  DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPRYETT AETTSGGLTG LTTSLSTLNA PALSRTQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTTNPRDTA FLSHLVQTVF FLRGIDVVSP ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSKGIK PTEGLMVDFS DIRPYGNHTG NSAPSVEADN
301 SHEGYGYSDE VVRQHRQGPX *

```

Computer analysis of the amino acid sequences gave the following results:

Homology with a predicted ORF from *N. meningitidis* *menA* with *menB*

ORF 406 shows 98.8% identity over a 320 aa overlap with a predicted ORF (ORF406.a) from *N. gonorrhoeae*:

g406/m406

	10	20	30	40	50	60
g406.pep	MRARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	:					
m406	MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFAVEQELVAASARA AVKMDLQALHGR					
	10	20	30	40	50	60
	70	80	90	100	110	120
g406.pep	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
m406	KVALYIATMGDQSGSLTGG RYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSGGLTG					
	70	80	90	100	110	120
	130	140	150	160	170	180
g406.pep	LTTSLSTLNAPALSRTQSDGSGSRSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
m406	LTTSLSTLNAPALSRTQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF					
	130	140	150	160	170	180
	190	200	210	220	230	240
g406.pep	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
m406	FLRGIDVVSPANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
g406.pep	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTGLMVDFS DIQPYGNHTGNSAPSVEADN					
m406	IKPKTNAFEAAAYKENYALWMGPYKVSKGIKPTGLMVDFS DIRPYGNHTGNSAPSVEADN					
	250	260	270	280	290	300
	310	320				
g406.pep	SHEGYGYSDEAVRQHRQGPX					
m406	SHEGYGYSDEVVRQHRQGPX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1329>:

a406.seq

```

1  ATGCAAGCAC GGCTGCTGAT ACCTATTCTT TTTTCAGTTT TTATTTTATC
51  CGCCTGCGGG AACTGACAG GTATTCCATC GCATGGCGGA GGTAAACGCT
101 TCGCGGTCGA ACAAGAACTT GTGGCCGCTT CTGCCAGAGC TGCCGTTAAA
151 GACATGGATT TACAGGCATT ACACGGACGA AAAGTTGCAT TGTACATTGC
201 AACTATGGGC GACCAAGGTT CAGGCAGTTT GACAGGGGGT CGCTACTCCA
251 TTGATGCACT GATTCGTGGC GAATACATAA ACAGCCCTGC CGTCCGTACC
301 GATTACACCT ATCCACGTTA CGAAACCACC GCTGAAACAA CATCAGGCGG
351 TTGACAGGT TTAACCACTT CTTATCTAC ACTTAATGCC CCTGCACCTC
401 CGCGCACCCA ATCAGACGGT AGCGGAAGTA AAAGCAGTCT GGGCTTAAAT
451 ATTGGCGGGA TGGGGGATTA TCGAAATGAA ACCTTGACGA CTAACCCGCG

```

730

```

501 CGACACTGCC TTTCTTTCCC ACTTGGTACA GACCGTATTT TTCCTGCGCG
551 GCATAGACGT TGTTCCTCCT GCCAATGCCG ATACGGATGT GTTTATAAAC
601 ATCGACGTAT TCGGAACGAT ACGCAACAGA ACCGAAATGC ACCTATACAA
651 TGCCGAAACA CTGAAAGCCC AAACAAACT GGAATATTTC GCAGTAGACA
701 GAACCAATAA AAAATTGCTC ATCAAACCAA AAACCAATGC GTTTGAAGCT
751 GCCTATAAAG AAAATTACGC ATTGTGGATG GGACCGTATA AAGTAAGCAA
801 AGGAATTAAA CCGACAGAAG GATTAATGGT CGATTTCCTC GATATCCAAC
851 CATACGGCAA TCATATGGGT AACTCTGCCC CATCCGTAGA GGCTGATAAC
901 AGTCATGAGG GGTATGGATA CAGCGATGAA GCAGTGCAGC GACATAGACA
951 AGGGCAACCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1330; ORF 406.a>:

```

a406.pep
  1 MQARLLIPIL FSVFILSACG TLTGIPSHGG GKRFVEQEL VAASARAAVK
 51 DMDLQALHGR KVALYIATMG DQSGSLTGG RYSIDALIRG EYINSPAVRT
101 DYTYPYRETT AETTSAGGLTG LTSSLSTLNA PALSRQSDG SGSKSSLGLN
151 IGGMGDYRNE TLTNPRDTA FLSHLVQTVF FLRGIDVVSF ANADTDVFIN
201 IDVFGTIRNR TEMHLYNAET LKAQTKLEYF AVDRTNKKLL IKPKTNAFEA
251 AYKENYALWM GPYKVSIGIK PTEGLMVDFF DIQPYGNHMG NSAPSVEADN
301 SHEGYGYSDE AVRRHRQGP *

m406/a406 98.8% identity in 320 aa overlap

      10      20      30      40      50      60
m406.pep MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
|||||
a406      MQARLLIPILFSVFILSACGTLTGIPSHGGGKRFVEQELVAASARAAVKDMDLQALHGR
      10      20      30      40      50      60

      70      80      90     100     110     120
m406.pep KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSAGGLTG
|||||
a406      KVALYIATMGDQSGSLTGGRYSIDALIRGEYINSPAVRTDYTYPRYETTAETTSAGGLTG
      70      80      90     100     110     120

      130     140     150     160     170     180
m406.pep LTSSLSTLNAPALSRQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF
|||||
a406      LTSSLSTLNAPALSRQSDGSGSKSSLGLNIGGMGDYRNETLTNPRDTAFLSHLVQTVF
      130     140     150     160     170     180

      190     200     210     220     230     240
m406.pep FLRGIDVVSFANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
|||||
a406      FLRGIDVVSFANADTDVFINIDVFGTIRNRTEMHLYNAETLKAQTKLEYFAVDRTNKKLL
      190     200     210     220     230     240

      250     260     270     280     290     300
m406.pep IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFDIRPYGNHTGNSAPSVEADN
|||||
a406      IKPKTNAFEAAAYKENYALWMGPYKVSIGIKPTEGLMVDFFDIQPYGNHMGNSAPSVEADN
      250     260     270     280     290     300

      310     320
m406.pep SHEGYGYSDEVVRQHRQGPX
|||||
a406      SHEGYGYSDEAVRRHRQGPX
      310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1331>:

```

g501.seq
  1 atggctcggac ggaccttgac cgcagatacc gacatatttg ttctgcttgc,
 51 ggcaggcgga gatggcaaga tgcagcatca ctttgacggc aggggttgct

```

731

```

101  tcgtcaaacg attcggacac caagccgctg tctcgggtcga ggccgaggggt
151  cagctgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcaatgcctt
301  aaccactgct tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  cgacgttggt cagacccatt tcgtcacgaa cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagctctcg gcaacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgtgccgc
501  cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggcaagc gttgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggatgc gtaaccggcg atgcggcgga
651  taatttcgcg tttcagttcg tcgtcttggt tgtcaaattc caacaaggct
701  ttcgggtgga tgccgatttg gcggttgatg ataaattcca tacgcgccaa
751  gccgatgcct tcgctgggca gattggcgaa gctgaatgcg agttcgggat
801  tgccgacgtt catcatgact ttgacgggtg cttttggcat attgtccaag
851  gcgacatcgg taatttgtac gtccagcagg ccggcataga taaagccgggt
901  atcgcccttc gcacaggata cggtaacttc ctgaccgttt tccaagagtt
951  cggtcgcatt gccgcagccg acgacggcag gaatacccag ttcgcgcgcg
1001 atgatggcgg cgtggcagggt gcgtccgccg cggttgggtca cgatggcgga
1051 agcacgtttc atcacgggtt cccaatccgg atcggtcatt tcggtaacca
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc tttaatcagg
1151 cgcaccttgc cctgaccgac tttttgaccg atggcacgac cttcgacaaa
1201 gacggttttt tcgccgttga tggcgtagcg gcgcaggttg cggctgcctt
1251 cttcttgagg tttgacggtt tcggggcggg cttgcaggat gtagagtttg
1301 ccgtccaggc cgtcgcgtcc ccattcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagcgctg agtgtgcaa ctcggtgatt tcttcgtcgg
1401 taatggagaa gcggttgccg tcttcttcgg ggacttcgac gttggttacc
1451 gatttgccgg cttcggcttt gtcggtgaaa atcattttga tgtgtttcga
1501 acccatggtc ttgcgcagga tggcggtttt gcctgctttg agcgtgggtt
1551 tgaacacata aaattcgtcc gggttgaccg cgccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acttggttgt agccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1332; ORF 501.ng>:

g501.pep

```

1  MVGRTLTA DT DIFVLLAAGG DGKMQHHFDG RFAFVKRFGH QAAVSVEAEG
51  QLGHVVRA DG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQCL
101 NHCFGFAQ SA DERNHDFDVG QTHFVTNAFQ GFAFQGETVF EALGNITRRT
151 TEAQHRVFF M RFVYAAADQV GVFGVFEVGH TDDGFTRINR CGKRCHAFGD
201 FIDVEVDRC G VTGDAADNFR FQFVVLVFKF QQGFRVDADL AVDDKFHTRQ
251 ADAFAGQIG E AECEFGIADV HHDFDGCFWH IVQGDIGNLY VQQAGIDKAG
301 IAFGTGYGN F LTVFQEFGR I AAADDGRNTQ FARDDGGVAG ASAAVGHDDG
351 STFHHGFPI R IGHVGNQYVA GFDGIHLGSI FNQAHLLALD FLTDGTTFAQ
401 DGFFAVDGV A AQVAAFFL G FDGFGAGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQRVVC Q LGDFFVNGE AVAVFFGDFD VGYRFAGFGF VGENHFDVFR
501 THGLAQDGG F ACFERGF EHI KFVRVDRALY DVFAQTVRGG NKDDL VVAGF
551 GVEGEHHT*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1333>:

m501.seq

```

1  atggtcggac sggccttgac cgcagatgcc gacatatttg ttctgcttgc
51  ggcaggcgga gatggcaagg tgcagcatca ctttgacggc aggggttgcg
101  tcgtcaaacg attcggatac caagccgctg tcgcgggtcga gaccgaggggt
151  cagttgggtc atgtcgttcg agccgatgga gaagccgtcg aagtattgca
201  ggaattgttc cgccaatacc gcgttgctcg gcagctcgca catcataatc
251  aggcgcaggc cgtttttgcc gcgttccaag ccgttttctt tcagggtctt
301  gacaacggmt tcggcttcgc ccaaagtgcg gacgaacgga atcatgattt
351  caacgttggy caaccccatc tcatcgcgga cgcgtttcaa ggctttgcat
401  tccaaggcga aacagtcttt gaagttgtcg gcgacataac gcgccgcacc
451  acggaagccc aacatcgggt tttcttcatt cggttcgtat acgttgccgc
501  cgaccagggt ggcgatttcg ttggatttga agtcggacat acggacgatg
551  gttttacgcg gataaaccga tgcggccaat gtcgccacgc cttcggcgat
601  tttatcgacg tagaagtcga caggggacgc gtaaccggcg atacggcggg
651  taatttcgcg ttttaattcg tcgtcttggt tgtcaaattc caacaargct

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```

701 ttgggggtgga taccgatttg gcggttgatg ataaattcca tacgcgccaa
751 gccgatgcct tcgctgggca ggttggcgaa gctgaatgcg agttcgggat
801 tgccgacggt catcatgact ttacaggtg ctttaggcatt attgtctaag
851 gcgacatcgg taatctgtac gtccaacaga ccggcataga taaagccggt
901 atcgcccttc gcacaggata cggttaactt ttgaccgttt ttcagcaatt
951 cggttgcatt gccgcagccg acaacggcag gaatgcccaa ttcacgcgcg
1001 atgatggcgg cgtggcaggt acggccgccc cggttggtaa cgatggcaga
1051 agcacgtttc atcacgggtt cccaatcccg atcggtcatg tcggtaacga
1101 gtacgtcgcc ggcttcgacg gaatccatct cggaagcatc ttaatacagg
1151 cgcaccttgc cctgaccgac ttctcgaccg atggcgcggc cttcgcataa
1201 tacggttttg tcgccgttga tggcgaagcg gcgcagggtg cggttgccct
1251 cttcttgagg ttttacggtt tcgggacggg cttgcaggat gtagagtttg
1301 ccgtccaagc cgtcgcgctc ccatcgata tccatcgggc ggccgtagtg
1351 tttttcgatg gtcagtgcgt aatgcgccaa ctcagtaatt tcttcgctcg
1401 taatggagaa gcggttgccg tcttcctcgg ggacatcgac gttggttacg
1451 gatttaccgg cttctgcttt gtcggtaaaa atcattttga tgtgtttga
1501 acccatggtt ttacgcagga tggcgggctt gcccgtyttg agcgtgggtt
1551 tgaacacatr aaattcgctc gggttgaccg caccttgtag gacgttttcg
1601 cccagaccgt aagaggaggt aacaaagacg acytgatcgt akccggattc
1651 ggtgtcgagg gtgaacatca cacctga

```

This corresponds to the amino acid sequence <SEQ ID 1334; ORF 501>:

```

m501.pep
1  MVGXALTADA DIFVLLAAGG DGKVQHHFDG RFAFVKRFGY QAAVAVETEG
51  QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFAFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFVGFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR FXFVVLVVKF QXFGVDTDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDFYRCFRH IVXGDIGNLY VQQTGIDKAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNAQ FTRDDGGVAG TAAAVGNDGR
351 STFHHGFPIR IGHVONEYVA GFDGIHLGSI FNQAHALTD FLTDGAFAFX
401 YGFVAVDGEA AQVAVALFLG FYGFGTGLQD VEFVQAVAS PFDIHRAAVV
451 FFDGQCVMRQ LSNFFVNGE AVAVFLGDID VGYGFTGFCF VGKNHFDVFX
501 THGFTQDGLL ARFERGFEXH KFRVVDRTLY DVFAQTVRGG NKDDLIVXGF
551 GVEGEHHT*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 501 shows 86.2% identity over a 558 aa overlap with a predicted ORF (ORF 501.ng) from *N. gonorrhoeae*:

m501/g501

```

              10      20      30      40      50      60
m501.pep  MVGXALTADADIFVLLAAGGDGKVQHHFDGRFAFVKRFGYQAAVAVETEGQLGHVVRADG
          ||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      MVGRTLTAADTDIFVLLAAGGDGKMQHFDGRFAFVKRFGHQAASVEAEGQLGHVVRADG
              10      20      30      40      50      60

              70      80      90     100     110     120
m501.pep  EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      EAVEVLQELFRQYRVARQLAHHNQAQAVFAAFQAVFFQCLNHCFGFAQSADERNHDFDVG
              70      80      90     100     110     120

              130     140     150     160     170     180
m501.pep  QPHFIADAFQGFQAFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH
          | ||::|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g501      QTHFVTNAFQGFQAFQGETVFEALGNITRRTTEAQHRVFFMRVYVAADQVGVFVGFEVGH
              130     140     150     160     170     180

              190     200     210     220     230     240
m501.pep  TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQXFGVDTDL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||

```

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g501	TDDGFTRINRCGKRCHAFGDFIDVEVDRGCVTGDAADNFRFQFVVLVFKFQQGFRVDADL
	190 200 210 220 230 240
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHIVXGDIIGNLYVQQTGIDKAG
	250 260 270 280 290 300
g501	AVDDKFHTRQADAFAGQIGAECEFGIADVHHDFDGCFWHIVQGDIGNLYVQQAGIDKAG
	250 260 270 280 290 300
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNAQFTRDDGGVAGTAAAVGNDGRSTFHHGFPPIR
	310 320 330 340 350 360
g501	IAFGTGYGNFLTTFVQEFGRIAAADNGRNTQFARDDGGVAGASAAVGHGDSSTFHHGFPPIR
	310 320 330 340 350 360
m501.pep	IGHVGNQYVAGFDGIHLGSI FNQAHALALTDFLTDGAFAFYGFVAVDGEAAQVAVALFLG
	370 380 390 400 410 420
g501	IGHVGNQYVAGFDGIHLGSI FNQAHALALTDFLTDGTTFAQDGFFAVDGVAAQVAALFLG
	370 380 390 400 410 420
m501.pep	FYGFGLQDVEFAVQAVASPFDIHRAAVVFFDQCVMRQLSNFFVNGEAVAVFLGDID
	430 440 450 460 470 480
g501	FDGFGAGLQDVEFAVQAVASPFDIHRAAVVFFDQQRVVCQLGDDFFVNGEAVAVFFGDFD
	430 440 450 460 470 480
m501.pep	VGYGFTGFVGVGNHFDVFXTHGFTQDGLARFERGFEXHKKFVRVDRTLVDVFAQTVRGG
	490 500 510 520 530 540
g501	VGYRFAGFGFVGENHFDVFRTHGLAQDGGFACFERGFEXIKFVRVDRALYDVFAQTVRGG
	490 500 510 520 530 540
m501.pep	NKDDLIVXGFGVEGEHHT
	550
g501	NKDDLIVVAGFGVEGEHHT
	550

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1335>:

a501.seq	(partial)
1	ATGGTCGGAC GGGCCTTGAC CGCAGATGCC GACATATTTG TTCTGCTTGC
51	GGCAGGCGGA GATGGCAAGG TGCAGCATCA CTTTGACGGC AGGGTTGCGT
101	TCGTCAAACG ATTCGGATAC CAAGCCGCTG TCGCGGTCGA GACCGAGGGT
151	CAGTTGGGTC ATGTCGTTTC AGCCGATGGA GAAGCCGTCG AAGTATTGCA
201	GGAATTGTTC CGCCAATACC GCGTTGCTCG GCAGCTCGCA CATCATAATC
251	AGGCGCAGGC CGTTTTTGCC GCGTTCCAAG CCGTTTTCTT TCAGGGCTTT
301	GACAACGGCT TCGGCTTCGC CCAAAGTGCG GACGAACGGA ATCATGATTT
351	CAACGTTGGT CAACCCCATC TCATCGCGGA CGCGTTTCAA GGCTTTGCAT
401	TCCAAGGCGA AACAGTCTTT GAAGTTGTCG GCGACATAAC GCGCCGCACC
451	ACGGAAGCCC AACATCGGGT TTTCTTCATG CCGTTTCGTAT ACGTTGCCGC
501	CGACCAGGTT GCGGTATTCG TTGGATTTGA AGTCGGACAT ACGGACGATG
551	GTTTTACGCG GATAAACCGA TGCGGCCAAT GTCGCCACGC CTTCGGCGAT
601	TTTATCGACG TAGAAGTCGA CAGGGGACGC GTAACCGGCG ATACGGCGGG
651	TAATTTCCGC TTTAATTTCG TCGCTTGTT TGTCAAATTC CAACAAGGCT
701	TTGGGGTGGG TACCGATTTG GCGGTTGATG ATAAATTCCA TACGCGCCAA
751	GCCGATGCCT TCGCTGGGCA GGTGGCGAA GCTGAATGCG AGTTCGGGAT
801	TGCCGACGTT CATCATGACT TTTACAGGTG CTTTAGGCAT GTTGTCCTAA
851	GCAACATCGG TAATTTGTAC GTCCAGCAGG CCGGAGTAGA TGAAGCCGGT
901	ATCGCCTTCG GCACAGGATA CGGTAACCTC TTGACCGTTT TTCAGCAATT
951	CGGTTGCATT GCCGCAGCCG ACAACGGCAG GAATACCCAG TTCGCGCGCG

```

1001 ATGATGGCGG CGTGGCAGGT ACGTCCGCCC CTGTTGGTCA CGATGGCGGA
1051 AGCGCGTTTC ATCACCAGGT CCCAATCTGG GTCGGTCATG TCGGTAACCA
1101 GTACGTCGCC GGCTTCGACG GAATCCATCT CGGAAGCATC TTTAATCAGG
1151 CGTACCTTGC CCTGACCGAC TTTCTGACCG ATGGCGCGGC CTTGCGACAA
1201 GACGGTTTTT TCGCCGTTGA TAGAAAAGCG GCGCAGGTTG CCGCTGCCTT
1251 CTTCTGCGGA TTTGACGGTT TCGGGACGGG CTTGCAGGAT GTAGAGTTTG
1301 CCGTCCAAGC CGTCGCGTCC CCATTTCGATG TCCATCGGGC GGCCGTAGTG
1351 TTTTTCGATG GTCAGTTCGT AATGCGCCAA CTCGGTGATT TCTTCGTCGG
1401 TAATGGAGAA GCGGTTGCGG TCTTCTTCGG GGACATCGAC GTTGGTTACC
1451 GATTTGCCGG CTTCTGCTTT GTCGGTAAAA ATCATTTTGA TGTGTTTTGA
1501 GCCCATGGTT TTGCGCAGGA TGGCAGGTTT GCCTGCTTTC AGCGTGGGTT
1551 TGAACACATA GAATTCGTCG GGATTGACTG CGCCTTGAC GACGTTTTCG
1601 CCCAGACCGT AGGATGAAGT GACAAAGACG ACTTGTCGT AACCGGATTC
1651 GGTATCGAGG GTGAACATCA C

```

This corresponds to the amino acid sequence <SEQ ID 1336; ORF 501.a>:

a501.pep

```

1 MVGRALTADA DIFVLLAAGG DGKVQHFDG RFAFVKRFGY QAAVAVETEG
51 QLGHVVRADG EAVEVLQELF RQYRVARQLA HHNQAQAVFA AFQAVFFQGF
101 DNGFGFAQSA DERNHDFNVG QPHFIADAFQ GFQFQGETVF EVVGDITRRT
151 TEAQHRVFFM RFVYVAADQV GVFGVFEVGH TDDGFTRINR CGQCRHAFGD
201 FIDVEVDRGR VTGDTAGNFR F*FVVLVVKF QQGFVVDL AVDDKFHTRQ
251 ADAFAGQVGE AECEFGIADV HHDYRCFRH VVQSNIGNLY VQAGVDEAG
301 IAFGTGYGNF LTVFQQFGCI AAADNGRNTQ FARDDGGVAG TSAPVGHG
351 SAFHHRFPIW VGHVGNQYVA GFDGIHLGSI FNQAYLALTD FLTDGAAFAQ
401 DGFFAVDRKA AQVAAFFLG FDGFGTGLQD VEFVAVAVAS PFDVHRAAVV
451 FFDGQCVMRQ LGDFFVNGE AVAVFFGDID VGYRFAGFCF VGKNHFDVF*
501 AHGFAQDGRF ACFQRGFEHI EFVGIDCALY DVFAQTVG*S DKDDLVTGTF
551 GIEGEHH

```

m501/a501 90.3% identity in 557 aa overlap

	10	20	30	40	50	60
m501.pep	MVGXALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
a501	MVGRALTADADIFVLLAAGGDGKVQHFDGRVAFVKRFGYQAAVAVETEGQLGHVVRADG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m501.pep	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
a501	EAVEVLQELFRQYRVARQLAHNQAQAVFAAFQAVFFQGFQDNGFGFAQSADERNHDFNVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m501.pep	QPHFIADAFQGFQFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGVFEVGH					
a501	QPHFIADAFQGFQFQGETVFEVVDITRRTTEAQHRVFFMRVYVAADQVGVFGVFEVGH					
	130	140	150	160	170	180
	190	200	210	220	230	240
m501.pep	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
a501	TDDGFTRINRCGQCRHAFGDFIDVEVDRGRVTGDTAGNFRFXFVVLVVKFQQXFGVDTDL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m501.pep	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
a501	AVDDKFHTRQADAFAGQVGEAECEFGIADVHHDFYRCFRHVVQSNIGNLYVQAGVDEAG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m501.pep	IAFGTGYGNFLTTFVQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPPIR					
a501	IAFGTGYGNFLTTFVQQFGCIAAADNGRNTQFARDDGGVAGTAAAVGNDGRSTFHHGFPPIR					
	310	320	330	340	350	360

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	370	380	390	400	410	420
m501.pep	IGHVGN EYVAGFDGIHLGSI FNQAH LALTDFLTDGA AFAXYGFVAVDGEAAQVA VALFLG					
a501	VGHVGNQYVAGFDGIHLGSI FNQAYLALTDFLTDGA AFADGFFAVDRKAAQVAAFFLG					
	370	380	390	400	410	420
m501.pep	FYGFGTGLQDVEFAVQAVASPFDIHRAAVVFFDGCVMRQLSNFFVGNGEAVAVFLGDID					
a501	FDGFGTGLQDVEFAVQAVASPFDVHRAAVVFFDGCVMRQLGDDFFVGNGEAVAVFFGDID					
	430	440	450	460	470	480
m501.pep	VGYGFTGFCFVGK NHFVFXTHGFTQDGG LARFERGF EHXKFVRVDR TLYDVFAQTVRGG					
a501	VGYRFAGFCFVGK NHFVFXAHGFAQDGRFACFQRGF EHFVGI DCALYDVFAQTVGXS					
	490	500	510	520	530	540
m501.pep	NKDDLIVXGFGVGEHHTX					
a501	DKDDLVTGFGIEGEHH					
	550	559				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1337>:

g502.seq

```

1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gttccgcac aggcgggcgc ggtggacgcg ctcaagcaat
101 tcaacaacga tgccgacggt atcagcgga cgttcaccca aaccgtccaa
151 agcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tctgcgccc
201 gggcctcttc aaatgggaat acactttgcc ctacagacag actattgtcg
251 gcgacggtca aaccgtttgg ctctacgatg ttgatttggc acaagtgacc
301 aagtcgtccc aagaccaggc catcgcgggc agccccgcgc ccatcctgtc
351 gaacaaaacc gccctcgaaa gcagttacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg cggggcaacg ccaaacgca acaacgcgg
451 ctaccaatac atccgcacgc gttcacaagg cggcaacctc gccgccatgc
501 agcttaa

```

This corresponds to the amino acid sequence <SEQ ID 1338; ORF 502.ng>:

g502.pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51  SKKKTQTAHG TFKILRPGLF KWEYTLPLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RGNAQTQRRR
151 LPIHPHRLQR RQPRRHAA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1339>:

m502.seq

```

1  atgatgaaac cgcacaacct gttccaattc ctgcccgttt gtcacctgac
51  cgtcgccgtc gttccgcac aggcgggcgc ggtagacgcg cttaagcaat
101 tcaacaacga tgccgacggt atcagcgga cgttcaccca amccgtccaa
151 wgcaaaaaga aaacccaaac cgcgcacggc acgttcaaaa tctgcgacc
201 gggccttttc aaatgggaat acaccaaact t.acaggcaa accatcgctc
251 gcgacggtca aacygtttgg ctmtacgatg tygatctggc acaagtgacc
301 aagtcgtccc aagaccaggc cataggcgsc agccccgcgc ccatcctgtc
351 gaacaaarcc gccctcgaaa gcagctacac gctgaaagag gacggttcgt
401 ccaacggcat cgattatgtg ggcaacgccc aaacgcaaca acgccggcta
451 ccaatacatc cgcacggcct tcaaaggcgg caacctcgcc gccatgcagc
501 tyaa

```

This corresponds to the amino acid sequence <SEQ ID 1340; ORF 502.ng>:

m502.pep

```

1  MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQXVQ
51  XKKKTQTAHG TFKILRPGLF KWEYTKLYRQ TIVGDGQTVW LYDVDLAQVT
101 KSSQDQAIGX SPAAILSNKX ALESSYTLKE DGSSNGIDYV GNAQTQRRR
151 PIHPHRLQRR QPRRHAA

```

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 502 shows 95.8% identity over a 168 aa overlap with a predicted ORF (ORF 502.ng) from *N. gonorrhoeae*:

m502/g502

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
g502	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
g502	TFKILRPGLFKWEYTLPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYV-GNAQTQQRRLPIHPHRLQRRQPRRHAA					
g502	ALESSYTLKEDGSSNGIDYVRGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1341>:

a502.seq

1	ATGATGAAAC	CGCACAACT	GTTCCAATTC	CTCGCCGTTT	GCTCCCTGAC
51	CGTCTCCGTC	GCTTCCGCAC	AGGCGGGCGC	GGTGGACGCG	CTCAAGCAAT
101	TCAACAACGA	TGCCGACGGT	ATCAGCGGCA	GCTTCACCCA	AACCGTCCAA
151	AGCAAAAAGA	AAACCCAAAC	CGCGCACGGC	ACGTTCAAAA	TCCTGCGCCC
201	GGGCCTCTTT	AAATGGGAAT	ACACTTCGCC	TTACAAACAG	ACTATTGTGC
251	GCGACGGTCA	AACCGTTTGG	CTCTACGATG	TCGATTTGGC	ACAAGTGACC
301	AAGTCGTCCC	AAGACCAGGC	CATAGGCGGC	AGCCCCGCCG	CCATCCTGTC
351	GAACAAAACC	GCCCTCGAAA	GCAGCTACAC	GCTGAAAGAG	GACGGTTCGT
401	CCAACGGCAT	CGATTATGTG	GGCAACGCCC	AAACGCAACA	ACGCCGGCTA
451	CCAATACATC	CGCATCGGCT	TCAAAGGCGG	CAACCTCGCC	GCCATGCAGC
501	TTAA				

This corresponds to the amino acid sequence <SEQ ID 1342; 502 217.a>:

a502.pep

1	MMKPHNLFQF	LAVCSLTVSV	ASAQAGAVDA	LKQFNNDADG	ISGSFTQTVQ
51	SKKKTQTAHG	TFKILRPGLF	KWEYTSFYKQ	TIVGDGQTVW	LYDVLDAQVT
101	KSSQDQAIGG	SPAAILSNKT	ALESSYTLKE	DGSSNGIDYV	GNAQTQQRRL
151	PIHPHRLQRR	QPRRHAA*			

m502/a502 95.2% identity in 167 aa overlap

	10	20	30	40	50	60
m502.pep	MMKPHNLFQFLAVCSLTVAVASQAQAGAVDALKQFNNDADGISGSFTQXVQXKKKTQTAHG					
a502	MMKPHNLFQFLAVCSLTVSVASQAQAGAVDALKQFNNDADGISGSFTQTVQSKKKKTQTAHG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m502.pep	TFKILRPGLFKWEYTKLYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGXSPAAILSNKX					
a502	TFKILRPGLFKWEYTSFYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
	130	140	150	160		
m502.pep	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
a502	ALESSYTLKEDGSSNGIDYVGNAQTQQRRLPIHPHRLQRRQPRRHAA					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1343>:

g502-1.seq

```

1 ATGATGAAAc cgcaCaacct gttccaaTtc CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTC AAATGGGAAT ACACTTTGCC CTACAGACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATCGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGTTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CGGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1344; ORF 502-1.ng>:

g502-1.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTLPLYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV RATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSISF GGLTNPQLS RGAFTFTPPK
201 GVDVLSN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1345>:

m502-1.seq

```

1 ATGATGAAAC CGCACAACT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCGCCGTC GCTTCCGCAC AGGCGGGCGC GGTAGACGCG CTTAAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGACC
201 GGGCCTTTTC AAATGGGAAT ACACCAAACC TTACAGGCAA ACCATCGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TTGATCTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGGCGGC AGCCCCGCCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ACCAAACCTC CATCAGTTTC GCGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1346; ORF 502-1>:

m502-1.pep

```

1 MMKPHNLFQF LAVCSLTVAV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTKPYRQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQAIGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSSISF GGLTNPQLS RGAFTFTPPK
201 GVDVLSN*

```

m502-1/g502-1 99.0% identity in 207 aa overlap

	10	20	30	40	50	60
m502-1.pep	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQTQVQSKKKTQTAHG				
g502-1	MMKPHNLFQFLAVCSLTVAVASAQAGAVDAL	LKQFNNDADGISGSFTQTQVQSKKKTQTAHG				
	10	20	30	40	50	60
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
g502-1	TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT					
	70	80	90	100	110	120
m502-1.pep	ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSSISF					
g502-1	ALESSYTLKEDGSSNGIDYVRATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSSISF					
	130	140	150	160	170	180

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```

                190      200
m502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
g502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190      200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1347>:

```

a502-1.seq
1  ATGATGAAAC CGCACAACTT GTTCCAATTC CTCGCCGTTT GCTCCCTGAC
51 CGTCTCCGTC GCTTCCGCAC AGGCGGGCGC GGTGGACGCG CTCAGCAAT
101 TCAACAACGA TGCCGACGGT ATCAGCGGCA GCTTCACCCA AACCGTCCAA
151 AGCAAAAAGA AAACCCAAAC CGCGCACGGC ACGTTCAAAA TCCTGCGCCC
201 GGGCCTCTTT AAATGGGAAT ACACTTCGCC TTACAAACAG ACTATTGTCG
251 GCGACGGTCA AACCGTTTGG CTCTACGATG TCGATTGGC ACAAGTGACC
301 AAGTCGTCCC AAGACCAGGC CATAGCGGCG AGCCCCGCG CCATCCTGTC
351 GAACAAAACC GCCCTCGAAA GCAGCTACAC GCTGAAAGAG GACGGTTCGT
401 CCAACGGCAT CGATTATGTG CTGGCAACGC CCAAACGCAA CAACGCCGGC
451 TACCAATACA TCCGCATCGG CTTCAAAGGC GGCAACCTCG CCGCCATGCA
501 GCTTAAAGAC AGCTTCGGCA ATCAAACCTC CATCAGTTTC GCGGGTTTGA
551 ATACCAATCC CCAACTCTCG CGCGGCGCGT TCAAGTTTAC CCCGCCCAAA
601 GCGGTGGACG TGTGAGCAA CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1348; ORF 502-1.a>:

```

a502-1.pep
1  MMKPHNLFQF LAVCSLTVSV ASAQAGAVDA LKQFNNDADG ISGSFTQTQVQ
51 SKKKTQTAHG TFKILRPGLF KWEYTSFYKQ TIVGDGQTVW LYDVLDAQVT
101 KSSQDQATGG SPAAILSNKT ALESSYTLKE DGSSNGIDYV LATPKRNNAG
151 YQYIRIGFKG GNLAAMQLKD SFGNQTSISF GGLNTNPQLS RGAFTFTPPK
201 GVDVLSN*

```

a502-1/m502-1 98.6% identity in 207 aa overlap

```

                10      20      30      40      50      60
a502-1.pep      MMKPHNLFQFLAVCSLTVSVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                |||||
m502-1          MMKPHNLFQFLAVCSLTVASAQAGAVDALKQFNNDADGISGSFTQTQVQSKKKTQTAHG
                10      20      30      40      50      60

                70      80      90      100     110     120
a502-1.pep      TFKILRPGLFKWEYTSFYKQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                |||||
m502-1          TFKILRPGLFKWEYTKPYRQTIVGDGQTVWLYDVLDAQVTKSSQDQAIGGSPAAILSNKT
                70      80      90      100     110     120

                130     140     150     160     170     180
a502-1.pep      ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                |||||
m502-1          ALESSYTLKEDGSSNGIDYVLATPKRNNAGYQYIRIGFKGGNLAAMQLKDSFGNQTSISF
                130     140     150     160     170     180

                190     200
a502-1.pep      GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                |||||
m502-1          GGLNTNPQLSRGAFKFTPPKGV DVL SNX
                190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1349>:

```

g503.seq
1  atgtccgcgc cgtcggcacg ggtaatcatt ttgttccatg ccgcttcgat
51 ttcggcatcg agctgttcgg ggaagggcgt gtccaaaatc cattggcgga
101 tttctttgcc gacgcgtgcc agttcggaaa cgtcttcgac atccaatttt
151 gccagagcgg cggaaatgcg ttcggttcaga ccgttggtg cgagaaatgc
201 gcggttag

```

This corresponds to the amino acid sequence <SEQ ID 1350; ORF 503.ng>:

```

g503.pep
1  MSAPSASVII LFHAASISAS SCSGKGVSKI HWRISLPTRA SSETSSSTSNF
51 ARAAEMRSFR PLCARNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1351>:

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```

m503.seq
  1  atgtccgcac cgccggcatc ggcaaccatt ttgttccatg ccgcttcgat
 51  ttccggcatcg agctgttcgg ggaaaggcgt atccaaaatc cattggcgga
101  tttctttgcc gacgcgtgcc agttcggcaa cgtcttcgac atccaatttt
151  gccagtgcgg cggaatgcg ttcgctcaga ccgttggtgt cgaggaatgc
201  gcggtag

```

This corresponds to the amino acid sequence <SEQ ID 1352; ORF 503>:

```

m503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51  ASAAEMRSLR PLCARNAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 503 shows 91.2% identity over a 68 aa overlap with a predicted ORF (ORF 503.ng) from *N. gonorrhoeae*:

```

m503/g503
      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          |||||:|||||
g503      MSAPSASVILFHAASISASSCSGKGVSKIHWRIPLTRASSETSTSNFARAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNAR
          |||||
g503      PLCARNAR

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1353>:

```

a503.seq
  1  ATGTCCGCGC CGCCGGCATC GGCAACCATT TTGTTCATG CCGCTTCGAT
 51  TTCGGCATCG AGCTGTTCGG GGAAGGGCGT GTCCAAAATC CATTGGCGGA
101  TTTCTTTGCC GACGCGTGCC AGTTCGGCAA CGTCTTCGAC ATCTAATTTT
151  GCCAGTGCGG CGGAAATGCG TTCGCTCAGA CCCTTGTGTG CGAGGAATGC
201  GCGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1354; ORF 503.a>:

```

a503.pep
  1  MSAPPASATI LFHAASISAS SCSGKGVSKI HWRISLPTRA SSATSSTSNF
 51  ASAAEMRSLR PLCARNAR*

```

m503/a503 100.0% identity in 68 aa overlap

```

      10      20      30      40      50      60
m503.pep  MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          |||||
a503      MSAPPASATILFHAASISASSCSGKGVSKIHWRIPLTRASSATSSTSNFASAAEMRSLR
          10      20      30      40      50      60

      69
m503.pep  PLCARNARX
          |||||
a503      PLCARNARX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1355>:

```

g503-1.seq
  1  ATGGCGCGGT CGTGTACAG GGAGGCGAAA ACGTGGCGCA TCGCTTTTTT
 51  AACGTTATCC AAGCCATTGA TATTCAGGAA GGTTTCCTGT TGGCCGGCAA
101  ATGATGCGTC GGGCAGGTCT TCGGCGGTTG CGGAAGAGCG TACGGCAACG
151  GAAATGTCCG CGCCGTCGGC ATCGGTAATC ATTTTGTTCC ATGCCGCTTC
201  GATTTTCGCA TCGAGCTGTT CGGGGAAGGG CGTGTCCAAA ATCCATTGGC
251  GGATTTCTTT GCCACGCGT GCCAGTTCGG AAACGTCTTC GACATCCAAT
301  TTTGCCAGAG CGGCGGAAAT GCGTTCGTTT AGACCGTTGT GTGCGAGAAA
351  TGGCGGGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1356; ORF 214.ng>:

g503-1.pep

```

1  MARSLYREAK TWRI AFLTSL KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPSASVI ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FARAAEMRSF RPLCARNAR*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1357>:

m503-1.seq

```

1  ATGGCACGGT CGTTATACAG GGAAGCGAAT ACATGGTGCA TCGCTTCTTT
51 AACGTTATCC AAGCCGTTGA TGTCAAGAA GGTTCCTGT TGTCCAGCGA
101 ATGATGCGTC CGGCAGGTCT TCGGCAGTTG CGGAAGAACG TACGGCAACG
151 GAAATGTCCG CACCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTATCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCCAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1358; ORF 503-1>:

m503-1.pep

```

1  MARSLYREAN TWCIALTSL KPLMFKKVSC CPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*
```

g503-1 / m503-1 89.9% identity in 119 aa overlap

	10	20	30	40	50	60
g503-1.pep	MARSLYREAKTWRI	AFLTSLKPLIFRKVSCWPANDASGRSSAVAEERTATE	MSAPSASVI			
m503-1	MARSLYREANTWCI	ASLTSLKPLMFKKVSCCPANDASGRSSAVAEERTATE	MSAPPASAT			
	10	20	30	40	50	60
	70	80	90	100	110	120
g503-1.pep	ILFHAASISASSCSGKGVSKI	IHWRI	SLPTRASSETSTSNFARAAEMRSFRPLCARNARX			
m503-1	ILFHAASISASSCSGKGVSKI	IHWRI	SLPTRASSATSTSNFASAAEMRSLRPLCARNARX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1359>:

a503-1.seq

```

1  ATGGCGCGGT CGTTGTACAG GGAGGCGAAT ACATGGCGCA TCGCTTCTTT
51 AACGTTTTCC AAGCCGTTGA TATTCAGGAA GGTTCCTGT TGGCCGGCAA
101 ATGATGCGTC GGGCAGGTCT TCGGCGGTG CGGAAGAGCG TACGGCAACG
151 GAAATGTCCG CGCCGCCGGC ATCGGCAACC ATTTTGTTC ATGCCGCTTC
201 GATTTCGGCA TCGAGCTGTT CGGGGAAAGG CGTGTCCAAA ATCCATTGGC
251 GGATTCTTTT GCCGACGCGT GCCAGTTCGG CAACGTCTTC GACATCTAAT
301 TTTGCCAGTG CGGCGGAAAT GCGTTCGCTC AGACCGTTGT GTGCGAGGAA
351 TGC GCGGTAG
```

This corresponds to the amino acid sequence <SEQ ID 1360; ORF 503-1.a>:

a503-1.pep

```

1  MARSLYREAN TWRIASLTFS KPLIFRKVSC WPANDASGRS SAVAEERTAT
51 EMSAPPASAT ILFHAASISA SSCSGKGVSK IHWRISLPTR ASSATSSTSN
101 FASAAEMRSL RPLCARNAR*
```

a503-1 / m503-1 95.8% identity in 119 aa overlap

	10	20	30	40	50	60
a503-1.pep	MARSLYREANTWRI	ASLTFSKPLIFRKVSCWPANDASGRSSAVAEERTATE	MSAPPASAT			
m503-1	MARSLYREANTWCI	ASLTSLKPLMFKKVSCCPANDASGRSSAVAEERTATE	MSAPPASAT			
	10	20	30	40	50	60
	70	80	90	100	110	120
a503-1.pep	ILFHAASISASSCSGKGVSKI	IHWRI	SLPTRASSATSTSNFASAAEMRSLRPLCARNARX			
m503-1	ILFHAASISASSCSGKGVSKI	IHWRI	SLPTRASSATSTSNFASAAEMRSLRPLCARNARX			
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1361>:

```

g504.seq
1  atgttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttgccagc gatattgaag
101 taacggacaa ggcaaccggg gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgaacctgt cgtgttgaag gcaacctcca tacaccagtt tccgttgga
301 atcggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gtgcggaacg ggaaaaaagc ctgaaatcca
401 ctctgaacga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccacgtgta ccgcacccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgatttt gcaggacaaa gattattttt
551 ggctgaccgg cacgcgcagc ggcttgagc agcaataaccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aagacgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaata tctttgcgca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaaag ggcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga accgtttcct
951 gctgcacagt atggatgctt atacggggct gacggaatat cccgcgccta
1001 tctgtctcca gcttgacggg ttttccgagg tgcgttcctc aggtttgcag
1051 atgaccggtt cgcggggtgc gcttttggtc tatctcggct cggattgtt
1101 ggttttggtt acagtattta tgttttatgt gcccaaaaaa cggcgctggg
1151 tattgttttc aaacdgcata atccggtttt ctatgtcttc ggccgcgagc
1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gcctgcaacg
1251 gctcggcaag gacttgaatc atgactga

```

This corresponds to the amino acid sequence <SEQ ID 1362; ORF 504.ng>:

```

g504.pep
1  MLVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFAWNLR DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPILQDK DYFWLTGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKDPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKGQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLHS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVFMFYVPPK RAWVLFNSKI RFAMSSARSE
401 RDLQKEFPKH VESLQRLGKD LNHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1363>:

```

m504.seq..
1  atatttggttc aggacttgcc ttttgaagtc aaactgaaaa aattccatat
51  cgattttttac aatacgggta tgccgcgcga ttttcgcccagc gatattgaag
101 tgacggacaa ggcaaccggg gagaaactcg agcgaccat ccgcgtgaac
151 catcctttga ccttgacagg catcacgatt tatcaggcga gttttgccga
201 cggcggttcg gatttgacat tcaaggcgtg gaatttgagg gatgcttcgc
251 gcgagcctgt cgtgttgaag gcaacatcca tacaccagtt tccgttgga
301 attggcaaac acaaatatcg tcttgagttc gatcagttca cttctatgaa
351 tgtggaggac atgagcgagg gcgcggaacg ggaaaaaagc ctgaaatcca
401 cgctgmmcga tgtccgcgcc gttactcagg aaggtaaaaa atacaccaat
451 atcggccctt ccattgttta ccgtatccgt gatgcggcag ggcaggcggg
501 cgaatataaa aactatatgc tgccgggttt gcaggaaacag gattattttt
551 ggattaccgg cacgcgcagc ggcttgagc agcaataaccg ctggctgcgt
601 atcccccttg acaagcagtt gaaagcggac acctttatgg cattgcgtga
651 gtttttgaaa gatggggaag ggcgcaaacg tctggttgcc gacgcaacca
701 aaggcgcacc tgccgaaatc cgcgaacaat tcatgctggc tgcggaaaaa
751 acgctgaaca tctttgcaca aaaaggctat ttgggattgg acgaatttat
801 tacgtccaat atcccgaaag agcagcagga taagatgcag ggctatttct
851 acgaaatgct ttacggcgtg atgaacgctg ctttgatga aaccatacgc
901 cggtagcggt tgcccgaatg gcagcaggat gaagcgcgga atcggttctc
951 gctgcacagt atggatgcgt acacgggttt gaccgaatat cccgcgccta
1001 tgctgctgca acttgatggg ttttccgagg tgcgttcgctc gggtttgcag

```

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1051 atgacccggt ccccggggtgc gcttttggtc tatctcggct cgggtgctggt
 1101 ggtattgggt acggtattga tgttttatgt gcgcgaaaaa cgggcgtggg
 1151 tattgttttc agacggcaaa atccgttttg ccatgtcttc ggcccgcagc
 1201 gaacgggatt tgcagaagga atttccaaaa cacgtcgaga gtctgcaacg
 1251 gctcggcaag gacttgaatc atga

This corresponds to the amino acid sequence <SEQ ID 1364; ORF 504>:

m504.pep.

1 ILVQDLPFVEV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
 51 HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
 101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLXDVRA VTQEGKKYTN
 151 IGPSIVYRIR DAAGQAVEYK NYMLPVLOEQ DYFWITGTRS GLQQQYRWLR
 201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
 251 TLNIFAQKGY LGLDEFITSN IPKEQQDKMQ GYFYEMLYGV MNAALDETIR
 301 RYGLPEWQQD EARNRFLHLS MDAYTGLTEY PAPMLQLDGF SEVRSSGLQ
 351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
 401 ERDLQKEFPK HVESLQRLGK DLNHD*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 504 shows 96.7% identity over a 425 aa overlap with a predicted ORF (ORF 504.ng) from *N. gonorrhoeae*:

m504/g504

	10	20	30	40	50	60
m504.pep	ILVQDLPFVEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN	HPLTLHGITI
g504	MLVQDLPFVEV	KLKKFHIDFY	NTGMPRDFAS	DIEVTDKATG	EKLERTIRVN	HPLTLHGITI
	10	20	30	40	50	60
	70	80	90	100	110	120
m504.pep	YQASFADGGS	DLTFKAWNLD	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEF	DQFTSMNVED
g504	YQASFADGGS	DLTFKAWNLD	DASREPVVLK	ATSIHQFPLE	IGKHKYRLEF	DQFTSMNVED
	70	80	90	100	110	120
	130	140	150	160	170	180
m504.pep	MSEGAREKSL	KSTLXDVR	AVTQEGKKY	TNIGPSIVY	RIRDAAGQ	AVEYKNYMLPVLOEQ
g504	MSEGAREKSL	KSTLNDVR	AVTQEGKKY	TNIGPSIVY	RIRDAAGQ	AVEYKNYMLPILQDK
	130	140	150	160	170	180
	190	200	210	220	230	240
m504.pep	DYFWITGTRS	GLQQQYRWLR	IPLDKQLKAD	TFMALREFLK	DGEGRKRLVA	DATKGAPAEI
g504	DYFWLTGTRS	GLQQQYRWLR	IPLDKQLKAD	TFMALREFLK	DGEGRKRLVA	DATKDAPAEI
	190	200	210	220	230	240
	250	260	270	280	290	300
m504.pep	REQFMLAAEN	TLNIFAQKGY	LGLDEFITSN	IPKEQQDKMQ	GYFYEMLYGV	MNAALDETIR
g504	REQFMLAAEN	TLNIFAQKGY	LGLDEFITSN	IPKGQQDKMQ	GYFYEMLYGV	MNAALDETIR
	250	260	270	280	290	300
	310	320	330	340	350	360
m504.pep	RYGLPEWQQD	EARNRFLHLS	MDAYTGLTEY	PAPMLQLDGF	SEVRSSGLQM	TRSPGALLV
g504	RYGLPEWQQD	EARNRFLHLS	MDAYTGLTEY	PAPMLQLDGF	SEVRSSGLQM	TRSPGALLV
	310	320	330	340	350	360
	370	380	390	400	410	420
m504.pep	YLGSVLLVLG	TVLMFYVREK	RAWVLFSDGK	IRFAMSSARS	ERDLQKEFPK	HVESLQRLGK
	370	380	390	400	410	420

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```

g504          YLGSVLLVLGTVFMFYVPPKKRAWVLFNS-KIRFAMSSARSERDLQKEFPKHVESLQRLGK
              370      380      390      400      410

m504.pep      DLNHD
              |||||
g504          DLNHD
              420

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1365>:

```

a504.seq
1  ATATTGGTTC AGGACTTGCC TTTTGAAGTC AAAGTAAAAA AATTCCATAT
51  CGATTTTAC AATACGGGTA TGCCGCGCGA TTTTGCCAGT GATATTGAAG
101 TAACGGATAA GGCAACCGGT GAGAACTCG AGCGCACCAT CCGCGTGAAC
151 CATCCTTTGA CCTTGACGG CATCACGATT TATCAGGCGA GTTTTGCCGA
201 CGGCGGTTTC GATTTGACAT TCAAGGCGTG GAATTTGGGT GATGCTTCGC
251 GCGAGCCTGT CGTGTGGAAG GCAACATCCA TACACCAGTT TCCGTTGGAA
301 ATGGCAAAC ACAATATCG TCTTGAGTTC GATCAGTTTA CTCTATGAA
351 TGTGGAGGAC ATGAGCGAGG GCGCGGAACG GGAAAAAGC CTGAAATCCA
401 CGCTGAACGA TGTCGCGGCC GTTACTCAGG AAGGTAAAAA ATACACCAAT
451 ATCGGCCCTT CCATTGTTTA CCGTATCCGT GATGCGGCAG GGCAGGCGGT
501 CGAATATAAA AACTATATGC TGCCGGTTTT GCAGGAACAG GATTATTTTT
551 GGATTACCGG CACGCGCAGC GGCTTGACAG AGCAATACCG CTGGCTGCGT
601 ATCCCTTGG ACAAGCAGTT GAAAGCGGAC ACCTTTATGG CATTGCGTGA
651 GTTTTGAAG GATGGGGAAG GCGCGAAACG TCTGGTTGCC GACGCAACCA
701 AAGGCGCACC TGCCGAAATC CGCGAACAAT TCATGCTGGC TGCGGAAAAC
751 ACGCTGAACA TCTTGCACA AAAAGGCTAT TTGGGATTGG ACGAATTTAT
801 TAGCTCCAAT ATCCCGAAAG AGCAGCAGGA TAAGATGCAG GGCTATTTCT
851 ACGAAATGCT TTACGGCGTG ATGAACGCTG CTTTGGATGA AACCATACGC
901 CGGTACGGCT TGCCCGAATG GCAGCAGGAT GAAGCGCGGA ATCGTTTCCT
951 GCTGCACAGT ATGGATGCGT ACACGGGTTT GACCGAATAT CCCGCGCCTA
1001 TGCTGCTGCA ACTTGATGGG TTTTCCGAGG TCGGTTTCGT GGGTTTGCAG
1051 ATGACCCGTT CCCCAGGTCG GCTTTTGGTC TATCTCGGCT CCGTGCTGTT
1101 GGTATTGGGT ACGGTATTGA TGTTTATGT GCGCGAAAAA CGGGCGTGGG
1151 TATGTTTTTC AGACGGCAAA ATCCGTTTTC CCATGTCTTC GGCCCGCAGC
1201 GAACGGGATT TGCAGAAGGA ATTTCCAAAA CACGTCGAGA GTCTGCAACG
1251 GCTCGGCAAG GACTTGAATC ATGACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1366; ORF 504.a>:

```

a504.pep
1  ILVQDLPEFV KLKKFHIDFY NTGMPRDFAS DIEVTDKATG EKLERTIRVN
51  HPLTLHGITI YQASFADGGS DLTFKAWNLG DASREPVVLK ATSIHQFPLE
101 IGKHKYRLEF DQFTSMNVED MSEGAREKS LKSTLNDVRA VTQEGKKYTN
151 IGPSIVYRIR DAAGQAVEYK NYMLPVLQEQ DYFWITGTRS GLQQQYRWLR
201 IPLDKQLKAD TFMALREFLK DGEGRKRLVA DATKGAPAEI REQFMLAAEN
251 TLNIFAQKGY LGLDEFITSN IPKEQDDKMQ GYFYEMLYGV MNAALDETIR
301 RYGLPEWQOD EARNRFLLS MDAYTGLTEY PAPMLLQLDG FSEVRSSGLQ
351 MTRSPGALLV YLGSVLLVLG TVLMFYVREK RAWVLFSDGK IRFAMSSARS
401 ERLQKEFPK HVESLQRLGK DLNHD*

```

m504/a504 99.8% identity in 425 aa overlap

```

              10      20      30      40      50      60
m504.pep      ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI
              |||||
a504          ILVQDLPEFVKLKKFHIDFYNTGMPRDFASDIEVTDKATGEKLERTIRVNHPLTLHGITI
              10      20      30      40      50      60

              70      80      90      100     110     120
m504.pep      YQASFADGGSDLTFKAWNLG DASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
              |||||
a504          YQASFADGGSDLTFKAWNLG DASREPVVLKATSIHQFPLEIGKHKYRLEFDQFTSMNVED
              70      80      90      100     110     120

              130     140     150     160     170     180
m504.pep      MSEGAREKSLKSTLXDVRVAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYK NYMLPVLQEQ

```

744

```

|||||
a504      MSEGAEEREKSLKSTLNDVRAVTQEGKKYTNIGPSIVYRIRDAAGQAVEYKKNYMLPVLQEQ
          130      140      150      160      170      180

          190      200      210      220      230      240
m504.pep  DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          |||||||
a504      DYFWITGTRSGLQQQYRWLRIPLDKQLKADTFMALREFLKDGEGRKRLVADATKGAPAEI
          190      200      210      220      230      240

          250      260      270      280      290      300
m504.pep  REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          |||||||
a504      REQFMLAAENTLNIFAQKGYLGLDEFITSNIPKEQQDKMQGYFYEMLYGVMNAALDETIR
          250      260      270      280      290      300

          310      320      330      340      350      360
m504.pep  RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          |||||||
a504      RYGLPEWQQDEARNRFLHSMDAYTGLTEYPAPMLLQLDGFSEVRSSGLQMTSPGALLV
          310      320      330      340      350      360

          370      380      390      400      410      420
m504.pep  YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK
          |||||||
a504      YLGSVLLVLGTVLMFYVREKRAWVLFSDGKIRFAMSSARSDRLQKEFPKHVESLQRLGK
          370      380      390      400      410      420

m504.pep  DLNHDX
          |||||
a504      DLNHDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1367>:

```

g505.seq
1   atgtttcggt tacaattcag gctgtttccc cctttgcgaa ccgccatgca
51  catcctgttg accgccctgc tcaaatgcct ctccctgctg tcgctttcct
101 gtctgcacac gctgggaaac cggctcggac atctggcggt ttacctttta
151 aaggaagacc gcgcgcgcat cgtcgccaat atgcggcagg cgggtttgaa
201 ccccgacacg cagacggtca aagccgtttt tgcggaaacg gcaaaatgcg
251 gtttgaact  tgccccgcg tttttcaaaa aaccggaaga catcgaaaca
301 atgttcaaag cggtacacgg ctgggaacac gtgcagcagg ctttggacaa
351 gggcgaaggg ctgctgttca tcacgccgca catcggcagc tacgatttgg
401 gcggacgcta catcagccag cagcttccgt tccacctgac cgccatgtac
451 aagccgccga aaatcaaagc gatagacaaa atcatgcagg cgggcagggt
501 gcgcggcaaa ggcaaaaccg cgcccaccgg catacaaggg gtcaaacaaa
551 tcatcaaggc cctgcgcgcg ggcgaggcaa ccatcatcct gcccgaccac
601 gtcccttctc cgcaggaagg cggcggcggt tgggcggatt ttttcggcaa
651 acctgcatac accatgacac tggcggcaaa attggcacac gtcaaaggcg
701 tgaaaaccct gtttttctgc tgcgaacgcc tgcccgcagg acaaggcttc
751 gtgttgacac tccgccccgt ccaaggggaa ttgaacggca acaaaagcca
801 cgatgccgcc gtgttcaacc gcaataccga atattggata cgccgttttc
851 cgacgcagta tctgtttatg tacaaccgct ataaaacgcc gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1368; ORF 505.ng>:

```

g505.pep
1   MFRLQFRLFP PLRTAMHILL TALLKCLSL SLSCLHTLGN RLGHlafyLL
51  KEDRARIVAN MRQAGLNPD TQTVKAVFAE AKCGLELAPA FFKKPEDIET
101 MFKAVHGW EH VQALDKGEG LLFITPHIGS YDLGGYISQ QLPFHLTAMY
151 KPPKIKAI DK IMQAGRVRGK GKTAPTGIQ VQKIIKALRA GEATIILPDH
201 VPSPQEGGGV WADFFGKPAY TMTLAAKLAH VKGVKTLFFC CERLPDGGQF
251 VLHIRPVQGE LNGNKAHDAA VFNRNTEYWI RRFPTQYLFM YNRYKTP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1369>:

745

```

m505.seq (partial)
  1  GGCATGTTTC GTTACAATT CAGGCTGTTT CCCCTTTGTC GAACCGCCAT
  51  GCACATCCTG TTGACCGCCC TGCTCAAATG CCTCTCCCTG CTGCCGCTTT
 101  CCTGTCTGCA CACGCTGGGA AACCGGCTCG GACATCTGGC GTTTTACCTT
 151  TTAAAGGAAG ACCGCGCGCG CATCGTCGCC AATATGCGGC AGGCGGGTTT
 201  GAACCCCGAC CCCAAAACGG TCAAAGCCGT TTTGCGGAA ACGGCAAAAG
 251  GCGGTTTGGA ACTTGCCCCC GCGTTTTTCA GAAAACCGGA AGACATAGAA
 301  ACAATGTTCA AAGCGGTACA CGGCTGGGAA CATGTGCAGC AGGCTTTGGA
 351  CAAACACGAA GGGCTGCTAT TCATCACGCC GCACATCGGC AGCTACGATT
 401  TGGGCGGACG CTACATCAGC CAGCAGCTTC CGTCCCGCT GACCGCCATG
 451  TACAAACCGC CGAAAATCAA AGCGATAGAC AAAATCATGC AGGCGGGCAG
 501  GGTTTCGCGC AAAGGAAAAA CCGCGCCTAC CAGCATACAA GGGGTCAAAC
 551  AAATCATCAA AGCCTGCGT TCGGGCGAGC AACCATCGTC CTGCCCGACC
 601  ACGTCCCTC CCCTCAAGAA GGCGGGGAAG GCGTATGGGT GGATTTCTTC
 651  GGCAAACCTG CCTATACCAT GACGCTGGCG GCAArATTGG CACACGTCAA
 701  AGGCGTGAAA ACCCTGTTTT TCTGCTGCGA ACGCCTGCCT GCGCGACAAG
 751  GTTTCGATTT GCACATCCGC CCCGTCCAAG GGAATTGAA CGGCGACAAA
 801  GCCCATGATG CCGCGTGTT CAACCGCAAT GCCGAATATT GGATACGCCG
 851  TTTTCCGACG CATATC....

```

This corresponds to the amino acid sequence <SEQ ID 1370; ORF 505>:

```

m505.pep (partial)
  1  MFRLQFRLFP PLRTAMHILL TALLKCLSLP LSLCLHTLGN RLGHAFYLL
  51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLELAPA FFRKPEDIE
 101  MFKAVHGEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPPPLTAMY
 151  KPPKIKAIK IMQAGVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
 201  VPSPQEGGEG VWVDFGKPA YTMTLAAXLA HVKGVKTLFF CCERLPGGQG
 251  FDLHIRPVQG ELNGDKAHDA AVFNRAEYW IRRFPTHI...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 505 shows 93.7% identity over a 287 aa overlap with a predicted ORF (ORF 505.ng) from *N. gonorrhoeae*:

m505/g505

	10	20	30	40	50	60
m505.pep	MFRLQFRLFP	PLRTAMHILL	TALLKCLSLP	LSLCLHTLGN	RLGHAFYLL	KEDRARIVAN
g505	MFRLQFRLFP	PLRTAMHILL	TALLKCLSLP	LSLCLHTLGN	RLGHAFYLL	KEDRARIVAN
	10	20	30	40	50	60
	70	80	90	100	110	120
m505.pep	MRQAGLNPD	PKTVKAVFAET	AKGGLELAPA	FFRKPEDIE	TMFKAVHGEH	VQQALDKHEG
g505	MRQAGLNPD	TQTVKAVFAET	AKCGLELAPA	FFKKPEDIE	TMFKAVHGEH	VQQALDKGEG
	70	80	90	100	110	120
	130	140	150	160	170	180
m505.pep	LLFITPHIGS	YDLGGYISQ	QLPFPLTAMY	KPPKIKAIK	IMQAGVRGK	GKTAPTSIQG
g505	LLFITPHIGS	YDLGGYISQ	LPFHLTAMY	KPPKIKAIK	IMQAGVRGK	GKTAPTGIQG
	130	140	150	160	170	180
	190	200	210	220	230	240
m505.pep	VKQIIKALRS	GEATIVLPDH	VPSPQEGGEG	VWVDFGKPA	YTMTLAAXLA	HVKGVKTLFF
g505	VKQIIKALR	AGEATII	LPDHVPSPQEGG	-GVWADFFGK	PAYMTLA	AKLAHVKGVKTLFF
	190	200	210	220	230	
	250	260	270	280	289	
m505.pep	CCERLPGGQG	FDLHIRPVQ	GELNGDKAHDA	AVFNRAEYW	IRRFPTHI	
g505	CCERLPDGGQ	FVLHIRPVQ	GELNGNKAHDA	AVFNNTTEY	WIRRFPTQYLF	MYNRYKTP
	240	250	260	270	280	290

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1371>:

a505.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGTCAGG CAGGCATGAA
201 TCCCGACCCC AAAACGGTCA AAGCCGTTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAACT TGCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTTGG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTTC GGCGAAGCAA CCATCGTCCT GCCCGACCAC
601 GTCCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTTGC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCCGTGTTCA ACCGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1372; ORF 505.a>:

a505.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGLHAFYLL
51  KEDRARIVAN MRQAGMNPDP KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGWEH VQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAIK IMQAGRVRGK GKTAPTSIQG VKQIIKALRS GEATIVLPDH
201 VPSPQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQG ELNGDKAHDA AVFNRNAEYW IRRFPTQYLF MYNRYKMP*

```

m505/a505 99.0% identity in 287 aa overlap

m505.pep	10	20	30	40	50	60
	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSLPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505.pep	70	80	90	100	110	120
	MRQAGLNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG					
a505	MRQAGMNPDPKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGWEHVQQALDKHEG					
	70	80	90	100	110	120
m505.pep	130	140	150	160	170	180
	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
a505	LLFITPHIGSYDLGGYISQQLPFPLTAMYPKPPKIKAIKIMQAGRVRGKGKTAPTSIQG					
	130	140	150	160	170	180
m505.pep	190	200	210	220	230	240
	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
a505	VKQIIKALRSGEATIVLPDHVPSPQEGGEGVWVDFFGKPAYTMTLAAKLAHVKGKTLFF					
	190	200	210	220	230	240
m505.pep	250	260	270	280		
	CCERLPGGQGFDLHIRPVQEGELNGDKAHDAVFNRNAEYWIRRFPTHI					
a505	CCERLPGGQGFDLHIRPVQEGELNGDKAHDAVFNRNAEYWIRRFPTQYLFMYNRYKMPX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1373>:

m505-1.seq

```

1  ATGTTTCGTT TACAATTCAG GCTGTTTCCC CCTTTGCGAA CCGCCATGCA
51  CATCCTGTTG ACCGCCCTGC TCAAATGCCT CTCCCTGCTG CCGCTTTCCT
101 GTCTGCACAC GCTGGGAAAC CGGCTCGGAC ATCTGGCGTT TTACCTTTTA
151 AAGGAAGACC GCGCGCGCAT CGTCGCCAAT ATGCGGCAGG CGGGTTTGAA
201 CCCCACCCCC AAAACGGTCA AAGCCGTTT TGCGGAAACG GCAAAAGGCG
251 GTTTGGAAC TCCCCCGCG TTTTTCAGAA AACCGBAAGA CATAGAAACA
301 ATGTTCAAAG CGGTACACGG CTGGGAACAT GTGCAGCAGG CTTTGGACAA
351 ACACGAAGGG CTGCTATTCA TCACGCCGCA CATCGGCAGC TACGATTGCG
401 GCGGACGCTA CATCAGCCAG CAGCTTCCGT TCCCGCTGAC CGCCATGTAC
451 AAACCGCCGA AAATCAAAGC GATAGACAAA ATCATGCAGG CGGGCAGGGT
501 TCGCGGCAAA GGAAAAACCG CGCTACCAG CATACAAGGG GTCAAACAAA
551 TCATCAAAGC CCTGCGTTCG GGCGAAGCAA CCATCGTCTT GCCCGACCAC
601 CCGCCCTCCC CTCAAGAAGG CGGGGAAGGC GTATGGGTGG ATTTCTTCGG
651 CAAACCTGCC TATACCATGA CGCTGGCGGC AAAATTGGCA CACGTCAAAG
701 GCGTGAAAAC CCTGTTTTTC TGCTGCGAAC GCCTGCCTGG CGGACAAGGT
751 TTCGATTGTC ACATCCGCCC CGTCCAAGGG GAATTGAACG GCGACAAAGC
801 CCATGATGCC GCGTGTTC ACGCAATGC CGAATATTGG ATACGCCGTT
851 TTCCGACGCA GTATCTGTTT ATGTACAACC GCTACAAAAT GCCGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1374; ORF 505-1>:

m505-1.pep

```

1  MFRLQFRLFP PLRTAMHILL TALLKCLSL LPLSCLHTLGN RLGLHAFYLL
51  KEDRARIVAN MRQAGLNPD P KTVKAVFAET AKGGLLELAPA FFRKPEDIET
101 MFKAVHGW EHVQQALDKHEG LLFITPHIGS YDLGGYISQ QLPFPLTAMY
151 KPPKIKAI DKIMQAGRVRGK GKTAPTSTIQ VKQIIKALRS GEATIVLPDH
201 VPSQEGGEG VWVDFFGKPA YMTLAAKLA HVKGVKTLFF CCERLPGGQG
251 FDLHIRPVQ G ELNGDKAHDA AVFNRAEYW IRRFPTQYLF MYNRYKMP*

```

m505-1/g505 94.3% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
g505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LSLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
m505-1.pep	MRQAGLNPD PKTVKAVFAETAKGGLLELAPAFFRKPEDIETMFKAVHGW EHVQQALDKHEG					
g505	MRQAGLNPD TQTVKAVFAETAKCGLELAPAFFKKPEDIETMFKAVHGW EHVQQALDKGEG					
	70	80	90	100	110	120
m505-1.pep	LLFITPHIGSYDLGGYISQQLPFPLTAM YKPPKIKAI DKIMQAGRVRGKGKTAPTSTIQG					
g505	LLFITPHIGSYDLGGYISQQLPFPLTAM YKPPKIKAI DKIMQAGRVRGKGKTAPTGTIQG					
	130	140	150	160	170	180
m505-1.pep	VKQIIKALRSGEATIVLPDHVPSQEGGEGVWVDFFGKPAYTMTLAAKLAHVKG VTKTLFF					
g505	VKQIIKALRAGEATII LPDHVPSQEGG-GVWADFFGKPAYTMTLAAKLAHVKG VTKTLFF					
	190	200	210	220	230	240
m505-1.pep	CCERLPGGQGF DLHIRPVQGELNGDKAHDA AVFNRAEYWIRRFPTQYLFMYNRYKMPX					
g505	CCERLPDGGQGFV LHIRPVQGELNGKHA DA AVFNRNTEYWIRRFPTQYLFMYNRYKTPX					
	240	250	260	270	280	290

m505-1/a505 99.7% identity in 298 aa overlap

	10	20	30	40	50	60
m505-1.pep	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
a505	MFRLQFRLFPPLRTAMHILLTALLKCLSL LPLSCLHTLGNRLGLHAFYLLKEDRARIVAN					
	10	20	30	40	50	60
	70	80	90	100	110	120

748

```

m505-1.pep  MRQAGLNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWEHVQQALDKHEG
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505         MRQAGMNPDPKTVKAVFAETAKGGLELAPAFFRKPEDIETMPKAVHGWEHVQQALDKHEG
              70      80      90      100     110     120

              130     140     150     160     170     180
m505-1.pep  LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTISIQQ
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505         LLFITPHIGSYDLGGYISQQLPFPPLTAMYKPPKIKAIKIMQAGRVRGKGTAPTISIQQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m505-1.pep  VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505         VKQIIKALRSGEATIVLPDHVPSPOEGGEGVWVDFFGKPAYTMTLAAKLAHVKGVKTLFF
              190     200     210     220     230     240

              250     260     270     280     290     299
m505-1.pep  CCEERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
a505         CCEERLPGGQGFDLHIRPVQGELNGDKAHDAAVFNRNAEYWIRRFPTQYLFMYNRYKMPX
              250     260     270     280     290

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1375>:

```

g506.seq
1  ATGGCGGTAT TTGATGAAGT CGGGCGCATC GCCCATGGCT GCGGCGGTGT
51 TGTCAAACAA AGCCTGTTTC TGC GCGTCGT TCATCAGGTT GAACAAGGCG
101 CGCGGTGGC TGAAGTAGTC GTCATCGTCT TGGCGGTAGT CCCAGTGTGC
151 CGCGTCGCCG TTGATTTTCA AAGGCGGTTC GCGGAAGTCG GGTGTGTGCT
201 GCCATTGGCC GAAGCTGTTG GGTTCGTAGT GCGGCAGGCT GCCGTAGTTG
251 CCGTCGCGCG GGCCTTGTCG GTCGCGCTGG TTGCTGTGAA CAGGGCAACG
301 CGGACGATTG ACGGGGATTT GCGGGAAGTT CACACCCAAG CGGTAACGTT
351 GCGCGTCGGC GTAATTGAAC AAACGGGCTT GCAACATTTT ATCCGGGCTC
401 GCGCCGATAC CGGGAACGAG GTTGCTCGGT GCGAAGGCGG ATTGTTCAC
451 ATCGGCGAAG AAGTTTTCGG GATTGCGGTT CAACTCGAAT TCGCCCACTT
501 CAATCAGCGG ATAGTCTTTT TTCGGCCAAA CTTTGGTCAA GTCAAACGGA
551 TGATAAGGCA CTTTTTCGGC ATCGGCTTCA GGCATGACTT GGATGTACAT
601 CGTCCATTTT GGGAACTCGC CGCGCTCGAT GGCTTCGTAC AGGTGCGGCT
651 GATGGCTTTC GCGGTCGTCG GCGATGATTT TTGCAGCTTC TTCGTGGTTC
701 AGGTTTTTAA TCCCTTGCTG GCTGCGGAAA TGGAAATTCA CCCAAAAACG
751 TTCGCCCGCT TCGTTCCAGA AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCTGGCGGGA ATACCGCGGT CGTCTATCAC GATGGTAACT
851 TGGTGCAGGG CTTGCGGCAG CAGCGTCCAG AAGTCCAGT TGTGTGTGGC
901 GGAACGCATA TTGGTGC GATCGCGTTT GACGGCTTTG TTCAGGTCCG
951 GGAATTTGCG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAT TTCAACGCAA AACC GCGGAT
1051 GTCGCGTTCC GCATCGGCTG CGCCGCGCTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGTGAAAAAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG TGTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTCAGCCAC AAATCTTGCG TCAGCAGGGG GCCGCGCGGG
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACGGCGCGC CGTTGTTTAT
1351 GGTCAGATGG GTTACGGGGC ATTTGGAGGT AGTCATCGCT CTTGTTCCCT
1401 TTCTCAGGTT GGTCAAATGG GGGGCAAACG GCTTACAGTA CGATTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GTAATAAATT TCTGAATCG
1501 ACATTTTATT TTCCTTTTGC AAAAATATG GATGCGATTA TACGCCAAGA
1551 TTTTCGTTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1376; ORF 506.ng>:

```

g506.pep
1  MAVFDEVGRI AHGCGGVVKQ SLFLRVVHGV EQGARLAEVV VIVLAVVPVC
51 RVAVDFQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGAALS VALVAVNRAT
101 RTIDGDLAEV HTQAVTLRVG VIEQTGLQHF IRARADTGNE VARCEGGLFH
151 IGEVFGIAV QLEFAHFNQR IVFRRPNFGQ VKRMIRHFFG IGRHDLDDVH

```

m506.seq

This corresponds to the amino acid sequence <SEQ ID 1378; ORF 506>:

1	MAVFDEVGRV	AHCGGGVAEQ	CLFLRVVHVQ	EQGARLAEIV	VIVLAVVPVC
51	<u>RVAVDFQRRF</u>	<u>GESGLLLPLA</u>	<u>EAVGFVVRQA</u>	<u>AXVAVGAALP</u>	<u>VAXXAVNXAT</u>
101	RTIDGNLAEV	YAQTVALCVG	VIEQTRLQHF	IXAGADTGNE	VARCEGGLFH
151	IGEEVFGIAV	QLEFAHFNQR	IVFFRPNFGQ	VKRMIRYFFR	VCFRHDLDVH
201	<u>RPFRKLAADF</u>	<u>GFXXVALMAF</u>	<u>AVUGDDFGGF</u>	<u>FVGQVFNALL</u>	<u>GAEMEFHPKT</u>
251	LACFVPEAVG	MRTEAVHMAV	AGGDAVAVAH	DGNLVQCFCQ	QRPEVPVVCG
301	RAHIGARVAF	DGFVQVGELT	RVAQEEHGRV	VADHIPVAFF	GIKFQGKTAD
351	VAFCICAAFA	ACHGGETGEH	LGFADFAED	FGAGVFGDVV	RYGKRTERAR
401	TFGVHTAFGD	DFAHEVGEFF	IQPQILRQQR	AARTGGQAVL	IVGNRRRAVVH
451	QMGYRAFFGG	SHRSCFSFSQ	QMGGKKRLTV	RFGGKRIRNR	FLDCNKFLES
501	TFYFPVKMTM	DATIRODFRY	*		

ORF 506 shows 89.2% identity over a 520 aa overlap with a predicted ORF (ORF 506.ng) from *N. gonorrhoeae*:

```

          10          20          30          40          50          60
m506.pep  MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVD FQRRF
          |||||:|  ||:|  |||||:|  |||||:|  |||||:|  |||||:|
g506      MAVFDEVGRIAHGCGGVVKQSLFLRVVHQVEQGARLAEVVVIVLAVVPVCRVAVD FQRRF
          10          20          30          40          50          60

```

	70	80	90	100	110	120
m506 . pep	GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG					
g506	GEVGLLLPLAEAVGFVVRQAQAVVAVGAALSVALVAVNRATRTIDGDLAEVHTQAVTLRVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m506 . pep	VIEQTRLQHFIXAGADTGNVEARCEGGLFHI GEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
g506	VIEQTGLQHFI RARADTGNVEARCEGGLFHI GEEVFGIAVQLEFAHFNQRIVFFRPNFGQ					
	130	140	150	160	170	180
	190	200	210	220	230	240
m506 . pep	VKRMIRYFFRVCFRHDL DVHRPFRKLAAFDGFX XVALMAFAVVGDDFGGFVQG VFNALL					
		:	:	:		:
g506	VKRMIRHFFGIGFRHDL DVHRPFR ELAALDGFVQVALMAFAVVGDDFCSFFVQG VFNPLL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m506 . pep	GAEMEFHPKTLACFVPEAVGMRTEAVHMAVAGGDA AVAHHDGNLVQCFGQQRPEVPVVCG					
	:	:		:		
g506	AAEMEFHPKTFARFVPEAVGMRTEAVHMAVAGGNTAVAHHDGNLVQFGQQRPEVPVVCG					
	250	260	270	280	290	300
	310	320	330	340	350	360
m506 . pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAF FGIK FQGKTADVAFCIGCAAF					
	:	:	:	:	:	:
g506	GTHIGARIAFDGFVQVG EFARVAQEEHGRVVADHIPVAF FGI E FQRTADVAFRIGCAAL					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506 . pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
		:				
g506	ACHGGETGEHLGFFADFAENFGAGVFGDVVCYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506 . pep	IQPQILRQQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFSQVQGMGGKRLTV					
		:				
g506	IQPQILRQQGAARAGGQAVLIVGNRAVVHGMGYGAFGGSHRSCSFSQVQGMGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506 . pep	RFGGKRIRNRFLDCNKFLESTFYFPFVKTM DATIRQDFRY					
g506	RFGGKRIRNRFLDCNKFLESTFYFPFAKTM DAIIRQDFRY					
	490	500	510	520		

a506.seq

1	ATGGCGGTAI	TTGATGAAGT	CGGGCGCGTC	GCCCATTGCG	GCGCGGGTGT
51	TGCCGAACAA	TGCGTGTTTC	TGCGCGTCGT	TCATCAGGTT	GAACAGGGCG
101	CGCGGTGGC	TGAAATGATC	GTCATCGTCT	TGGCGGTAGT	CCCACTGCGC
151	GCGCTCGCG	TTGATTTTCA	AAGGCGGTTT	GCGCAAGTCG	GGCTGCTGCT
201	GCCATTGGCC	GAAGCTGTTG	GGTTCGTAGT	GCGGCAGGCT	GCGGTAGTTG
251	CCGTGCGGCG	GTCCTTGTC	GTCGCGCTGG	TTGCTGTGAA	CAGGGCAACG
301	CGGACGGTTG	ACAGGGATTT	GCGCGAAGTT	CACGCCCCAG	CGGTAGCGTT
351	GCGCGTCGCG	GTAATTTGAAC	AAACGCGCCT	GCAACATTTT	ATCTGGGCTG
401	GCGCCGACAC	CGGGAACGAG	GTTGCTCGGT	GCGCAAGGCG	ATTGTTCCAC
451	ATCGGCGAAG	AAGTTTTCGG	GATTGCGGTT	CAACTCGAAT	TCGCCCCACTT
501	CAATCAGCGG	ATAGTCTTTT	TTCGGCCAAA	CTTTGGTCAA	GTCAAACGGA
551	TGATACGGCA	CTTTTTCGCG	ATCGGCTTCA	GCGATGACTT	GGATGTACAT
601	CGTCCATTTT	GGAAACTCGC	CGCGCTCGAT	GGCTTCGTAC	AGGTCGCGCT

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```

651 GATGGCTTTC ACGGTCGTCG GCGATGATTT TGGCGGCTTC TTCGTTGGTC
701 AGGTTTTTAA TGCCTTGTG GGTGCGGAAA TGGAAATTTCA CCCAAAAACG
751 CTCGCCTGCT TCGTTCAGAG AGCTGTAGGT ATGCGAACCG AAGCCGTGCA
801 TATGGCGGTA GCCGGCGGGG ATGCCGCGGT CGCTCATCAC GATGGTAACT
851 TGGTGCAGTG CTTCGGGCAG CAGCGTCCAG AAGTCCAGT TGTTTGTGGC
901 AGAGCGCATA TTGGTGCGCG GGTGCGGTTT GACGGCTTTG TTCAGGTCGG
951 GGAACCTTACG CGGGTCGCGC AGGAAGAACA CGGGCGTGTT GTTGCCGACC
1001 ACATCCAGT TGCCTTCTTC GGTATAGAAC TTCAACGAA AACCGCGGAT
1051 GTCGCGTTCT GCATCGGCTG CGCCGCGTTC GCCTGCCACG GTGGTGAAAC
1101 GGGCGAACAT CTCGGTTTTT TTGCCGACTT CGCTGAAGAT TTTGGCGCGG
1151 GTGTATTTGG TGATGTCGTG CGTTACGGTA AACGTACCGA ACGCGCCCGA
1201 ACCTTTGGCG TGCATACGGC GTTCGGGGAT GACTTCGCGC ACGAAGTCGG
1251 CGAGTTTTTC ATTACGCCAC AAATCCTGCG CCAGCAGAGG GCCGCGAGGA
1301 CCGGCGGTCA GGCTGTTTTG ATTGTCGGCA ACAGGCGCGC CGTTGTTTAT
1351 GGTACAGATG GTTACAGGGC ATTTGGAGGT ANTCATCGCT CTTGTTCCCT
1401 TTCTCAGGTT GGTCAAAT.G GGGGTAAACG GCTTACAGTA CGATTTGGCG
1451 GAAAGCGTAT TCGTAACCGG TTTCTTGATT GCAATAAATT TCTTGAATCG
1501 ACATTTTATT TCCCTTTTGT AAAAATATG GATGCGACTA TACGCCAAGA
1551 TTTTCGCTAT TAA

```

This corresponds to the amino acid sequence <SEQ ID 1380; ORF 506.a>:

```

a506.pep
1 MAVFDEVGRV AHCGGGVAEQ CLFLRVVHQV EQGARLAEIV VIVLAVVPVR
51 RVAVDFOQRRF GEVGLLLPLA EAVGFVVRQA AVVAVGASLS VALVAVNRAT
101 RTVDRDLAEV HAQAVALRVG VIEQTRLQHF IWAGADTGNE VARCEGGLFH
151 IGEEVFGIAV QLEFAHFNQR IVFFRPNFGQ VKRMIRHFFR IGRHDLVDVH
201 RPFRKLAALD GFVQVALMAF TVVGDDFGGF FVGQVFNALL GAEMEFHPKT
251 LACFVPEAVG MRTEAVHMAV AGGDAVAHH DGNLVQCFGQ QRPEVPVVC
301 RAHIGARVAF DGFVQVGELT RVAQEEHGRV VADHIPVAFF GIELQRKTAD
351 VAFICIGAAF ACHGGETGEH LGFFADFAED FGAGVFGDVV RYGRTERAR
401 TFGVHTAFGD DFAHEVGEFF IQPQILRQQR AARTGGQAVL IVGNRRRAVVH
451 GQMGYRAFGG XHRSCSFSQV GQXGGKRLTV RFGGKRIRNR FLDCNKFLES
501 TFYFPEVKTMDATIRQDFRY *

```

m506/a506 94.8% identity in 520 aa overlap

```

              10      20      30      40      50      60
m506.pep    MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVCRVAVDFQRRF
              |||
a506         MAVFDEVGRVAHCGGGVAEQCLFLRVVHQVEQGARLAEIVVIVLAVVPVRRVAVDFQRRF
              10      20      30      40      50      60

              70      80      90     100     110     120
m506.pep    GESGLLLPLAEAVGFVVRQAAXVAVGAALPVAXXAVNXATRTIDGNLAEVYAQTVALCVG
              |||
a506         GEVGLLLPLAEAVGFVVRQAAXVAVGASLSVALVAVNRATRTVDRDLAEVHAQAVALRVG
              70      80      90     100     110     120

              130     140     150     160     170     180
m506.pep    VIEQTRLQHFIXAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
              |||
a506         VIEQTRLQHFIWAGADTGNEVARCEGGLFHIGEEVFGIAVQLEFAHFNQRIVFFRPNFGQ
              130     140     150     160     170     180

              190     200     210     220     230     240
m506.pep    VKRMIRYFFRVCFRHDLDVHRPFRKLAALDGFXXVALMAFAVVGDDFGGFVVGQVFNALL
              |||
a506         VKRMIRHFFRIGFRHDLVHRPFRKLAALDGFVQVALMAFTVVGDDFGGFVVGQVFNALL
              190     200     210     220     230     240

              250     260     270     280     290     300
m506.pep    GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC
              |||
a506         GAEMEFHPKTLACFVPEAVGMRTAVHMAVAGGDAVAHHDGNLVQCFGQQRPEVPVVC
              250     260     270     280     290     300

```

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	310	320	330	340	350	360
m506.pep	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIKFQGKTADVAFICGCAAF					
a506	RAHIGARVAFDGFVQVGELTRVAQEEHGRVVADHIPVAFFGIELQKRTADVAFICGCAAF					
	310	320	330	340	350	360
	370	380	390	400	410	420
m506.pep	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
a506	ACHGGETGEHLGFFADFAEDFGAGVFGDVVRYGKRTERARTFGVHTAFGDDFAHEVGEFF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m506.pep	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGSHRSCSFQVGMGGKRLTV					
a506	IQPQILRQRAARTGGQAVLIVGNRRRAVVHGMGYRAFGGXHRSCSFQVGMGXGGKRLTV					
	430	440	450	460	470	480
	490	500	510	520		
m506.pep	RFGGKRIRNRFDCNKFLESTFYFPFVKTM DATIRQDFRYX					
a506	RFGGKRIRNRFDCNKFLESTFYFPFVKTM DATIRQDFRYX					
	490	500	510	520		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1381>:

g507.seq

```

1  ATGCTCTTGC CGGCTTTGCA ACAAGGCGGC GGCTTCCTGA GCGGCGGCGG
51  TTTCGGCCTC GTCGGGCAGG TTCAGGGCTT GGTTCCTCTG CTTCAGACGG
101 CCTTTGCGCT CTTCGTGCTT GGCAACGGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGA AAGCAGCGTT AGCGTGGCTT GGACTTCTTC CAATTCGGGC
251 AGACGCTCTT CGTGTTCGGC AACCTGCATC GCCCATTCCT CCAATTCGGT
301 TTGCTTTTCT TCGACCTGCA ACTCGTTTTC CTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC CTGCGCGATG CGTTGCAACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCG TCGCTTGGTG CAGGTTTTCG CCGTGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGTTTGTTC CTCAATTCGT
501 GTACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TTATTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1382; ORF 507.ng>:

g507.pep

```

1  MLLPALQQGG GFLSGGGFGL VGQVQGLVFL LQTAFALFVL GNRLFQGMGKL
51  LLLQRQFAAD AVCLVLLGLE GSVERGLDFF QFGQTLFVFG NLHRPFRQFG
101 LLFFDLQLVF LKLHADLLLL LPDALQLRLR CLLVAFDALV QVLPVADLFF
151 QTGNLLAQHA AFVAQFVYCL LLRLFGSLQG VYFVI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1383>:

m507.seq

```

1  ATGCTCTTGC TGACTTTGCA ACAAGGCGGC TGCTTCCTGC GCGGCGGCGG
51  TTTCGGCTTC GTCGGGCAGG TTTAAGGCTT GGTTCCTCTG TTTCAGACGA
101 CCTTTGCGCT CTTCGTGCTT GGCAATCGTT TGTTCGGCAT GGGCAAGCTG
151 CTGCTGCTTC AACGCCAGTT CGCGGCGGAT GCGGTTTGCC TCGTCCTGCT
201 GGGTTTGGA AAGCAGCGTT AGCGTGGCTT GGGCTTCTTC CAATTCGGGC
251 AGACGCTCCT CGTGTTCGGC AACCTGCATC GCCCATTCCT CCAGCTCGGT
301 TTGTTTTTCT TCGACCTGCA ACTCGTTTTC TTCAAGCTGC ACGCGGATTT
351 GCTGCTGCTC TTGATGAATG CGTTGTA ACT GCGCCTGCGC TGCCTGCTTG
401 TCGCGTTTCG TCGCTTGGTG CAGGTTTTCG TGATGGCGGA TTTGTTCTTC
451 CAAACGGGCA ATCTGCTCGC GCAACACGCC GCGCTTGTTC CTCAATTCAT
501 GCACTGCCTG CTGCTGCGAC TGTTCGGCAG TCTGCAAGGC GTGTACTTCG
551 TCGTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1384; ORF 507>:

m507.pep

```

1  MLLLTLLQQGG CFLRGGGFGF VGQVXGLVFL FQTTAFALFVL GNRLFQGMGKL

```

51 LLLQRQFAAD AVCLVLLGLE GGVERGLGFF QFGQTLTVFG NLHRPFRQLG
101 LFFFDLQLVF FKLHADLLLL LMNALXLRRL CLLVAFDALV QVLLMADLFF
151 QTGNLLAQHA ALVAQFMHCL LLRLFGSLQG VYFVV*

ORF 507 shows 87.0% identity over a 185 aa overlap with a predicted ORF (ORF 507.ng) from *N. gonorrhoeae*:

		10	20	30	40	50	60
m507.pep		MLLLTLQQGGCFLRGGGFGFVGQVXGLVFLFQTTFAFLFVLGNRLFIMGKLLLLLQRFQFAAD					
		: : : :					
g507		MLLPALQQGGGFLSGGGFGLVGVQGLVFLQLQTAFALFVLGNLFGMGKLLLLLQRFQFAAD					
		10	20	30	40	50	60
		70	80	90	100	110	120
m507.pep		AVCLVLLGLEGGVERGLGFFQFGQTLLVFGNLHRPFRQLGLFFFDLQLVFFKLHADLLLL					
		: : : :					
g507		AVCLVLLGLEGSVERGLDFFQFGQTLFVFGNLHRPFRQFGLLFFFDLQLVFLKLHADLLLL					
		70	80	90	100	110	120
		130	140	150	160	170	180
m507.pep		LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG					
		: : : :					
g507		LPDALQLRLRCLLVAFDALVQVLPVADLFFQTGNLLAQHAAFVAQFVYCLLLRLFGSLQG					
		130	140	150	160	170	180
m507.pep		VYFVV					
		:					
g507		VYFVI					

a507.seq

1	ATGCTCTTGC	TGGCTTTGCA	ACAAGGCGGC	AGCTTCCTGC	GCGGCGGCGG
51	TTTCGGGCTC	GTCAGGCAGA	TTCAGGGCTT	GGTTTTCCTG	TTTCAGACGA
101	CCTTTGCGTT	CTTCGTGCTT	GGCAACGGTT	TGTTCCGCAT	GGGCAAGCTG
151	CTGCTGCTTC	AACGCCAGTT	CGCGGCGGAT	GCGGTTTGCC	GCTGCTGCT
201	GGGTTTGGAA	GGCGGCATTG	AGTGTGGCTT	GGGTTTCTTC	CAATTCCGGG
251	AGACGCTCTT	CGTGTTCCGC	AACCTGCACT	GCCCATTCCG	CCAATTCGGT
301	TGCTCTTTCT	TCCGCCTGCA	ACTCGTTTTT	TTCGAAGCTG	ACGCGGATTT
351	GCTGCTGCTC	CTGATGGATG	CGCTGCATCT	GCGCCTGCGC	CGCCTGCTTG
401	TCGCGTTTCGA	TGCGTTGGTG	CAGGTTTTGC	TGATGGCGGA	TTTGTTCTTC
451	CAAACGGGCA	ATCTGTTTCG	GCAACACGCC	GCGTTTGTTG	CCAATTCGTT
501	GCACCGCCCT	CTGCTGCGAC	TGTTCCGGCAG	TCTGCAAGGC	GTGTACTTCG
551	TCGTTTTAA				

a507.pep

1	MLLLALQQGG	SFLRGGGGGF	VRQIQGLVFL	FQTTFALFVL	GNGLFGMGKL
51	LLLQRQFAAD	AVCLVLLGLE	GGIECGLGFF	QFGQTLFVFG	NLHRPFRQFG
101	LLFFRLQLVF	AKLHADLLLL	LMDALHLRL	RLVAFDALV	QVLLMADLFF
151	QTGNLFAQHA	AFVAQFVHRL	LLRLFGSLOG	RYFVVV*	

	10	20	30	40	50	60
m507.pep	MLLLTLQGGCFLRGGGFGVGVQVXGLVFLFQTTFALFVLGNRLFIMGKLLLLLQRFQFAAD					
	: :					
a507	MLLLALQGGGSFLRGGGFGFVRQIQGLVFLFQTTFALFVLGNLFGMGKLLLLLQRFQFAAD					
	10	20	30	40	50	60
	70	80	90	100	110	120

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```

m507.pep  AVCLVLLGLEGGVERGLGFFQFGQTLVFGNLRPFRQLGLFFFDLQLVFFKLHADLLLL
          |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       AVCLVLLGLEGGIECGLGFFQFGQTLFVFGNLRPFRQFGLLFFRLQLVFFKLHADLLLL
          70      80      90      100     110     120

          130      140      150      160      170      180
m507.pep  LMNALXLRRLRCLLVAFDALVQVLLMADLFFQTGNLLAQHAALVAQFMHCLLLRLFGSLQG
          ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a507       LMDALHLRLRLRLVAFDALVQVLLMADLFFQTGNLFAQHAAFAVQFVHRLLLRLFGSLQG
          130      140      150      160      170      180

m507.pep  VYFVVX
          |||||
a507       VYFVVX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1387>:

```

g508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCCTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGGCAGCT TGGTTTGACG GGTTTGTACG
101 CGGGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTTCTCTG
151 CACGGCGATG TATTCTTCGT CCAGCGTGTG TACGGTTTCG GTCAACTCGT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTTTGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCCGGCGTTC CTGCCAGTCC AGGGTTTGCT GTTCGAGCCG
301 GCGGATTGTC TGCCGGTAGT TTTGTTTTTG CGGGTTGAGT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA GCGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1388; ORF 508.ng>:

```

g508.pep
1  MVAFGVDQGL LLLQQGGLGG GLKLRQLGLQ GLYAGVLLPA LFLNLRFFFL
51  HGDVFFVQRV YGFGQLVELD VLLVVLELGF IGEGKLLPAF LPVQGLLFEP
101 GDLLPVVLFL RVEFVDGDFG KPVLA VG FQ GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQSSDVV

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1389>:

```

m508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TCGGGCAGCT TGGTTTGACG GGTTTGTACT
101 TTAGCGTATT GCTCCCTGCC CTGTTCTCTGA ATCTGCGCGA GTTTCTCTTG
151 CACAACAATA TATTCTTCGT CCAAGGTCTG TACGGCTTCG CTTAATTCTT
201 CAAGCTTGAT GTGCTGCTCG TCGTTTTTGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAGTCG AGGGTTTGCT GTTCAAGCTG
301 GCGGATTGTC TGCCGGTAGT TTTGTTTTTG CTGGTTGACT TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGGCCTTG CTGCTCTTGG CGGCTGTGCG CGGTGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAAGTA ACGATGTCGT
501 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1390; ORF 508.ng>:

```

m508.pep
1  MVAFGVDQGF LLLQQGGLGG GLKLRQLGLQ GLHFSVLLPA LFLNLRFFLL
51  HNNIFFVQGL YGFAXFFKLD VLLVVLELGF IGEGKLLAF LPVEGLLFKL
101 GDLLPVVLFL LVEFVDGDFG KPVLA VG FQ GKLRLFQTAL LLLAAVRGGL
151 LLVFEFGGGF LQNDVV*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 508 shows 86.8% identity over a 167 aa overlap with a predicted ORF (ORF 508.ng) from *N. gonorrhoeae*:

m508/g508

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	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
g508	MVAFGVDQGLLLQGGGLGGGLKLRQLGLQGLYAGVLLPALFLNLREFFLHGDVFFVQRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKLGDLLPVVLFLLVEFVDGDFG					
g508	YGFQQLVELDVLLVVLELGFIGEGKLLPAFLPVQGLLFEPGDLLPVVLFLLRVEFVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGN DVV					
g508	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQSS DVV					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1391>:

```
a508.seq
1  ATGGTAGCGT TTGGCGTTGA TCAGGGCTTC CTGCTGCTGC AACAGGGCGG
51  TTTGGGTGGC GGCCTGAAGC TGCGGCAGCT TGGTTTGAG GGTTTGTACG
101 CGGGCGTATT GTTCCCTACC CTGCTCCTGA ATCTGCGCGA GTTCTCCTG
151 TACGACAATA TATTCTTCGT CCAAACTCTG TACGGCTTCG CTCAACTCTT
201 CGAGCTTGAT GTGCTGCTCG TCGTTTGGGA ACTCGGTTTC ATAGGCGAGG
251 GCAAGCTCTT GCTGGCGTTC CTGCCAATCG AAGGTTTGTT GTTCAAGCTG
301 GGCAATTTGC TGTGGTAGT TTTGTTTTTG CTGGTTGAGC TTGTGGACGG
351 CGACTTCGGC AAGCCCGTAT TGGCGGTTGG CTTCCAACAG GGCAAGCTGC
401 GCCTGTTTCA GACGACCTTG CTGCTCTTGG CGGCTGTGCG CGGCGGTTTG
451 CTGCTGGTGT TCGAGTTCGG CGGCGGCTTC CTGCAAATG GCGATGTCGT
501 CTGA
```

This corresponds to the amino acid sequence <SEQ ID 1392; ORF 508.a>:

```
a508.pep
1  MVAFGVDQGF LLLQGGGLGG GLKLRQLGLQ GLYAGVLFPT LLLNLREFLL
51  YDNIFFVQTL YGFAQLFELD VLLVVLELGF IGEGKLLLAFL LPIEGLLFLK
101 GNLLLVVFL LVELVDGDFG KPVLA VG FQ QG KLR L FQTLL LLAAVRGGL
151 LLVFEFGGGF LQNGDVV*
```

m508/a508 88.6% identity in 167 aa overlap

	10	20	30	40	50	60
m508.pep	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLHFSVLLPALFLNLREFLLHNNIFFVQGL					
a508	MVAFGVDQGFLLQGGGLGGGLKLRQLGLQGLYAGVLFPTLLNLREFLLYDNIFFVQTL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m508.pep	YGFAXFFKLDVLLVVLELGFIGEGKLLLAFLPVEGLLFLKLGDLLPVVLFLLVEFVDGDFG					
a508	YGFAQLFELDVLVVLELGFIGEGKLLLAFLPIEGLLFLKLGNNLLVVLFLLVELVDGDFG					
	70	80	90	100	110	120
	130	140	150	160		
m508.pep	KPVLA VG FQ QG KLR L FQTALLLLAAVRGGLLVFEFGGGFLQGN DVVX					
a508	KPVLA VG FQ QG KLR L FQTLLLLAAVRGGLLVFEFGGGFLQNG DVVX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1393>:

g509.seq

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```

1   atggctcgctg tatgtgatga acgggctgta cagcggacgt tgggtggccca
51  attcgcgcaa caaggcggct tgtttttgct cttcgttcag gctgtttag
101 tcttccaagc ctgcgtgttg gaaaagctcg gcaaccacat cggcgtgttt
151 gcctgcgtgt tggcgcaggt cgagcggcat catgtggaag ccgaacacgg
201 acacggaacg gatgaggtct gccaaacggc cttcggcaag caggcggctg
251 ccgttgtcga taagggaacg ttgcaatttt ttcaaatacat cgagaaattt
301 ttgggcccga gcataaggct cgagaaagcc gaatttgacg cccatgccca
351 aaccgagcga gcgcgctttg cccatagcgc gcgccataat gtaggcaatg
401 gcgcggcggt aagggtcttc ggtgcgggcg atttcttcgt caggcgagag
451 ggctgccagt gccattacgt cgtcgttgac tttgacgcgg cggatggaaa
501 gcggcagttc gcggtaaagt ttgtcgagtt cgtgcggta aaaacggaac
551 acggcatcgg cgtggcggcg gaaggcaaaag cgcagggttt cgccagaaac
601 aaacggattg ccgtcgcggg cgccgccgat ccagccgccg attttaagga
651 tattcggaac gcggacatcg ggataggccg tctgaaagtc gtgtccatc
701 ttgcggtaga gtttgggcag ggcttcaaaa aagctcatcg ggaagatgga
751 cagccggttg ttgatttcgt cgttgacgct gagtttgttg cggcgcgttt
801 cgtcgttctg ccacaagccc agaagcacgg tgcgatttc gcggcgcagc
851 cgtgccagcg cgtcggcatt ggtgcagcgt tcgcgttgcg gcagcagcgc
901 gcggatgcgg cggttgaaat tcaaaacggg ttggcgttgc acttcggctg
951 ggtgcgcggg caaaacggcg gtaacggacg tattgtccaa ctgccgtctg
1001 accgatttgc cgtcggcttt ccccgctttg agcctgcgga cggttccgt
1051 caggctgcct tctgctgcgt tgtggccggc atcttcgttg atttggcggc
1101 ggcgttcgtg gtgcacgtct tcggcgatat tcagaatctg ggcgaaacagc
1151 ccgcaggcaa gcgtcagatc gtaggtctgc cgttcgtcca attgcggcaa
1201 tactttttca atcaatgccg cgtgtcgtc ggaagtggac aagagtttga
1251 ccgttttcgac aaccaacggc gaggtctctt cgtgcaggag gttgaacagg
1301 gactgtttca aaaattccgc gtcgcgcgc aaagccgcgt ccttcggatt
1351 gttcaggata tgcagttgca tgattttcct ctcattgccg taaatactgt
1401 aaatgtacct caaatgccgc atccgtgcca aaccgttcac actttaacca
1451 ctcattgtcc gaaatgccgt ctgaagttag acgccgcccg acggcggcgt
1501 tacaatcgcc cgcaactgtt tttttccgaa catcatcatg accgcgaccg
1551 aacacgacaa cgacgacgca ctctgctgc ggtacagccg ccacatcctc
1601 ttggacgaaa tcggcatcga agggcagcag aagctttccg ccgcgcatac
1651 tttggtcgtc ggctgcggcg gattgggccc cgcgcgccct gccctatctc
1701 gccgcctcgg gggtcggcac gctga

```

This corresponds to the amino acid sequence <SEQ ID 1394; ORF 509.ng>:

g509.pep

```

1   MVAVCDERAV ORTLVAQFAQ QGGLFLLFVQ AVVVVFQACVL EKLGNHIGVF
51  ACVLAQVERH HVEAEHGHGT DEVCQTAFGK QAAAVVDKGT LQFFQIIIEKF
101 LGRSIRLEKA EFAAHAQTER ARFAHSARHN VGNGAAVRFF GAGDFFVRRE
151 GCQCHYVVVD FDAADGKRQF AVKFVEFAAV KTEHGIGVAA EGKAQGFARN
201 KRIAVAVAAD PAADFKDIRN ADIGIGRLKV VFHLAVEFGQ GFKKAHREDG
251 HAVVDFVVD AEFVAARFAGL PQAQKHGVDF AAQPCQRVGI GAAAFALRQR
301 ADAAVEIQNG LALHFGRVRG QNGGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFCCVVAG IFVDLAAAFV VHVFGDIQNL GEQPAGKRQI VGLPFVQLRQ
401 YFFNQCRVVV GSGQEFDRFD NQRRGFFVQE VEQGLFQKFR VRRQSRVLRI
451 VQDMQLHDFP LIAVNTVNVP QMPHPCQTVH TLTHVTPKCR LKLNAARRRR
501 YNRPQLFFSE HHHRDRDRTRQ RRRTPAAVQP PHPLGRNRHR RAAEAFRRAY
551 FGRRLLRRIGR RRPCISPPIR GSAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1395>:

m509.seq

```

1   ATGGTCGCTG TATGTGATAA ACGGGCTGTA CAGAGGACGT TGATGGCTCA
51  ATTCGCGCAA CAGGGCGGTT TGTTTTGTCT CTTCGTTCAG GCGGTTGTAG
101 TCTTCCAAGC CTGCGTGTGT GAAAAGCTCG GCAACCACAT CGGCGTGTTC
151 GCCTGCGTGT TGGCGCAAGT CGAGCGGCAT CATGTGAAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCCGCAAG CAGACGGCTG
251 CCGTTGTGCA TAAGGGAACG TTGCAATTTT TTCAAATCAT CCAGAACTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCGATG
401 GCGCGGCGGT AGGGTTCTTC GGCGCGGGCG ATTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCGTTACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGATT CGCCGCGATA GAAGCGGAAC

```

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```

551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAG CGCAGGGTTT CGGCAGAAAC
601 AAACGGATTG CCGTCGCGGT CGCCGCCGAT CCAGCCGCCG ATTTTGAGGA
651 TGTCCGGAAC GCGGACGCCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCGAAA AAGCTCATCG GGAAGATGGA
751 CACGCCGT TGATTTCGT CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTtC GCgGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTGCAGCGT TCgCGTTGCG GCAACAGTGC
901 GCGGATGCGG CGGTTGAAGC TTAAGACGGT TTGGCGTTGC ACTTCGGTCG
951 GGTGCGCGGT CAAAACGGCG GTAACGGACG TATTGTCCAA CTGCCGCTGC
1001 ACCGATTTGC CGTCGGCTTT CCCCCTTTG AGCCTGCCGA CGGTTTCCGT
1051 CAGGCTGCC'T TCCGCGCCGC CGCGTCCGGC TTCTTCGTGG ATTTGGCGGC
1101 GCGGTTCTGT GTGCACGTCT TCGGCGATGT TCAAAATCTG GGCGAACAGG
1151 CCGCAGGCCA AGGTTAAATC GTGGGTTTGT TGTTCTGTTCA ATTGCGGCAA
1201 TACTTTTTCA ATCAATGCCG CGCTGTCGTC GGAAGTGGAC AAGAGTTTGA
1251 CTGTTTCGAC AACCAACGGC GAGGCTTCTT CGTGCAGGAG GTTGAACAGG
1301 GATTGTTTCA GAAATTCCGC GTCCGCCGCC AAAGCCGCGT CCTTTGGATT
1351 GTTCAGAATA TGCAGTTGCA TGATTTTTCT CTCTCGTCTG CCGTAAATAT
1401 TGTAATGTA CCCCCAATGC CGCATCCGTG CCAAACCGTT CACACTTTAA
1451 CCGCCCGTGT CCCGAAATGC CGTCTGAAGT TGAACGCCGC CCGACGGCAG
1501 CGTTACAATC GCCCGCAACT GTTTTtTTCC GAACATCATC ATGACCACGA
1551 CCGAACACGA CAACGACGAT GCATTCTGTC TCGGTTACAG CCGCCACATC
1601 CTCTTGACG AAATCGGCAT CGAAGGGCAG CAGAACTTT CCGCCGCGCA
1651 TATTTTGGTC GTCGGCTGCG GCGGTTTGGG TGCCGCCGCA CT.GCCCTAC
1701 CTTGCCGCTT CGGGTGTGCG CACGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1396; ORF 509>:

```

m509.pep
1  MVAVCDKRAV QRTLMAQFAQ QGGLFLLFVQ AVVVVFQACVL EKLGNHIGVF
51 ACVLAQVERH HVKAEHGYGT DEVCQTAFGK QTAAVVDKGT LQFFQIIQKL
101 LCRSIRLEKA EFAAHTQTER ARFAHSARHN VGDGAAVGFF GAGDFFVGRF
151 VGQRRYIAVD FDAADGERQF AVEFVEFAAI EAEHGIGVAA EGKAQGFGRN
201 KRIAVAVAAD PAADFEDVRN ADAGIGRLKV VFHLAVELGQ GFKAHREDG
251 HAVVDFVDA EFVAARFAGL PQAQQDSVDF AAQPCQRVGI GAAFALRQQC
301 ADAAVEAXDG LALHFGVRG QNGNGRIVQ LPLHRFAVGF PRFEPADGFR
351 QAAFRAAASG FFVDLAAAFV VHVFGDVQNL GEQAAGQGXI VGLLFVQLRQ
401 YFFNQCRVV GSGQEFDCFQ NQRRGFFVQE VEQGLFQKFR VRRQSRVLWI
451 VQNMQLHDFS LSSAVNIVNV PQMPHPCQTV HTLTARVPKC RLKLNARRQ
501 RYNRPQLFFS EHHHDHRT RRCIPAAVQ PPHPLGRNRH RRAAETFRRA
551 YFGRRLRRFG CRRTXPTLPL RVSAR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 509 shows 87.8% identity over a 575 aa overlap with a predicted ORF (ORF 509.ng) from *N. gonorrhoeae*:

```

m509/g509
      10      20      30      40      50      60
m509.pep MVAVCDKRAVQRTLMAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNIHIGVFACVLAQVERH
|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g509      MVAVCDERAVQRTLVAQFAQQGGLFLLFVQAVVVVFQACVLEKLGNIHIGVFACVLAQVERH
      10      20      30      40      50      60

      70      80      90      100     110     120
m509.pep HVKAEHGYGTDEVCQTAFGKQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER
||:||||:|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g509      HVEAEHGHGTDEVCQTAFGKQAAAVVDKGTLQFFQIEKFLGRSIRLEKAEFAAHAQTER
      70      80      90      100     110     120

      130     140     150     160     170     180
m509.pep ARFAHSARHNVDGAAGVFFGAGDFFVGRFVGQRRYIAVDFDAADGERQFAVEFVEFAAI
|||||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
g509      ARFAHSARHNVDGNAAVRFFGAGDFFVRREGCQCHYVVVDFDAADGKRQFAVKFVEFAAV
      130     140     150     160     170     180

```

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	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFGRNKR IAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
	:: : : : : : : : : : : : : : : : : : :					
g509	KTEHGIGVAAEGKAQGFARNKR IAVAVAADPAADFKD I RNADIGIGRLKVVFHLAVEFGQ					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GF EKAHREDGHAVVDFVVD AEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAAAFALRQQC					
	: : : : : : : : : : : : : : : :					
g509	GFKKAHREDGHAVVDFVVD AEFVAARFAGLPQAQKHGVDFAAQPCQRVGIGAAAFALRQQR					
	250	260	270	280	290	300
	310	320	330	340	350	360
m509.pep	ADA AVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFRAAASG					
	: : : : : : : : : : : : : : :					
g509	ADA AVEIQNGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPFRFEPADGFRQAAFCVVAG					
	310	320	330	340	350	360
	370	380	390	400	410	420
m509.pep	FFVDLAAAFVHVFGDVQN LGEQAAGQGXI VGLLFVQLRQYFFNQCRAVVSGSQEFDCFD					
	: : : : : : : : : : : : : : : :					
g509	IFVDLAAAFVHVFGDIQN LGEQPAKGRQIVGLPFVQLRQYFFNQCRAVVSGSQEFDRFD					
	370	380	390	400	410	420
	430	440	450	460	470	480
m509.pep	NQR RGFFVQEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMHPHCQTV					
	: : : : : : : : : : : : : : :					
g509	NQR RGFFVQEVEQGLFQKFRVRRQSRVLRIQDMQLHDFPLI - AVNTVNVPQMHPHCQTV					
	430	440	450	460	470	
	490	500	510	520	530	540
m509.pep	HTLTARVPKCR LKLNAARRQRYNRPQLFFSEHHHDH DTRQRR CIPAAVQPPHPLGRNRH					
	: : : : : : : : : : : : : : :					
g509	HTLTTHVPKCR LKLNAARRRRYNRPQLFFSEHHHDH DTRQRRRTPAAVQPPHPLGRNRH					
	480	490	500	510	520	530
	550	560	570			
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTCPTLPLRV SAR					
	: : : : : : : : : : : :					
g509	RRAAEAFRRAYFGRRLRRIGRRRPCISP PRGSAR					
	540	550	560	570		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1397>:

```

a509.seq
1   ATGGTCGCTG TATGTGATGA ACGGACTGTA CAGTGGACGT TGATGGCTCA
51  ATTCCGCAAG CAGGGCGGCT TGTTTTTGCT CTTCGTTGAG GCTGTTGTAG
101 TCTTCCAAGC CTGCGTGTTG GAAAAGCTCG GCAACCATAT CGGCGTGTTT
151 GCCTGCGTGT TGGCGCAGGT CGAGCGGCAT CATGTGGAAG CCGAACACGG
201 ATACGGAACG GATGAGGTCT GCCAAACGGC CTTCGGCAAG CAGGCGGCTG
251 CCGTTGTCGA TAAGGGAATG TTGCAATTTT TTCAAATCAT CGAGAAATTC
301 TTGTGCCGAA GCATAAGGCT CGAGAAAGCC GAATTTGCAG CCCATACCCA
351 AACCGAGCGC GCGCGCTTTG CCCATAGCGC GCGCCATAAT GTAGGCAATG
401 GCGCGACGGT AGGGTTCTTC GGCGCGGGCG GTTCTTCGT CGGGCGATTT
451 GTCGGACAAC GCCATCACAT CGCCGTTGAC TTTGACGCGG CGGATGGAGA
501 GCGGCAGTTC GCGGTAGAGT TTGTGAGTTC CGCCACGGTA AAAACGGAAC
551 ACGGCATCGG CGTGGCGGCG GAAGGCAAAA CGCAAGGTTT CGGCAGAAAC
601 AACCGGATTG CCGTCGCGGT CGCCGCGCAT CCAGCCGCGG ATTTTGAGGA
651 TGTCCGGAAC GCGGACATCG GGATAGGCCG TCTGAAAGTC GTGTTCCATC
701 TTGCGGTAGA GCTTGGGCAG GGCTTCAAAA AAGCTCATCG GAAAGATGGA
751 CACGCCGTTG TTGATTTCTG CGTTGACGCT GAGTTTGTGG CGGCGCGTTT
801 CGCTGGTCTG CCACAAGCCC AGCAGGATAG TGTCGATTTT CGGCGCGCAGC
851 CGTGCCAGCG CGTCGGCATT GGTACAGCGT TCGCGTTGCG GCAGCAGCGC

```


a509.pap

m509/a509 93.0% identity in 575 aa overlap

	10	20	30	40	50	60
m509.pep	MVAVCDKRAVQRTLMAQFAQQGGFLFLFVQAVVVFOACVLEKLGNHIGVFACVLAQVERH					
a509	::: :::					
	10	20	30	40	50	60
	70	80	90	100	110	120
m509.pep	HVKAEHGYGTDEVQCQTAFGKGQTAAVVDKGTLQFFQIIQKLLCRSIRLEKAEFAAHTQTER					
a509	::: ::: :::					
	70	80	90	100	110	120
	130	140	150	160	170	180
m509.pep	ARFAHSARHNVGDDGAAGVFFFGAGDFFVGRFVGQRRIYAVDFDAADGERQFAVEFVEFAAI					
a509	: : : : : :					
	130	140	150	160	170	180
	190	200	210	220	230	240
m509.pep	EAEHGIGVAAEGKAQGFRGNKRIAVAVAADPAADFEDVRNADAGIGRLKVVFHLAVELGQ					
a509	: : : :					
	190	200	210	220	230	240
	250	260	270	280	290	300
m509.pep	GFEKAHREDGHAVVDFVVDAAEFVAARFAGLPQAQQDSVDFAAQPCQRVGIGAALRQQC					
a509	: : :					
	250	260	270	280	290	300
	310	320	330	340	350	360

760

m509.pep	ADAAVEAXDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPREFPADGFRQAAFRAAASG
a509	ADAAVEIQDGLALHFGRVRGQNGNGRIVQLPLHRFAVGFPREFPADGFRQAAFRAAASG
	310 320 330 340 350 360
m509.pep	FFVDLAAAFVVHVFGDVQNLGEQAAGQGIXIVGLLFLVQLRQYFFNQCRVVGSGQEFDCFD
a509	FFVDLAAAFVVHVFGDVQNLGEQAAGQGIXIVGLLFLVQLRQYFFNQCRVVGSGQEFDRFD
	370 380 390 400 410 420
m509.pep	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLSSAVNIVNVPQMPHPCQTV
a509	NQRRGFFVQVEVEQGLFQKFRVRRQSRVLWIVQNMQLHDFSLI-AVNTVNVPQMPHPCQTV
	430 440 450 460 470 480
m509.pep	HTLTARVPKCRLLKLNAAARRQRYNRPLQFFSEHHHDHRTQRRCIPAAVQPPHPLGRNRH
a509	HTLTARVPKCRLLKLNAAARRQRYNRPLQFXSEHHHDHRTQRRCIPAAVQPPHPLGRNWH
	480 490 500 510 520 530
m509.pep	RRAAETFRRAYFGRRLRRFGCRRTXPTLPLRV SARX
a509	RRAAETFRRAYFGRRLRRFGCRXPCPISPLPASARX
	540 550 560 570

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1399>:

```

g510.seq
1  atgccttcgc ggacaccgca gggaaaaagg ggttattcct gccccaaagcg
51 ggatagtgcc ttttgccagg cgttgtccat atcggttatt ttacgcgcaa
101 aatcgccgat tgccaaatcg ccgccgttca gggaggtttt caataggctcg
151 tggacgacgt tgagcgcggc cataatgacg attttttcgc tgcgcgcgac
201 gcggccgcct tcgcggatgg ctteggcttt gccgttgagc attccgactg
251 cctgcaacag tgtgtctttt tcttctgccg gcgtgttgac agtcagccgg
301 ggcgtgcatg acttcgatgt agacttgctc gatgttcac ctttaatcct
351 tattgctgcg tttcctgccg ttgggggagg cgcgctgccg gtgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1400; ORF 510.ng>:

```

g510.pep
1  MPSRTPQGKR GYSCPKRDSA FWQALSISVI LRAKSPIAKS PPFREVFNRS
51  WTTL SAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVHDFD VDLF DVHPLILIAA FPAVGGGALP VR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1401>:

```

m510.seq
1  ATGCCTTCGC GGACACCGCA GGGnAAAAGG GGTATTCTCT GCGCCAAGCG
51  GGATAGTGCT TTTTGCCAGG CGTTGTCCAT ATCGGCTATT TTACGCGCAA
101 AATCGCCGAT TGCCAAATCG CCGCCGTCA GGGAGGTTT CAACAGGTCG
151 TGGACGACGT TGAGCGCGGC CATAATGACG ATTTTTCGCG GTCCGCGAC
201 GCGTCCGCCT TCGCGGATGG CTTCGGCTTT GCCGTGAGC ATTCGCACTG
251 CCTGCAACAG TGTGTCTTT TCTTCTGCCG GCGTGTGAC GGTCAGCCGG
301 GCGGTGCAW ACTTCsAtGT GGA CTGTGTC GATGTTCAT CTTTAATCCT
351 TATTGCTGCG TTTCCTGCCA TTGGGGGAGG CGCGCTGCCA GTGCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1402; ORF 510>:

```

m510.pep
1  MPSRTPQGKR GYSCAKRDSA FWQALSISAI LRAKSPIAKS PPFREVFNRS
51  WTTL SAAIMT IFSLSATRPP SRMASALPLS IPTACNSVSF SSAGVLTVSR
101 GVXDFX VDLF DVHPLILIAA FPAIGGGALP VR*

```

Computer analysis of this amino acid sequence gave the following results:

761

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 510 shows 96.2% identity over a 132 aa overlap with a predicted ORF (ORF 510.ng) from *N. gonorrhoeae*:

m510/g510

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFAWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	:					
g510	MPSRTPQGKRGYSCPKRDSAFAWQALSISVILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
	:					
g510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
g510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1403>:

a510.seq

1	ATGCCTTCGC	GGACACCGCA	GGGAAAAAGG	GGTTATTCCT	CGGCCAAGCG
51	GGATAGTGCT	TTTTGGCAGG	CGTTGTCCAT	ATCGGCTATT	TTACGCGCAA
101	AATCGCCGAT	TGCCAAATCG	CCGCCGTTCA	GGGAGGTTT	CAACAGGTCG
151	TGGACGACGT	TGAGCGCGGC	CATAATGACG	ATTTTTTCGC	TGTCCGCGAC
201	GCGTCCGCCT	TCGCGGATGG	CTTCGGCTTT	GCCGTTGAGC	ATTCCGACTG
251	CCTGCAACAG	TGTGTCTTTT	TCTTCTGCCG	GCGTGTGAC	GGTCAGCCGG
301	G.CGTGCATG	ACTTCGATGT	GGACTTGTTT	GATGTTTCATC	CTTTAATCCT
351	TATTGCTGCG	TTTCTGCGG	TTGGGGGAGG	CGCGCTGCCA	GTGCGCTGA

This corresponds to the amino acid sequence <SEQ ID 1404; ORF 510.a>:

a510.pep

1	MPSRTPQGKR	GYSCAKRDSA	FWQALSISAI	LRAKSPIAKS	PPFREVFNR
51	WTTLSAAIMT	IFSLSATRPP	SRMASALPLS	IPTACNSVSF	SSAGVLTVSR
101	XVHDFDVLDF	DVHPLILIAA	FPAVGGGALP	VR*	

m510/a510 97.0% identity in 132 aa overlap

	10	20	30	40	50	60
m510.pep	MPSRTPQGKRGYSCAKRDSAFAWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	:					
a510	MPSRTPQGKRGYSCAKRDSAFAWQALSISAILRAKSPIAKSPPFREVFNRSWTTLSAAIMT					
	10	20	30	40	50	60
	70	80	90	100	110	120
m510.pep	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRGVXDFXVDLFDVHPLILIAA					
	:					
a510	IFSLSATRPPSRMASALPLSIPTACNSVSFSSAGVLTVSRXVHDFDVLFDVHPLILIAA					
	70	80	90	100	110	120
	130					
m510.pep	FPAIGGGALPVRX					
	:					
a510	FPAVGGGALPVRX					
	130					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1405>:

g512.seq

1	atgaaagtgc	ttgttttagg	tgcgggtggt	gccggcgat	cctccgtgtg
---	------------	------------	------------	-----------	------------

g512.pep

m512.seq (partial)

m512.pep (partial)

m512/g512

```

                                10      20      30
m512.pep                      VLERYGVPPYRLKPEECAEFEPALARVTAK
                                |||||
g512      TDMNFEGRRKKGTLQIFRQTEEVEAAKQDIAVLERYGVPPYRLKPEECAEFEPALARVTAK
              130      140      150      160      170      180

              40      50      60      70      80      90
m512.pep    IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
              |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g512      IVGGLHLPADATGDCRLFTENLYKLCQEKGVRFYFNQTISRIDHNGLRIKAVETKQGGLK
              190      200      210      220      230      240

              100      110      120
m512.pep    QMPLSARSVASAGRFRWSWISICPFIPSKAIP
              |||||||:|||||
g512      QMPLSARSAASAGLCWRWSWISICPFIPSKAIP

```

763

250

260

270

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1409>:

```
a512.seq
1  ATGAAAGTGC TTGTTTTAGG TGCTGGTGTT GCCGGCGTAT CTTCCGCGTG
51  GTATCTGGCA GAGGCAGGAC ATGAAGTAAC GGTCATCGAC CGCGCCGAGG
101 GCGTGGCGAT GGAACCAGT TTTGCCAACG CAGGCCAGCT TTCTTACGGC
151 TATACCACGC CTTGGGCTGC ACCCGGTATT CCGACCAAAG CACTGAAATG
201 GCTGTTTAAA AGCCATCCGC CTTTGCTGTT TCGCCCCGAC GGCAGCCTGT
251 ATCAAATCGA ATGGCTGTGG CAGATGCTGC AACACTGCAC GGCAGCGCGC
301 TATCAAATCA ATAAAGAGCG CATGGTCAGG ATGTCCGAAT ACAGCCGTGA
351 AATGTTCCGC CGTTTTGAAG CGCAAACCGG CATGAATTTT GAGGGACGCA
401 AAAAAGGGAC GTTGCAGATT TTCCGCCAAA CCAAAGAAGT CGAAGCGGCA
451 AAACAAGACA TTGCCGTTTT GGAACGCTAC GGCCTGCCGT ACCGCCGTCT
501 GAAGCCCGAA GAATCGCGAG AATTCGAGCC TGCCTGGCA CGCGTTACCG
551 CAAAATTGCG CGGCGGCGCT CACCTGCCCC CAGACGCGAC CGGCGACTGC
601 CGCCTCTTCA CTGAAAACCT GTACAAATTG TGTCAAGAAA AGGGCGTACG
651 GTTTCATTTT AACCAAACCA TCAGCCGCAT CGACCACAAC GGGCTGCGCA
701 TCAAACCGT TGAACGAAA CAGGGCGGTT TGAAGCAGAT GCCGTTGTCT
751 GCGCGCTCGG CTGCTTCAGC AGGACGGTTT TGGCGCAACT GGATCTCAAT
801 CTGCCGATTT ATCCCGTCAA AGGCTATTCC TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1410; ORF 512.a>:

```
a512.pep
1  MKVLVLGAGV AGVSSAWYLA EAGHEVTVID RAEGVAMETS FANAGQLSYG
51  YTPWAAPGI PTKALKWLFK SHPPLFRPD GSLYQIEWLW QMLQHCTAAR
101 YQINKERMVR MSEYSREMFR RFEAQTMNF EGRKKGLQI FRQTKVEEAA
151 KQDIAVLERY GVPYRLKPE ECAEFEPALA RVTAKIAGGL HLPADATGDC
201 RLFTENLYKL CQEKGVRFHF NQTISRIDHN GLRIKTVETK QGGLKQMPLS
251 ARSAASAGRF WRKWISICRF IPSKAIP*
```

m512/a512 95.9% identity in 122 aa overlap

```
m512.pep                                10      20      30
                                VLERYGVVPYRLKPEECAEFEPALARVTAK
a512                                |||||
                                130      140      150      160      170      180
                                TGMNFEGRKKGTLQIFRQTKVEEAAKQDIAVLERYGVVPYRLKPEECAEFEPALARVTAK

                                40      50      60      70      80      90
m512.pep                        IAGGLHLPADATGDWRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK
a512                        |||||
                                190      200      210      220      230      240
                                IAGGLHLPADATGDCRLFTENLYKLCQEKGVRFHFNQNISRIDHNGLRIKTVETKQGGLK

                                100      110      120
m512.pep                        QMPLSARSVASAGRFWRWSISICPFIPSKAIPX
a512                        |||||:|||||:|||||
                                250      260      270
                                QMPLSARSAASAGRFWRKWISICRFIPSKAIPX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1411>:

```
g513.seq
1  ATGGGTTCGG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
51  TTCGAAGGT ATGATTCAAA TGCTGGGCGT GTTGTCGAT ACCATCATCG
101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
301 AAAAGCCATT GGCTGATTAC CGCGTTTTTC CGTATGCTGG TTTTGGCGTG
351 GGTCTATTTT GGC GCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
401 ATATGGCGAT GGGCATCATG GCGTGGATCA ACCTCGTCGC CATCCTGCTG
451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
```

501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1412; ORF 513.ng>:

g513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKM GK DPEFKLSEHP GLKRRIKSDV W*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1413>:

m513.seq

1 ATGGGTTCCG CGCCGAACGC CGCCGCCGCC GCCGAAGTGA AACACCCTGT
 51 TTCGCAAGGT ATGATTCAA TGCTGGGCGT GTTGTGCGAT ACCATCATCG
 101 TTTGTTCTTG CACCGCCTTC ATCATCTTGA TTTACCAACA GCCTTATGGC
 151 GATTTGAGCG GTGCGGCGCT GAcgcAGGCG GCGATTGTCA GCCAAGTGGG
 201 GCAATGGGGC GCGGGTTTCC TCGCCGTCAT CCTGTTTATG TTTGCCTTTT
 251 CCACCGTTAT CGGCAACTAT GCCTATGCCG AGTCCAACGT CCAATTCATC
 301 AAAAGCCATT GGCTGATTAC CGCCGTTTTC CGTATGCTGG TTTTGGCGTG
 351 GGTCTATTTC GGCGCGGTTG CCAATGTGCC TTTGGTCTGG GATATGGCGG
 401 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 451 CTCTCGCCat TGGCGTTTAT GCTGCTGCGC GATTACACCG CCAAGCTGAA
 501 AATGGGCAAA GACCCCGAGT TCAAACTTTc cgAACATCCG GGCCTGAAAC
 551 GCCGCATCAA ATCCGATGTT TGGTAA

This corresponds to the amino acid sequence <SEQ ID 1414; ORF 513>:

m513.pep

1 MGSAPNAAAA AEVKHPVSQG MIQMLGVFVD TIIVCSCTAF IILIYQQPYG
 51 DLSGAALTQA AIVSQVGQWG AGFLAVILFM FAFSTVIGNY AYAESNVQFI
 101 KSHWLITAVF RMLVLAWVYF GAVANVPLVW DMADMAMGIM AWINLVAILL
 151 LSPLAFMLLR DYTAKLKM GK DPEFKLSEHP GLKRRIKSDV W*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 513 shows 99.5% identity over a 191 aa overlap with a predicted ORF (ORF 513.ng) from *N. gonorrhoeae*:

m513/g513

	10	20	30	40	50	60
m513.pep	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
g513	MGSAPNAAAAAEVKHPVSQGM IQMLGVFVD TIIVCSCTAF IILIYQQPYGDLSGAALTQA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m513.pep	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
g513	AIVSQVGQWGAGFLAVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFRMLVLAWVYF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m513.pep	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMXLRDYTAKLKM GK DPEFKLSEHP					
g513	GAVANVPLVWDMADMAMGIMAWINLVAILLSPLAFMLLRDYTAKLKM GK DPEFKLSEHP					
	130	140	150	160	170	180
	190					
m513.pep	GLKRRIKSDVW					
g513	GLKRRIKSDVW					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1415>:

a513.seq

765

```

1  ATGAACGAGA ACTTTACCGA ATGGCTGCAC GGCTGGGTCG GCGCCATCAA
51  CGATCCGATG TGGTCATACT TGGTTATNT GCTTTTGGGT ACGGGGCTTT
101 TCTTCACCGT AACCACGGGC TTTGTCCAAT TCCGCCTGTT CGGGCGCAGC
151 ATCAAAGAAA TGCTCGGCGG CCGCAAACAG GGGGACGACC CTCACGGCAT
201 CACGCCGTTT CAGGCATTGT TAACCGGCCT TGCCAGCCGC GTGGGCGTGG
251 GCAATATCGC GGGCGTGGCC ATCGCCATCA AAGTCGGCGG ACCGGGCGCG
301 GTGTTTTGGA TGTGGGTAAC CGCCTTAATC GGTATGAGTT CGGCGTTTGT
351 CGAATCTTCG CTGGCGCAGC TCTTTAAAGT CCGCGACTAC GACAACCACC
401 ATTTCCGGGG CGGCCCTGCC TACTACATCA CTCAAGGGCT GGGGCAGAAA
451 TGGCTGGGCG TGTTGTTTCG CCTGAGCCTG ATTTTCTGTT TCGGCTTTGT
501 GTTTGAAGCG GTTCAGACCA ATACCATTGC CGATACCGTC AAAGCGGCGT
551 GGGGTTGGGA GCCTCATTAT GTCGGCGTCG CCCTGGTGAT TTTAACCGCG
601 CCGATTATCT TCGGCGGCAT CAGGCGCATA TCTAAAGCGG CGGAATATCGT
651 CGTCCCCCTG ATGGCGGTTT TGTACCTCTT TATCGCGCTT TTCATCATTT
701 TGACCAATAT TCCGATGATT CCGGACGTGT TCGGTGAGAT TTTTTCGGGC
751 GCGTTCAAAT TCGACGCGGC AGCAGGCGGC TTA CTGCGGCG GTCTGATTTC
801 GCAAACGATG ATGATGGGCA TCAAACGCGG CCTGTATTCC AACGAGGCGG
851 GTATGGGTTC CGCGCCGAAC GCCGCCGCCG CCGCCGAAGT GAAACACCCCT
901 GTTTCGCAAG GTATGATTCA AATGCTGGGC GTGTTTGTCT ATACCATCAT
951 CGTTTGTCTT TGCACCGCCT TCATCATCTT GATTTACCAA CAGCCTTACG
1001 GCGATTTGAG CGGTGCGGCG CTGACGCAGG CGGCGATTGT CAGCCAAGTG
1051 GGGCAATGGG GCGCGGGCTT CCTCGCGCTC ATCCTGTTTA TGTTTGCTTT
1101 TTCCACCGTT ATCGGCAACT ATGCCTATGC CGAGTCCAAC GTCCAATTCA
1151 TCAAAGCCA TTGGCTGATT ACCGCCGTTT TCCGTATGCT GGTTTTGCGG
1201 TGGGTCTATT TCGGCGCGGT TGCCAATGTG CTTTGTGCTT GGGATATGGC
1251 GGATATGGCG ATGGGCATTA TGGCGTGGAT CAACCTTGTC GCCATCCTGC
1301 TGCTCTCGCC CTTGGCGTTT ATGCTGCTGC GCGATTACAC CGCCAAGCTG
1351 AAAATGGGCA AAGACCCCGA GTTCAAACCT TCCGAACATC CGGGCCTGAA
1401 ACGCCGTATC AAATCCGACG TTTGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1416; ORF 513.a>:

```

a513.pep
1  MNENFTEWLH GWVGAINDPM WSYLVYXLLG TGLFFTVTG EVQFRLFGRS
51  IKEMLGGRKQ GDDPHGITPF QAFVTGLASR VGVGNIAGVA IAIKVGPGPA
101 VFWMWVTALI GMSSAFVESS LAQLFKVRDY DNHHFRGGPA YYITQGLGQK
151 WLGVLFALSL IFCFGFVFEA VQNTIADTV KAAWGWEPHY VGVALVILTA
201 PIIFGGIRRI SKAAEIVVPL MAVLYLFIAL FIILTNPIMI PDVFGQIFSG
251 AFKFDAAGG LLGGLISQTM MMGIKRGLYS NEAGMGSAPN AAAAAEVKHP
301 VSQGMQMLG VFVDTIIVCS CTAFIILYQ QPYGDLGAA LTQAAIVSQV
351 QQWAGFLAV ILFMFAFSTV IGNYAYAESN VQFIKSHWLI TAVFRMLVLA
401 WVYFGAVANV PLVWDMADMA MGIMAWINLV AILLLSPLAF MLLRDYTAKL
451 KMGKDPEFKL SEHPGLKRRI KSDVW*

```

m513/a513 100.0% identity in 191 aa overlap

```

m513.pep
10 20 30
MGSAPNAAAAAEVKHPVSQGMQMLGVFVD
|||||

a513
260 270 280 290 300 310
DAAAGLLGLISQTM MMGIKRGLYS NEAGMGSAPNAAAAAEVKHPVSQGMQMLGVFVD

40 50 60 70 80 90
TIIIVCSCTAFIILYQ QPYGDLGAA LTQAAIVSQV QWAGFLAVILFMFAFSTVIGNY
|||||

a513
320 330 340 350 360 370
TIIIVCSCTAFIILYQ QPYGDLGAA LTQAAIVSQV QWAGFLAVILFMFAFSTVIGNY

100 110 120 130 140 150
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL
|||||

a513
380 390 400 410 420 430
AYAESNVQFIKSHWLI TAVFRMLVLAWVYFGAVANV PLVWDMADMA MGIMAWINLVAILL

160 170 180 190
LSPLAFMLLRDYTAKL KMGKDPEFKL SEHPGLKRRI KSDVW
|||||

```

a513 LSPLAFMLLRDY TAKLKMKG DPEFKLSEHPGLKRRIKSDVWX
 440 450 460 470

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1417>:

g515.seq
 1 atggttcaaa tacaggttgt gcgcgcgcgc gccgttgccc gtggtctgca
 51 ttccgagttt gcgcgcgcgc taactgccga ggaaatagcc ttcgacaatg
 101 ccgttttgaa tcacgaagcg cggcgcggtg gcaacacctt ccgcatcaaa
 151 atagctgctg cggaaagagc ggggatgtg cggttcttcg cgcaggttga
 201 ggaaatcggg caggactttt ttgccgatgc tgcgatcag gaaactgctt
 251 tggcggtaga gcgcgcgcgc ggagagtgtg ccgacgaggt gtccgatcag
 301 cccgcccga aacggtggtat cgaagaggac ggggtagctg cctgtcggga
 351 tgctgcggct gccgagtcgg cgcgaagtgc gccgggcggc ggtttgaccg
 401 atggtttcgg ggctgtccat atccggatgg cggcaggcgg aatcgtacca
 451 gtatgcgcgc tgcattccgt ttctcgtcgc gccgacgacg ctgcaggaaa
 501 tgctgtggtg cgtgctttgc cgggtgtcgc caaaaccgtg ggtgttgccg
 551 taaacgtatt ggtactgtcc ggtttgcacc gccgcgcctt cggagttttc
 601 gatgcggctg tccgtgtcca acgctgcctg ttcgcattgt ttgccaagc
 651 cgacggcggc ttccgtatcc aaatcccat cgtggtaaa gtcggggtcg
 701 ccgatgtgtt gcgccatcaa ctccgggtcg gcaagtccgg cgcaaccgtc
 751 ttcggcggtg tggcgggcga tgcgcggcgc gccgcggacg gtgtcgcgca
 801 gggcttggtt ggagaagtcg gcggtgccgc cgcggccttt gcgtttgccg
 851 acgtaaacgg taatgtccag cgatttgcct tgctggaact cgatttgttc
 901 gatttcgccc aagcgcacgc tgacgctttg tccgagcgat tcgctgaagt
 951 cggttcggc gccggtcgcg cccgctgctt ttgccaagtc gagcgtcggg
 1001 cggcagaggt cgaggagttc ggaagcgggt tggttgaaca gcataacaat
 1051 ctttcttggg ggagcgttgt gccattttaa

This corresponds to the amino acid sequence <SEQ ID 1418; ORF 515.ng>:

g515.pep
 1 MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
 51 IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERRA GECADVSDQ
 101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
 151 VVALHSVFVG GDDAAGNAV V RALPVCCKTV GVAVNVLVLS GLHRRAFGVF
 201 DAAVRVQRCL FALFCQADGG FRIQIPFVK VGVADVLRHQ LGVGKSGATV
 251 FGGVAGDVGG GADGVAQGLF GEVGGAGAAF AFADVNGNVQ RFVLLLELDLF
 301 DFAQAHADAL SERFAEVGFG GGRARCFCQV ERAAAEVEEF GSGVVEQHNN
 351 LSWSVVAF*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1419>:

m515.seq (partial)
 1 ..GGAAAGAGCG GGGGATGTGC GTTCTTCGCG CAGGTTGAGG AAATCGGGCA
 51 GGACTTTTCT GCCGATGCTG TCGATCAGGA AACTGCTTTG GCGGTAGAGC
 101 GCGCCGCCGG AGAGTGCGCC GACGAGGTGT CCGATAAGAC CGCCGAAAC
 151 GGTGGTATCG AAGAGGACGG GGTAGCTGCC TGTCGGGATG CTGCGGCTGC
 201 CGAGTCGGCG CAAAGTGC GGCGCGCGG TTTGACCGAT GGTTCGGGG
 251 CTGTCCATAT CCGGATGGCG GCAGGCGGAA TCGTACCAGT AGTCGCGCTG
 301 CATGCCGTTT TCGTCGGCGG CAACGACGCT GCAGGAAATG CTGTGGTGCG
 351 TGCTTGCGCG GTGTGCGGCA AAACCGTGGG TGTGCGCGTA AACGTATTGG
 401 TAATGGCCGG TTTGCACCGC CGCGCCTTCG GAGTTTTCGA TCGCTCATC
 451 CTCGTTACAG GCGGCTTGTT CGCATTGTTT TGCCAAGCCG ACGCGGCTK
 501 CCGTATCCAA ATCCCATTCG TGGTAAAGGT CGGGGTCGCC GATGTGTTTT
 551 GCCATCAGAC AGGCATCGGC AAGTCCGGCG CAACCGTCTT CGGCGGTGTG
 601 GCGGGCGATG TCGATGGCGG CTTTGACGGT GTCTTGACAG GCTTTTTCGG
 651 AGAAGTCGGC AGTACTGGCG CGGCCTTTGC GTTTGCCGAC GTAAACGGTA
 701 ATGTCCAGCG ACTTGTCTCG CTGGAACTCG ATTTGTTsGA TTTsGCCAG
 751 CCGCACGCTG ACGCTTTGTC CCAATGATTC GCTGAAATCG GCTTCGGCGG
 801 CGGTTGCGCC CGTCGCTTTT GCCAAGTCGA GCGTGC GGCG GCAGAGGTG
 851 AGGAGTTCGG AAGCGGTGTG GTTgAACAGC ATAGAAATCT TTCTTGATGA
 901 TGCTTGCGCG CATTTTAA

This corresponds to the amino acid sequence <SEQ ID 1420; ORF 515>:

m515.pep (partial)

767

```

1  ..GKSGGCAFFA QVEEIGQDFS ADAVDQETAL AVERAAGECA DEVSDKTARN
51  GGIEEDGVAA CRDAAAESA QSAAGGGLTD GFGAVHIRMA AGGIVPVVAL
101 HAVFVGGNDA AGNAVVRALP VCGKTVGVAV NVLVMAGLHR RAFGVFDALI
151 LVQGGFLFALF CQADGGXRIQ IPFVVKVGVA DVFCHQTGIG KSGATVFGGV
201 AGDVDGGFDG VLQGGFGEVG STGAFAFAD VNGNVQRLVL LELEDLXDXAQ
251 PHADALSQXF AEIGFGGGCA RRFCQVERAA AEVEEFGSGV VEQHRNLSXX
301 CFAAF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 515 shows 85.9% identity over a 304 aa overlap with a predicted ORF (ORF 515.ng) from *N. gonorrhoeae*:

m515/g515

```

                                10      20      30
m515.pep                      GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                ::|  |||||  |||||  |||||  |||||  |||||
g515                          AEEIAFDNAVLNHEARRGGNTFRIKIAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
                                30      40      50      60      70      80

                                40      50      60      70      80      90
m515.pep                      VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          VERAAGECADEVSDQPARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
                                90     100     110     120     130     140

                                100     110     120     130     140     150
m515.pep                      GGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
                                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          GGIVPVVALHSVFVGGDDAAGNAVVRALPVCCKTVGVAVNVLSGLHRRAFGVFDAAVR
                                150     160     170     180     190     200

                                160     170     180     190     200     210
m515.pep                      VQGGFLFALFCQADGGXRIQIPFVVKVGVAADVDFCHQTGIGKSGATVFGGVAGDVDGGFDGV
                                ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          VQRCFLFALFCQADGGFRIQIPFVVKVGVAADVLRHQLGVGKSGATVFGGVAGDVGGGADGV
                                210     220     230     240     250     260

                                220     230     240     250     260     270
m515.pep                      LQGGFGEVGSTGAFAFADVNGNVQRLVLELEDLXDXAQPHADALSQXFAEIGFGGGCGAR
                                ||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          AQGLFGEVGGAGAAFAFADVNGNVQRFVLELEDLFDFAQAHADALSERFAEVGFGGGGRAR
                                270     280     290     300     310     320

                                280     290     300
m515.pep                      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAF
                                |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
g515                          CFCQVERAAAEVEEFGSGVVEQHNNLSWWSVVAF
                                330     340     350

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1421>:

a515.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGGTTGCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTGAAT TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGC CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTGCGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GGCGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTGCGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTTGCCG

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768

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551 TAAACGTATT GGTAATGGCC GGTTCGCACC GCCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCNNNNGC GGCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTCC TGCTGAAACT CGATTGTGTT
901 GATTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGAT TCGCTGAAAT
951 CGGCTTCGGC GCGGTTGCG CCCGTCGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAGAAAT
1051 CTTTCTTGAT GATGCTTTGC GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1422; ORF 515.a>:

```

a515.pep
1 MVQIKVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RCGGNAFRIK
51 IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLMMA GLHRRAFGVF
201 DALILVQGGF FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVXX GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*FAEIGFG GGCARRFCQV ERAAAEVEEF GSGVVEQHRN
351 LS**CFAAF*

```

m515/a515 92.1% identity in 304 aa overlap

```

m515.pep                                10      20      30
                                         GKSGGCAFFAQVEEIGQDFSADAVDQETALA
                                         :| | | | | | | | | | | | | | | | | |
a515      AEEIAFDNAVLNHEARCGGNAFRIKIAAAERAGDVRFFAQVEEIGQDFFADAVDQETALA
              30      40      50      60      70      80

              40      50      60      70      80      90
m515.pep    VERAAGECADEVSDKTARNGGIEEDGVAACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
              |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VERSAGECADEVSDKTARNGGIEEDGVVACRDAAAESAQSAAGGGLTDGFGAVHIRMAA
              90      100     110     120     130     140

              100     110     120     130     140     150
m515.pep    GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      GGIVPVVALHAVFVGNDAAAGNAVVRALPVCCKTVGVAVNVLMAGLHRRAFGVFDALIL
              150     160     170     180     190     200

              160     170     180     190     200     210
m515.pep    VQGGFLFALFCQADGGXRIQIPFVVKVGVADV FCHQTGIGKSGATVFGGVAGDV DGGFDGV
              | | | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      VQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQLGVGKSGATVFGGVAGDVXXGADGV
              210     220     230     240     250     260

              220     230     240     250     260     270
m515.pep    LQGGFFGEVSGTGAAFAFADVNGNVQRLVLLLELDLXDXAQPHADALSQXFAEIGFGGGCAR
              ||:| | | | | | | | | | | | | | | | | | | | | | | | | |
a515      AQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLFDFAQPHADALSQXFAEIGFGGGCAR
              270     280     290     300     310     320

              280     290     300
m515.pep    RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
              | | | | | | | | | | | | | | | | | | | | | | | | | |
a515      RFCQVERAAAEVEEFGSGVVEQHRNLSXXCFAAFX
              330     340     350     360

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1423>:

```

g515-1.seq
1 ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA

```

```

51  TTCCGAGTTT GCGCGCGCTG TAACTGCCGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGCGCGGTG GCAACACCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATCAG
301 CCCGCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATTCCGT TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGCG
551 TAAACGTATT GGTAGTGTCC GGTTTGCACC GCGCGCCTT CGGAGTTTTC
601 GATGCGGCTG TCCGTGTCCA ACGCTGCCTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAGTCG GCGGTGCGCG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGATTGTGCC TGCTGGAACG CGATTGTGTC
901 GATTTGCGCC AAGCGCACGC TGACGCTTTG TCCGAGCGAT TCGCTGAAGT
951 CCGCTTCGGC GCGGTGCGCG CCCGTGCTT TTGCCAAGTC GAGCGTGCGG
1001 CGGCAGAGGT CGAGGAGTTC GGAAGCGGTG TGGTTGAACA GCATAACAAT
1051 CTTTCTTGTT GGAGCGTTGT GGCATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1424; ORF 515-1.ng>:

g515-1.pep

```

1  MVQIQVVRAA GVARGLHSEF ARAVTAEIEA FDNAVLNHEA RRGNTFRIK
51  IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDQ
101 PARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVVS GLHRRAFGVF
201 DAAVRVQRCL FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEVVGAGAAF AFADVNGNVQ RFLVLELDLF
301 DFAQAHADAL SERFAEVGFG GGRARCFQCV ERAAAEVEEF GSGVVEQHNN
351 LSWWSVVAFF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1425>:

m515-1.seq

```

1  ATGGTTCAAA TACAGGTTGT GCGCGCCGCC GCGGTTGCCC GTGGTCTGCA
51  TACCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAAATCGGG CAGGACTTTT TTGCCGATGC TGTCGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCGCCGCC GGAGAGTGTG CCGACGAGGT GTCCGATAAG
301 ACCGCCCGAA ACGGTGGTAT CGAAGAGGAC GGGGTAGCTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTTGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CCGCAGGCGG AATCGTACCA
451 GTAGTTCGCG TGCAATGCCG TTTCTGCGGC GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTGC CGGTGTGCGG CAAAACCGTG GGTGTGCGCG
551 TAAACGTATT GGTAAATGCC GGTTTGCACC GCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTCGCATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATT CGTGGTAAAG GTCGGGGTCG
701 CCGATGTGTT TTGCCATCAG ACAGGCATCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGGCGGGCGA TGTCGATGGC GGCTTTGACG GTGCTTGTGA
801 GGGCTTTTTT GGAGAAGTCG GCAGTACTGG CGCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGGAACG CGATTGTGTC
901 GATTTGCGCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1426; ORF 515-1>:

m515-1.pep

```

1  MVQIQVVRAA GVARGLHTEF ARAVTAEIEA FDNAVLNHEA RCGGNAFRIK
51  IAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERAA GECADDEVSDK
101 TARNGGIEED GVAACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHSAFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALLLVQGG FALFCQADGG FRIQIPFVVK VGVADVFC HQ TGIGKSGATV
251 FGGVAGDVGG GFDGVLQGF GEVVGSTGAAF AFADVNGNVQ RLVLELDLF
301 DFAQPHADAL SQ*

```

m515-1/g515-1 91.7% identity in 312 aa overlap

```

              10      20      30      40      50      60
g515-1.pep  MVQIQVVRAAGVARGLHSEFARA VTAEIEAFD NAVLNHEARRGGNTFR IKIAAERAGDV
              |||
m515-1      MVQIQVVRAAGVARGLHTEFARA VTAEIEAFD NAVLNHEARCGGNAFRIKIAAERAGDV
              10      20      30      40      50      60

```

770

	70	80	90	100	110	120
g515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDQPARNGGIEEDGVAAACRDAAA					
m515-1	RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNNGGIEEDGVAAACRDAAA					
	70	80	90	100	110	120
g515-1.pep	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHSVFVGGNDAAGNAVVRALPVCCKTV					
m515-1	AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAFVVGNDAGNAVVRALPVCCKTV					
	130	140	150	160	170	180
g515-1.pep	GVAVNVLVVSGLHRRAFGVFDAAVRVQRCLFALFCQADGGFRIQIPFVVVKGVADVLRHQ					
m515-1	GVAVNVLVMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVVKGVADVFCCHQ					
	190	200	210	220	230	240
g515-1.pep	LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEVGGAGAAFAFADVNGNVQRFLVLELDF					
m515-1	TGIGKSGATVFGGVAGDVDDGFDVLQGGFGEVGGSTGAFAFADVNGNVQRLVLELDF					
	250	260	270	280	290	300
g515-1.pep	DFAQAHADALSERFAEVGFGGGRARCFQVERAAAEVEEFGSGVVEQHNNLSWWSVVAFX					
m515-1	DFAQPHADALSQX					
	310	320	330	340	350	360

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1427>:

a515-1.seq

```

1  ATGGTTCAAA TAAAGTTGT GCGCGCCGCC GCGCTTGCCC GTGGTCTGCA
51  TTCCGAGTTT GCGCGCGCTG TAACTGCTGA GGAAATAGCC TTCGACAAATG
101 CCGTTTTGAA TCACGAAGCG CGGTGCGGTG GCAACGCCTT CCGCATCAAA
151 ATAGCTGCTG CGGAAAGAGC GGGGGATGTG CGGTTCTTCG CGCAGGTTGA
201 GGAATCGGG CAGGACTTTT TTGCCGATGC TGTGATCAG GAAACTGCTT
251 TGGCGGTAGA GCGCTCCGCC GGAGAGTGCG CCGACGAGGT GTCCGATAAG
301 ACCGCCCCGA ACGGTGGTAT CGAAGAGGAC GGGGTAGTTG CCTGTCGGGA
351 TGCTGCGGCT GCCGAGTCGG CGCAAAGTGC GCGGGGCGGC GGTTCGACCG
401 ATGGTTTCGG GGCTGTCCAT ATCCGGATGG CGGCAGGCGG AATCGTACCA
451 GTAGTCGCGC TGCATGCCGT TTTCGTCGCG GGCAACGACG CTGCAGGAAA
501 TGCTGTGGTG CGTGCTTTGC CGGTGTGCGG CAAAACCGTA GGTGTGCGCG
551 TAAACGTATT GGTAATGGCC GGTTCGACC GCGCGCCTT CGGAGTTTTC
601 GATGCGCTCA TCCTCGTTCA GGGCGGCTTG TTGCGATTGT TTTGCCAAGC
651 CGACGGCGGC TTCCGTATCC AAATCCCATC CGTGGTAAAG GTCGGGGTGC
701 CCGATGTGTT GCGCCATCAA CTCGGGGTCG GCAAGTCCGG CGCAACCGTC
751 TTCGGCGGTG TGCGGGCGCA GTGCGGCGGC GCGCGGACG GTGTCGCGCA
801 GGGCTTGTTT GGAGAAATCG GCGGTGCCGG CCGGCCTTT GCGTTTGCCG
851 ACGTAAACGG TAATGTCCAG CGACTTGTC TGCTGAAACT CGATTGTGTC
901 GATTTCGCCC AGCCGCACGC TGACGCTTTG TCCCAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1428; ORF 515-1.a>:

a515-1.pep

```

1  MVQIKVVRAA GVARGLHSEF ARAVTAEEIA FDNVNLNHEA RCGGNAFRIK
51  IAAAERAGDV RFFAQVEEIG QDFFADAVDQ ETALAVERSA GECADDEVSDK
101 TARNNGGIEED GVVACRDAAA AESAQSAAGG GLTDGFGAVH IRMAAGGIVP
151 VVALHAVFVG GNDAAAGNAV RALPVCCKTV GVAVNVLVMA GLHRRAFGVF
201 DALILVQGG FALFCQADGG FRIQIPFVVK VGVADVLRHQ LGVGKSGATV
251 FGGVAGDVGG GADGVAQGLF GEIGGAGAAF AFADVNGNVQ RLVLLKLDLF
301 DFAQPHADAL SQ*

```

m515-1/a515-1 94.9% identity in 312 aa overlap

	10	20	30	40	50	60
a515-1.pep	MVQIKVVRAAGVARGLHSEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
m515-1	MVQIQVVRAAGVARGLHTEFARAVTAEEIAFDNAVNLNHEARCGGNAFRIKIAAAERAGDV					
	10	20	30	40	50	60
a515-1.pep	RFFAQVEEIGQDFFADAVDQETALAVERSAGECADEVSDKTARNNGGIEEDGVVACRDAAA					

```

m515-1      RFFAQVEEIGQDFFADAVDQETALAVERAAGECADEVSDKTARNGGIEEDGVAACRDAAA
              70          80          90          100          110          120

a515-1.pep   130          140          150          160          170          180
AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
|||||
m515-1      AESAQSAAGGGLTDGFGAVHIRMAAGGIVPVVALHAVFVGGNDAAGNAVVRALPVCCKTV
              130          140          150          160          170          180

a515-1.pep   190          200          210          220          230          240
GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
|||||
m515-1      GVAVNVLMAGLHRRAFGVFDALILVQGGFLFALFCQADGGFRIQIPFVVKVGVADVLRHQ
              190          200          210          220          230          240

a515-1.pep   250          260          270          280          290          300
LGVGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
|:|||||
m515-1      TGIGKSGATVFGGVAGDVGGGADGVAQGLFGEIGGAGAAFAFADVNGNVQRLVLLKLDLF
              250          260          270          280          290          300

a515-1.pep   310
DFAQPHADALSQX
|||||
m515-1      DFAQPHADALSQX
              310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1429>:

```

g516.seq
1  atgttggtcc gtaaaacgac cgccgccggt ttggcggcaa ccttgatact
51  gaacggctgt acgatgatgt tgcgggggat gaacaacccg gtcagccaaa
101 caatcacccg caaacacggt gacaaagacc aaatccgcgc cttcgggtgtg
151 gttgccgaag acaatgccca attggaaaag ggcagcctgg tgatgatggg
201 cgggaaatac tggttcgccg tcaatcccga agattcggcg aagctgacgg
251 gccttttgaa ggccgggttg gacaagccct tccaaatagt tgaggatacc
301 ccgagctatg cccgccacca agccctgccg gtcaaattcg aagcggcccg
351 cagccagaat ttcagtaccg gaggtctttg cctgcgctat gataccggca
401 gacctgacga catcgccaag ctgaaacagc ttgagtttaa agcgggtcaa
451 ctcgacaatc ggaccattta cgcgcgtgct gtatccgcca aaggcaaata
501 ctacgccacg ccgcaaaaac tgaacgccga ttatcatttt gagcaaagt
551 tgcccgccga tatttattat acggttactg aaaaacatac cgacaaatcc
601 aagctgtttg gaaatatctt atatacgccc cccttggtga tattggatgc
651 ggcggccgct gtgctggtct tgcctatggc tctgattgca gccgcgaatt
701 cctcagacaa atga

```

This corresponds to the amino acid sequence <SEQ ID 1430; ORF 516.ng>:

```

g516.pep
1  MLFRKTTAAV LAATLILNGC TMMLRGMNPN VSQTITRKHV DKDQIRAFGV
51  VAEDNAQLEK GSLVMMGGKY WFAVNPEDSA KLTGLLKAGL DKPFQIVEDT
101 PSYARHQALP VKFEAPGSQN FSTGGLCLRY DTGRPDIAK LKQLEFKAVK
151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEKHTDKS
201 KLFGNILYTP PLLILDAAAA VLVLPMALIA AANSSDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1431>:

```

m516.seq
1  ATGTTGTTCC GTAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGCT
51  GAACGGCTGT ACGTTGATGT TGTGGGGAAT GAACAACCCG GTCAGCGAAA
101 CAATCACCCG CAAACACGTT GACAAAGACC AAATCCGC GCCTTCGGTGTG
151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
201 CGGAAAATAC TGGTTCGTCG TCAATCCCGA AGATTCGGCG AAGCTGACGG
251 GCATTTTGAA GGCAGGGCTG GACAAACCCT TCCAAATAGT TGAGGATACC
301 CCGAGCTATG CTCGCCACCA AGCCCTGCCG GTCAAACCTG AATCGCCTGG
351 CAGCCAGAAT TTCAGTACCG AAGGCCTTTG CCTGCGCTAC GATACCGACA
401 AGCCTGCCGA CATGCCAAG CTGAAACAGC TCGGGTTTGA AGCGGTCAAA
451 CTCGACAATC GGACCATTTA CACGCGCTGC GTATCCGCCA AAGGCAAATA

```

```

501 CTACGCCACA CCGCAAAAAC TGAACGCCGA TTACCATTTT GAGCAAAGTG
551 TGCCTGCCGA TATTTATTAC ACGGTTACTG AAGAACATAC CGACAAATCC
601 AAGCTGTTTG CAAATATCTT ATATACGCCC CCCTTTTGA TACTGGATGC
651 GCGGGCGCG GTACTGGCCT TGCCTGCGGC GGCTCTGGGT GCGTCTGTGG
701 ATGCCGCCCC CAAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1432; ORF 516>:

```

m516.pep
  1 MLFRKTTAAV LAATLMLNGC TLMLWGMNPN VSETITRKHV DKDQIRAFGV
  51 VAEDNAQLEK GSVLMMGGKY WFFVNPEDSA KLTGILKAGL DKPFQIVEDT
 101 PSYARHQALP VKLESPGSQN FSTEGLCRLY DTDKPADIAP LKQLGFQAVK
 151 LDNRTIYTRC VSAKGKYYAT PQKLNADYHF EQSVPADIYY TVTEHTDKS
 201 KLFANILYTP PFLILDAAGA VLALPAAALG AVVDAARK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 516 shows 90.0% identity over a 231 aa overlap with a predicted ORF (ORF 516.ng) from *N. gonorrhoeae*:

```

m516/g516
      10      20      30      40      50      60
m516.pep MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK
g516      MLFRKTTAAVLAATLILNGCTMMLRGMNPNVSQTITRKHVDKDQIRAFGVVAEDNAQLEK
      10      20      30      40      50      60
      70      80      90     100     110     120
m516.pep GSVLMMGGKYWFFVNPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
g516      GSVLMMGGKYWFAVNPEDSAKLTGLLKAGLDKPFQIVEDTPSYARHQALPVKFEAPGSQN
      70      80      90     100     110     120
      130     140     150     160     170     180
m516.pep FSTEGLCRLYDTDKPADIAPKLKQLGFQAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF
g516      FSTGGLCRLYDTGRPDIAKLEFQAVKLDNRTIYTRCVSAKGKYYATPQKLNADYHF
      130     140     150     160     170     180
      190     200     210     220     230     239
m516.pep EQSVPADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARK
g516      EQSVPADIYYTVTEKHTDKSKLFGNILYTPPLLILDAAGAVLALPAAALGAVVDAARK
      190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1433>:

```

a516.seq
  1 ATGTTGTTCG GTAAAACGAC CGCCGCCGTT TTGGCGGCAA CCTTGATGTT
  51 GAACGGCTGT ACGGTAATGA TGTGGGGTAT GAACAGCCCG TTCAGCGAAA
 101 CGACCGCCCG CAAACACGTT GACAAGGACC AAATCCGCGC CTTCGGTGTG
 151 GTTGCCGAAG ACAATGCCCA ATTGGAAAAG GGCAGCCTGG TGATGATGGG
 201 CGGGAAATAC TGGTTCGTCTG TCAATCCTGA AGATTCGGCG AAGCTGACGG
 251 GCATTTTGAA GGCCGGGTTG GACAAGCAGT TTCAAATGGT TGAGCCCAAC
 301 CCGCGCTTTG CCTACCAAGC CCGCCGGTCT AAATCGAAT CGCCCGCCAG
 351 CCAGAATTTC AGTACCGAAG GCCTTTGCCT GCGCTACGAT ACCGACAGAC
 401 CTGCCGACAT CGCCAAGCTG AAACAGCTTG AGTTTGAAGC GGTGGAAGT
 451 GACAATCGGA CCATTTACAC GCGCTGCGTC TCCGCCAAAG GCAAATACTA
 501 CGCCACACCG CAAAACTGA ACGCCGATTA TCATTTTGAG CAAAGTGTGC
 551 CTGCCGATAT TTATTACACG GTTACGAAAA AACATACCGA CAAATCCAAG
 601 TTGTTTGAAA ATATTGCATA TACGCCACAC ACGTTGATAC TGGATGCGGT
 651 GGGCGCGGTG CTGGCCTTGC CTGTCGCGGC GTTGATTGCA GCCACGAATT
 701 CCTCAGACAA ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1434; ORF 516.a>:

a516.pep

773

```

1  MLFRKTTAAV LAATLMLNGC TVMMWGMNSP FSETTARKHV DKDOIRAFGV
51 VAEDNAQLEK GSLVMMGGKY WFVVPEDSA KLTGILKAGL DKQFQMVPEPN
101 PRFAYQALPV KLESPASQNF STEGLCLRYD TDRPADIAKL KQLEFEAVEL
151 DNRTIYTRCV SAKGKYATP QKLNADYHFE QSVADIYYT VTKKHTDKSK
201 LFENIAYTPT TLILDAVGAV LALPVAALIA ATNSSDK*

```

m516/a516 86.1% identity in 238 aa overlap

```

              10      20      30      40      50      60
m516.pep      MLFRKTTAAVLAATLMLNGCTLMLWGMNPNVSETITRKHVDKDQIRAFGVVAEDNAQLEK
              |||||:|||||:| |||:|||||
a516           MLFRKTTAAVLAATLMLNGCTVMMWGMNSPFSETTARKHVDKDQIRAFGVVAEDNAQLEK
              10      20      30      40      50      60

              70      80      90      100     110     120
m516.pep      GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKPFQIVEDTPSYARHQALPVKLESPGSQN
              |||||:|||||:| |||:|:|:|:|
a516           GSLVMMGGKYWFVVPEDSAKLTGILKAGLDKQFQMVPEPNRFA-YQALPVKLESPASQN
              70      80      90      100     110

              130     140     150     160     170     180
m516.pep      FSTEGCLCLRYDTPDKPADIAKLKQLGFQAVKLDNRTIYTRCVSAKGKYATPQKLNADYHF
              |||||:|||||:| |||:|||||
a516           FSTEGCLCLRYDTPDRPADIAKLKQLEFEAVELDNRTIYTRCVSAKGKYATPQKLNADYHF
120           130     140     150     160     170

              190     200     210     220     230     239
m516.pep      EQSVADIYYTVTEHTDKSKLFANILYTPPFLILDAAGAVLALPAAALGAVVDAARKX
              |||||:|||||:| |||:|||||:|
a516           EQSVADIYYTVTKKHTDKSKLFENIAYTPTTLILDAVGAVLALPVAALIAATNSSDKX
180           190     200     210     220     230

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1435>:

```

g517.seq
1  atgcatcggg tttcagacgg cattggagtg tcagtcgtgt tctgccgatt
51 cgtaggcttc gacgattttt tgcaccagag gatgccggac aacgtcttcg
101 ccggtgaagg tatggaaata cagtcctgcc acgccgtgca gtttctcacg
151 tgcgtctttc aatcccgaatt tgatgttttt gggcaggctc atttggtctg
201 tgtcgccggt aatgacggct ttcgcgccga agccgatgcg ggtcaggaaac
251 attttcattt gttcgggctt ggtgttttgc gtttcgtcga ggatgatgta
301 tgcgccgttg agcgtcctgc cgcgcatata ggcgagcggg gcgatttcaa
351 tcaggccttt ttcaatcagc ttggttacac ggtcaaagcc catcagggtca
401 tagagggcat cataaagcgg acggaggtag ggtcgactt tttgggtcag
451 gtctccgggc aggaagccca gtttctcacc ggcttcgacg gcaggccgaa
501 ctaa

```

This corresponds to the amino acid sequence <SEQ ID 1436; ORF 517.ng>:

```

g517.pep
1  MHRVSDGIGV SVVFCRFVGF DDFLHQRMPD NVFAGEGMEI QSCHAVQFLT
51 CVFQSRFDVF GQVDLAGVAG NDGFRAEADA GQEHFHLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TEVGVDFLGQ
151 VSGQEAQFLT GFDGRPN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1437>:

```

m517.seq
1  ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTT TGCACCAAAG GATGCCGGAC AACGCTTTCG
101 CCGGTAAAGG TGTGAAATA CAGCCCTTCC ACCTGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCATT TGATGTTTTT GGGCAGGTCG ATTTGCTCTG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTGCA GGATGATGTA
301 TGCGCCGTTG AGCGTCCTGC CGCGCATATA GGCGAGCGGG GCGATTTCOA
351 TCAGGCCTTT TTCAATCAGC TTGGTTACAC GGTCAAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG

```

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451 GTCTCCGGGC AGGAAGCCCA GTTCTCGCC GGCTTCGACG GCTGgGCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1438; ORF 517>:

m517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHVQFLT
51 RIFXSRFDVF GQVDLAGVAG NDGFRAEADA QGEHFHFLFGR GVLRFVEDDV
101 CAVERPAAHI GERGDFNQAF FNQLGYTVKA HQVIEGIIKR TKVGIDFLGQ
151 VSGQEAQFLA GFDGWAH*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 517 shows 92.7% identity over a 164 aa overlap with a predicted ORF (ORF 517.ng) from *N. gonorrhoeae*:

m517/g517

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
g517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGEGMEIQSCHAVQFLTCVFQSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
g517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	70	80	90	100	110	120
	130	140	150	160		
m517.pep	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAH					
	: : : : :					
g517	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGRPN					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1439>:

a517.seq
1 ATGCATCGGG TTTCAGACGG CATTGGAATG TCAGTCGTGT TCTGCCGATT
51 CGTAGGCTTC GACGATTTTT TGCACCAAAG GATGCCGGAC AACGTCTTCG
101 CCGGTAAGG TGTGGAAATA CAGCCCTTCC ACGCCGTGCA GTTCTCACG
151 CGCATCTTTT AATCCCGATT TGATGTTTTT GGGCAGGTCG ATTTGGCTGG
201 TGTCGCCGGT AATGACGGCT TTCGCGCCGA AGCCGATGCG GGTCAGGAAC
251 ATTTTCATTT GTTCGGGCGT GGTGTTTTGC GCTTCGTCGA GGATGATGTA
301 TCGCGCGTTG AGCGTCCTGC CGCGCATATA GGCAGCGGG GCAATCTCAA
351 TCAGACCTTT TTCAATCAGC TTGGTGACAC GGTCTGAAGCC CATCAGGTCA
401 TAGAGGGCAT CATAAAGCGG ACGAAGGTAG GGATCGACTT TCTGGGTCAG
451 GTCACCGGGC AGAAAACCCA GTTCTCGCC GGCTTCGACG GCAGGCCGCA
501 CTAA

This corresponds to the amino acid sequence <SEQ ID 1440; ORF 517.a>:

a517.pep
1 MHRVSDGIGM SVVFCRFVGF DDFLHQMPD NVFAGKGVEI QPFHAVQFLT
51 RIF*SRFDVF GQVDLAGVAG NDGFRAEADA QGEHFHFLFGR GVLRFVEDDV
101 CAVERPAAHI GERGNLNQTF FNQLGDTVEA HQVIEGIIKR TKVGIDFLGQ
151 VTGQKTQFLA GFDGRPH*

m517/a517 93.4% identity in 167 aa overlap

	10	20	30	40	50	60
m517.pep	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHVQFLTRIFXSRFDVF					
	: : : : :					
a517	MHRVSDGIGMSVVFCRFVGFDDFLHQMPD NVFAGKGVEIQPFHAVQFLTRIFXSRFDVF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m517.pep	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGDFNQAF					
	: : : : :					
a517	GQVDLAGVAGNDGFRAEADAGQEHFHLFGRGVLRFVEDDVCAVERPAAHIGERGNLNQTF					

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	70	80	90	100	110	120
m517.pep	130	140	150	160		
	FNQLGYTVKAHQVIEGIIKRTKVGIDFLGQVSGQEAQFLAGFDGWAHX					
a517	130	140	150	160		
	FNQLGDTVEAHQVIEGIIKRTKVGIDFLGQVTGQKTQFLAGFDGRPHX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1441>:

```

g518.seq
1   atgacgtttt cggcggcaaa gctcaacatt tcggcactga tgttgtgtct
51  ttcggcagga atgaccgttt tactttccgc ttttttactg ctccgaccgg
101 aaggcagcat cttattcaac cattttttca gcataaatat tctgacccca
151 agagcggcat ctccacgggc aaccgtgttc agactgcatac aggcggtagc
201 attccacaag atgccgaaaa ccataagcaa aatgcgtaga aactacgccg
251 tccgaatcac gccgcctcct cggcggcaca cgcttcatta taacagattg
301 ccccttaaaa aatcagaccc tgcttttgtg gcggagtctg aaatttga

```

This corresponds to the amino acid sequence <SEQ ID 1442; ORF 518.ng>:

```

g518.pep
1   MTFSAAKLNI SALMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RLHQAVRFHK MPKTISKMRN NYAVRITPPP RAATLHYNRL
101 PLKKSDFPAFV AESEI*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1443>:

```

m518.seq
1   ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACGTTTT TACTTTCCGC TTTTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTGACCCGA
151 AGAGCGGCAT CTCCACAGGC AACCGTGTTT AGACGGCATC AGGCGCGGTT
201 TGCAAGATGC CGTACCATAA ACAAAGGCG TAGAACTAC GCCGTCGAA
251 TCACGCCGCC CTCGCG.GCG GCAACGCGTC ATTATAACAG ATTGCCCTCC
301 GCGGCAGGCT TAGTGCGGCG GGAGCGCCGC CGTTGCGCAG TAATATTGTC
351 TAACGGGAGG AAAAAATCAG ACCCTGCTTT TGTGGCAGAG TCTGAAATTT
401 GA

```

This corresponds to the amino acid sequence <SEQ ID 1444; ORF 518>:

```

m518.pep
1   MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPQATVF RRHQARFARC RTINKRRRNY AVRITPPSXA ATRHYNRLPS
101 AAGLVRERRR RCAVILSNR KKSDFPAFAE SEI*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 518 shows 74.1% identity over a 135 aa overlap with a predicted ORF (ORF 518.ng) from *N. gonorrhoeae*:

```

m518/g518

m518.pep      MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF
g518          MTFSAAKLNISALMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF
               10      20      30      40      50      60

m518.pep      RRHQA-RFARC-RTINKRRRNYAVRITPPSXAATRHYNRLPSAAGLVRERRRRCAVILSN
g518          RLHQAVRFHKMPKTISKMRNRYAVRITPPRAATLHYNRLPL-----
               70      80      90      100     110

m518.pep      120      130
g518          GRKKSDPAFVAESEI
               |||||
g518          --KKSDPAFVAESEI
               110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1445>:

```
a518.seq
1  ATGACGTTTT CGGCGGCAAA GCTCAACATT TCGGCACGGA TGTGTGTCT
51  TTCGGCAGGA ATGACCGTTT TACTTTCCGC TTTTCTACTG CTCCGACCGG
101 AAGGCAGCAT CTTATTCAAC CATTTTTTCA GCATAAATAT TCTAACCCGA
151 AGAGCGGCAT CTCCACGGGC AACCGTGTTC AGACGGCATC AGGCGGTACG
201 ATCCGCAAG ATGCCGACCA TAAACAAAAG GCGTAGAAAC TACGCCGTCC
251 GAATCACGCC GTCCTCG.CG GCGGCAACGC GTCATTATAA CAGATTGCCC
301 TCC.....
351 .....AAAAAAT CAGACCCTGC TTTTGTGGCA GAGTCTGAAA
401 TTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1446; ORF 518.a>:

```
a518.pep
1  MTFSAAKLNI SARMLCLSAG MTVLLSAFLL LRPEGSILFN HFFSINILTR
51  RAASPRATVF RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP
101 S..... .KKSDPAFVA ESEI*
```

m518/a518 79.9% identity in 134 aa overlap

	10	20	30	40	50	60
m518.pep	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPOATVF					
a518	MTFSAAKLNISARMLCLSAGMTVLLSAFLLLRPEGSILFNHFFSINILTRRAASPRATVF					
	10	20	30	40	50	60
	70	80	90	100	110	119
m518.pep	RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP SAAGLVRRERRRCAVILSNG					
a518	RRHQAVRFRK MPTINKRRRN YAVRITPSSX AATRHYNRLP S-----					
	70	80	90	100		
	120	130				
m518.pep	RKKSDPAFVAESEIX					
a518	-KKSDPAFVAESEIX					
		110				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1447>:

```
g519.seq
1  atggaatttt tcattatcctt gttggcagcc gtcgcccgttt tcggcttcaa
51  atcctttgtc gtcacccccc agcaggaagt ccacgttgct gaaaggctcg
101 ggcgtttcca tcgcgccctg acggccggtt tgaatatatt gattcccttt
151 atcgaccgcg tcgcctaccg ccattcgctg aaagaaatcc ctttagacgt
201 acccagccag gtctgcatca cgcgcgataa tacgcaattg actgttgacg
251 gcatcatcta tttccaagta accgatccca aactcgcctc atacggttcg
301 agcaactaca ttatggcaat taccagctt gcccaaacga cgtgcgttc
351 cgttatcggt cgtatggagt tggacaaaac gtttgaagaa cgcgacgaaa
401 tcaacagtac cgtcgtctcc gccctcgatg aagccgcccg ggcttggggg
451 gtgaaagtcc tccgttacga aatcaaggat ttggttccgc cgcaagaaat
501 ccttcgcgca atgcaggcac aaattaccgc cgaacgcgaa aaacgcgccc
551 gtattgccga atccgaaggc cgtaaaatcg aacaaatcaa ccttgccagt
601 ggtcagcgtg aagccgaaat ccaacaatcc gaaggcgagg ctgaggtcgc
651 ggtcaatcgc tccaatgcg agaaaatcgc ccgcatcaac cgcgccaaag
701 gcgaagcgga atccctgcgc cttgttgccg aagccaatgc cgaagccaac
751 cgtcaaattg ccgccgccct tcaaacccaa agcggggcgg atgcggtcaa
801 tctgaagatt gcgggacaat acgttaccgc gttcaaaaat cttgccaaag
851 aagacaatac gcggattaag cccgccaaag ttgccgaaat cgggaaccct
901 aattttcggc ggcatgaaaa attttcgcca gaagcaaaaa cggccaaata
951 a
```

This corresponds to the amino acid sequence <SEQ ID 1448; ORF 519.ng>:

```
g519.pep
1  MEFFIILLAA VAVFGFKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSI KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
```

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101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGQAQAVNA SNAEKIARIN RAKGEAESLR LVAEANAEN
 251 RQIAAALQTQ SGADAVNLKI AGQYVTAFAKN LAKEDNTRIK PAKVAEIGNP
 301 NFRRHEKFSP EAKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1449>:

m519.seq (partial)
 1 ..TCCGTTATCG GCGGTATGGA GTTGGACAAA ACCTTTGAAG AACGCGACGA
 51 AATCAACAGT ACTGTTGTTG CGGCTTTGGA CGAGGCGGCC GGGgCTTgGG
 101 GTGTGAAGGT TTTGCGTTAT GAGATTAAAG ACTTGGTTCC GCCGCAAGAA
 151 ATCCTTCGCT CAATGCAGGC GCAAATTACT GCCGAACGCG AAAAACGCGC
 201 CCGTATCGCC GAATCCGAAG GTCGTAAAAT CGAACAAATC AACCTTGCCA
 251 GTGGTCAGCG CGAAGCCGAA ATCCAACAAT CCGAAGGCGA GGCTCAGGCT
 301 GCGGTCAATG CGTCAAATGC CGAGAAAATC GCCCGCATCA ACCGCGCCAA
 351 AGGTGAAGCG GAATCCTTGC GCCTTGTGTC CGAAGCCAAT GCCGAAGCCA
 401 TCCGTCAAAT TGCCGCGGCC CTTCAAACCC AAGGCGGTGC GGATGCGGTC
 451 AATCTGAAGA TTGCGGAACA ATACGTCGCT GCGTTCAACA ATCTTGCCAA
 501 AGAAAGCAAT ACGCTGATTA TGCCCGCCAA TGTTGCCGAC ATCGGCAGCC
 551 TGATTCTGTC CGGTATGAAA ATTATCGACA GCAGCAAAAC CGCCAAaTAA

This corresponds to the amino acid sequence <SEQ ID 1450; ORF 519>:

m519.pep (partial)
 1 ..SVIGRMELDK TFEERDEINS TVVAALDEAA GAWGVKVLRY EIKDLVPPQE
 51 ILRSMQAQIT AEREKRARIA ESEGRKIEQI NLAGQREAE IQQSEGEAQA
 101 AVNASNAEKI ARINRAKGEA ESLRLVAEAN AEAIRQIAAA LQTQGGADAV
 151 NLKIAEQYVA AFNNLAKESN TLIMPANVAD IGSLISAGMK IIDSSKTAK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 519 shows 87.5% identity over a 200 aa overlap with a predicted ORF (ORF 519.ng) from *N. gonorrhoeae*:

m519/g519

m519.pep				10	20	30
				SVIGRMELDKTFEERDEINSTVVAALDEAA		
g519	YFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA					
	90	100	110	120	130	140
m519.pep		40	50	60	70	80
		GAWGVKVLRYEIKDLVPPQEILRSMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
g519		GAWGVKVLRYEIKDLVPPQEILRAMQAQITAEREKRARIAESEGRKIEQINLAGQREAE				
		150	160	170	180	190
m519.pep		100	110	120	130	140
		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA AEAIRQIAAALQTQGGADAV				
g519		IQQSEGEAQA AVNASNAEKIARINRAKGEAESLRLVAEANA EANRQIAAALQTQSGADAV				
		210	220	230	240	250
m519.pep		160	170	180	190	200
		NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL-ISAGMKIIDSSKTAK				
g519		NLKIAEQYVTAFAKNLAKEDNTRIKPAKVAEIGNPNFRRHEKFSP EAKTAK				
		270	280	290	300	310

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1451>:

a519.seq
 1 ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
 51 ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
 101 GGCGTTTCCA TCGCGCCCTG ACGGCCGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTAGACGT

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201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGC GTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCGG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCGG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGTGGCG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1452; ORF 519.a>:

```

a519.pep
1  MEFFIILLAA VVVFQKSFV VIPQQEVHVV ERLGRFHRAL TAGLNILIPF
51  IDRVAIRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIFYQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAIAI
251 RQIAAALQTO GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519/a519 99.5% identity in 199 aa overlap

```

m519.pep                               10      20      30
                               SVIGRMELDKTFEERDEINSTVVAALDEAA
a519      YFOVTDPKLASYGSSSNYIMAITQLAQTTLRSVIGRMELDKTFEERDEINSTVVSALDEAA
           90      100     110     120     130     140

m519.pep           40      50      60      70      80      90
GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
a519      GAWGVKVLRYEIKDLVPPQEILRSMAQITAEREKRARIAESEGRKIEQINLASGQREAE
           150     160     170     180     190     200

m519.pep           100     110     120     130     140     150
IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
a519      IQQSEGEAQAAVNASNAEKIARINRAKGEAESLRLVAEANAIAIRQIAAALQTQGGADAV
           210     220     230     240     250     260

m519.pep           160     170     180     190     200
NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
a519      NLKIAEQYVAAFNNLAKESNTLIMPANVADIGSLISAGMKIIDSSKTAKX
           270     280     290     300     310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1453>:

```

g519-1.seq
1  ATGGAATTTT TCATTATCTT GTTGGCAGCC GTCGCCGTTT TCGGCTTCAA
51  ATCCTTTGTC GTCATCCCCC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCGTTTCCA TCGCGCCCTG ACGGCCGTTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGATAA TACGCAATTG ACTGTTGACG
251 GCATCATCTA TTTCCAAGTA ACCGATCCCA AACTCGCCTC ATACGGTTTCG
301 AGCAACTACA TTATGGCAAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGTAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG GGCTTGGGGT
451 GTGAAAGTCC TCCGTTACGA AATCAAGGAT TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCGCA ATGCAGGCAC AAATTACGCG CGAACGCGAA AAACGCGCCC
551 GTATTGCCGA ATCCGAAGGC CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAAGCTG AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
651 GGTCAATGCG TCCAATGCCG AGAAAATCGC CCGCATCAAC CGCGCCAAAG
701 GCGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCCGCCCT TCAAACCCAA GCGGGGCGG ATGCGGTCAA

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801 TCTGAAGATT GCGGAACAAT ACGTAGCCGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GCATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1454; ORF 519-1.ng>:

g519-1.pep

1 MEFFIILLAA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRA MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1455>:

m519-1.seq

1 ATGGAATTTT TCATTATCTT GTTGGTAGCC GTCGCCGTTT TCGGTTTCAA
 51 ATCCTTTGTT GTCATCCAC AACAGGAAGT CCACGTTGTC GAAAGGCTGG
 101 GGCCTTTCCA TCGCGCCCTG ACGGcCGGTT TGAATATTTT GATTCCCTTT
 151 ATCGACCGCG TCGCCTACCG CCATTGCTG AAAGAAATCC CTTTAGACGT
 201 ACCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
 251 GCATCATCTA TTTCCAAGTA ACCGACCCA AACTCGCCTC ATACGTTTCG
 301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
 351 CGTTATCGGG CGTATGGAGT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
 401 TCAACAGTAC TGTGTGTCG GCTTTGGACG AGGCGGCCGG GGCTTGGGGT
 451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
 501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC CGAACGCGAA AAACGCGCCC
 551 GTATCGCCGA ATCCGAAGGT CGTAAATCG AACAAATCAA CCTTGCCAGT
 601 GGTCAAGCGC AAGCCGAAAT CCAACAATCC GAAGGCGAGG CTCAGGCTGC
 651 GGTCAATGCG TCAATGCGG AGAAAATCG CCGCATCAAC CGCGCCAAAG
 701 GTGAAGCGGA ATCCTTGCGC CTGTGTGCGG AAGCCAATGC CGAAGCCATC
 751 CGTCAAATTG CCGCGCCCT TCAAAACCAA GGCGGTGCGG ATGCGGTCAA
 801 TCTGAAGATT GCGGAACAAT ACGTCGCTGC GTTCAACAAT CTTGCCAAAG
 851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
 901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

This corresponds to the amino acid sequence <SEQ ID 1456; ORF 519-1>:

m519-1.

1 MEFFIILLVA VAVFGFKSFV VIPQQEVHV ERLGRFHRAL TAGLNILIPF
 51 IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIIYFQV TDPKLASYGS
 101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVA ALDEAAGAWG
 151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
 201 GQREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
 251 RQIAAALQTQ GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
 301 ISAGMKIIDS SKTAK*

m519-1/g519-1 99.0% identity in 315 aa overlap

	10	20	30	40	50	60
g519-1.pep	MEFFIILLAAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
m519-1	MEFFIILLVAVAVFGFKSFVVIPQQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL					
	10	20	30	40	50	60
g519-1.pep	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYSNYSNYIMAITQLAQTTLRSVIG					
m519-1	KEIPLDVPSQVCITRDNTQLTVDGIIYFQVTDPKLASYSNYSNYIMAITQLAQTTLRSVIG					
	70	80	90	100	110	120
g519-1.pep	RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRAMQAQITAERE					
m519-1	RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMAQQAQITAERE					
	130	140	150	160	170	180
g519-1.pep	KRARIAESEGKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
m519-1	KRARIAESEGKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR					
	190	200	210	220	230	240
g519-1.pep						
m519-1						

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```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
g519-1.pep  LVAEANAEAIRQIAAALQTGGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTGGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
g519-1.pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1457>:

```

a519-1.seq
1  ATGGAATTTT TCATTATCTT GCTGGCAGCC GTCGTTGTTT TCGGCTTCAA
51  ATCCTTTGTT GTCATCCAC AGCAGGAAGT CCACGTTGTC GAAAGGCTCG
101 GGCGTTTCCA TCGCGCCCTG ACGCGCGGTT TGAATATTTT GATTCCCTTT
151 ATCGACCGCG TCGCTACCG CCATTCGCTG AAAGAAATCC CTTTAGACGT
201 ACCCAGCCAG GTCTGCATCA CGCGCGACAA TACGCAGCTG ACTGTTGACG
251 GTATCATCTA TTTCCAAGTA ACCGACCCCA AACTCGCTC ATACGTTTCG
301 AGCAACTACA TTATGGCGAT TACCCAGCTT GCCCAAACGA CGCTGCGTTC
351 CGTTATCGGG CGTATGGAAT TGGACAAAAC GTTTGAAGAA CGCGACGAAA
401 TCAACAGCAC CGTCGTCTCC GCCCTCGATG AAGCCGCCGG AGCTTGGGGT
451 GTGAAGGTTT TGCGTTATGA GATTAAAGAC TTGGTTCCGC CGCAAGAAAT
501 CCTTCGCTCA ATGCAGGCGC AAATTACTGC TGAACGCGAA AAACGCGCCC
551 GTATCGCCGA ATCCGAAGGT CGTAAAATCG AACAAATCAA CCTTGCCAGT
601 GGTCAGCGCG AAGCCGAAAT CCAACAATCC GAAGCGGAGG CTCAGGCTGC
651 GGTCAATGCG TCAATGCCG AGAAAATCGC CGCATCAAC CGCGCCAAAG
701 GTGAAGCGGA ATCCTTGCGC CTTGTTGCCG AAGCCAATGC CGAAGCCATC
751 CGTCAAATTG CCGCGCCCT TCAAACCCAA GGCGGTGCGG ATGCGGTCAA
801 TCTGAAGATT GCGGAACAAT ACGTCGCCGC GTTCAACAAT CTTGCCAAAG
851 AAAGCAATAC GCTGATTATG CCCGCCAATG TTGCCGACAT CGGCAGCCTG
901 ATTTCTGCCG GTATGAAAT TATCGACAGC AGCAAAACCG CCAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1458; ORF 519-1.a>:

```

a519-1.pep.
1  MEFFIILLAA VVVFGRKSFV VIPQEVHV ERLGRFHRAL TAGLNILIPF
51  IDRVAYRHSL KEIPLDVPSQ VCITRDNTQL TVDGIYFQV TDPKLASYGS
101 SNYIMAITQL AQTTLRSVIG RMELDKTFEE RDEINSTVVS ALDEAAGAWG
151 VKVLRYEIKD LVPPQEILRS MQAQITAERE KRARIAESEG RKIEQINLAS
201 QREAEIQQS EGEAQAAVNA SNAEKIARIN RAKGEAESLR LVAEANAEAI
251 RQIAAALQQT GGADAVNLKI AEQYVAAFNN LAKESNTLIM PANVADIGSL
301 ISAGMKIIDS SKTAK*

```

m519-1/a519-1 99.0% identity in 315 aa overlap

```

              10      20      30      40      50      60
a519-1.pep  MEFFIILLAAVVVFGRKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              |||||
m519-1      MEFFIILLVAVAVFGFKSFVVIPQEVHVVERLGRFHRALTAGLNILIPFIDRVAYRHSL
              10      20      30      40      50      60

              70      80      90      100     110     120
a519-1.pep  KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              |||||
m519-1      KEIPLDVPSQVCITRDNTQLTVDGIYFQVTDPKLASYGSSNYIMAITQLAQTTLRSVIG
              70      80      90      100     110     120

              130     140     150     160     170     180
a519-1.pep  RMELDKTFEERDEINSTVVSALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              |||||
m519-1      RMELDKTFEERDEINSTVVAALDEAAGAWGVKVLRYEIKDLVPPQEILRSMQAQITAERE
              130     140     150     160     170     180

              190     200     210     220     230     240
a519-1.pep  KRARIAESEGRKIEQINLASGQREAEIQQSEGEAQAAVNASNAEKIARINRAKGEAESLR
              |||||

```

```

m519-1      KRARIAESEGRKIEQINLASGQREAEIQQSEGEAAVNASNAEKIARINRAKGEAESLR
              190      200      210      220      230      240

              250      260      270      280      290      300
a519-1 .pep  LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              |||||
m519-1      LVAEANAEAIRQIAAALQTQGGADAVNLKIAEQYVAAFNNLAKESNTLIMPANVADIGSL
              250      260      270      280      290      300

              310
a519-1 .pep  ISAGMKIIDSSKTAKX
              |||||
m519-1      ISAGMKIIDSSKTAKX
              310

```

Expression of ORF 519

The primer described in Table 1 for ORF 519 was used to locate and clone ORF 519. ORF 519 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 4A shows the results of affinity purification, and Figure 4B shows the expression in E.coli. Purified Nis-fusion protein was used to immunize mice whose sera were used for ELISA (positive result), FACS analysis (Figure 4C), western blot (Figure 1E), and a bactericidal assay (Figure 4D). These experiments confirm that 519 is a surface-exposed protein and that it is a useful immunogen. The hydrophilicity plots, antigenic index, and amphipatic regions of ORF 519 are provided in Figure 8. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 519 and the amino acid sequence encoded thereby as provided herein.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1459>:

```

g520.seq
1  atgcctgcgc ttctttcaat acgtcgggca aacgcgctgc ctttttcgcg
51 catttcggaa aggatgaagt tgctgggtgcc gttaataatg ccggcgatgg
101 atttaatcct gtttgccgcc aaaccttcgc gcacggcttt gatgattggg
151 ataccgcccg ctactgccgc ttcaaattgg acgatgacgt tttgtttttc
201 cgccagcggg aagatttcgt tgccgtattc ggcgagcagt tttttgttgg
251 cggtaacgat gtgtttgccg ttttcaatgg ctttcaacac cgcttctttg
301 gcaatgcccg tgccgccgaa caattcgacc aagacatcga cgtctttacg
351 cgcgaacagt tcgaacggat cttttgacaa gggcggggcga cgggcccatt
401 ttggcgggct ttttcttcgc ttaagtcgca catggcagaa atacggattt
451 cgcgccccaa gcggcgggaa atttctctcg cgttgtcccc caacacggca
501 gccgcaccgc cgccgaccgt acctaacgct aaaagaccga tgtttactgg
551 cttcattgtg tctccttgta agccgactga aatgtaaata ttga

```

This corresponds to the amino acid sequence <SEQ ID 1460; ORF 520.ng>:

```

g520.pep
1  MPALLSIRRA NALPFSRISE RMKLLVPLIM PAMDILILFAA KPSRTALMIG
51 IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101 AMPVFPNNST KTSTSLRANS SNGSFDKGG RADFGLFLR LSRTWQKYGF
151 RAPSGGKFPL RCPATRQPHR RRPYLSLKDR CLLASLCLLV SRLKCKY*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1461>:

```

m520.seq
1  ATGCCTGCGC TTCTTTCAGT ACATCG.GCA AACGCGCTGC CTTTTTCGCG
51 CATTTCCGGrk AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101 ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTTT GATGATTGGG
151 ATACCGCCCG CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTTC
201 CGCCAGCGGG AAGATTTTCTG TGCCGTATTG GCGGAGCAGT TTTTGTGGG
251 CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG

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```

301  GCAATGCCGG TACCGCCGaa CAATTCGACG ACGACATCGA CGTCTTCACG
351  TGCGACCAGT TCGAACGGAT CTTTGACAAA GGCTGc.CGG ACGGGCAGGT
401  TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451  CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCSG CAACACGGCA
501  GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551  CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1462; ORF 520>:

```

m520.pep
  1  MPALLSVHXA NALPFSRISX RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101  AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF
151  RAPSDGKFPP RCXATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 520 shows 87.3% identity over a 197 aa overlap with a predicted ORF (ORF 520.ng) from *N. gonorrhoeae*:

```

m520/g520
      10      20      30      40      50      60
m520.pep  MPALLSVHRANALPFSRISXRMKLLVPLIMPAMDILFAAKPSRRALMIGIPPATAASNW
          |||||::||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520      MPALLSIRANALPFSRISERMKLLVPLIMPAMDILFAAKPSRTALMIGIPPATAASNW
          10      20      30      40      50      60

      70      80      90      100     110     120
m520.pep  TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g520      TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTKTSTSLRANS
          70      80      90      100     110     120

      130     140     150     160     170     180
m520.pep  SNGSLTKAARTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYNLKDR
          |||:|:|:|:| |||||:| ||||| ||||| ||||| |||||:| |||||
g520      SNGSFDKGGRRADFGGLFLRLSRTWQKYGFRAPSGGKFPLRCPATRQPHRRRPYLSLKDR
          130     140     150     160     170     180

      190
m520.pep  CLLASLCLLVSRKCKY
          ||||| ||||| ||||| |||||
g520      CLLASLCLLVSRKCKY
          190

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1463>:

```

a520.seq
  1  ATGCCTGCGC TTCTTTCAGT ACATCGG.CA AACGCGCTGC CTTTTTCGCG
 51  CATTTCCGAG AGGATGAAGT TGCTGGTGCC GTTAATAATG CCGGCGATGG
101  ATTTAATCCT GTTTGCCGCC AAACCTTCGC GCAGGGCTT GATGATTGGG
151  ATACCGCCCC CTACTGCCGC TTCAAATTGG ACGATGACGT TTTGTTTTC
201  CGCCAGCGGG AAGATTTCTG TGCCGTATTC GGCGAGCAGT TTTTGTGTTG
251  CGGTAACGAT GTGTTTGCCG TTTTCAATGG CTTTCAACAC CGCATCTTTG
301  GCAATGCCGG TACCGCCGAA CAATTCGACG ACGACATCGA CGTCTTCACG
351  TGCGACCAGT TCGAACGGAT CTTTGACAAA GGCTG..CGG ACGGGCAGGT
401  TTGTCGGGCT TTTTCTTCAC TCAAATCGCA CACGGCAGAA ATACGGATTT
451  CGCGCCCCAA GCGACGGGAA ATTTCTCCG CGTTGTCCG CAACACGGCA
501  GCCGTACCGC CGCCGACCGT ACCCAAACCT AAAAGACCGA TGTTTACTGG
551  CTTCATTGTG TCTCCTTGTA AGCCGACTGA AATGTAAATA TTGA

```

This corresponds to the amino acid sequence <SEQ ID 1464; ORF 520.a>:

```

a520.pep
  1  MPALLSVHRX NALPFSRISE RMKLLVPLIM PAMDILFAA KPSRRALMIG
 51  IPPATAASNW TMTFCFSASG KISLPYSASS FLLAVTMCLP FSMAFNTASL
101  AMPVPPNNST TTSTSSRATS SNGSLTKAXR TGRFVGLFLH SNRTRQKYGF

```


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151 RAPSDGKFPP RCPATRQPYR RRPYPNLKDR CLLASLCLLV SRLKCKY*

m520/a520 98.0% identity in 197 aa overlap

	10	20	30	40	50	60
m520.pep	MPALLSVHXANALPFSRISXRMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
a520	MPALLSVHRXNALPFSRISERMKLLVPLIMPAMDILILFAAKPSRRALMIGIPPATAASNW					
	10	20	30	40	50	60
	70	80	90	100	110	120
m520.pep	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
a520	TMTFCFSASGKISLPYSASSFLLAVTMCLPFSMAFNTASLAMPVPPNNSTTTSTSSRATS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m520.pep	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCXATRQPYRRRPYNLKDR					
a520	SNGSLTKAXRTGRFVGLFLHSNRTRQKYGFRAPSDGKFPPRCPATRQPYRRRPYNLKDR					
	130	140	150	160	170	180
	190					
m520.pep	CLLASLCLLVSRLLKCKYX					
a520	CLLASLCLLVSRLLKCKYX					
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1465>:

g520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGCG CAGCGGGAAG
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC TTCTTTGGCA ATGCCCGTGC
251 CGccgAACAA TTCGACGACG ACATCGACGT CTTTACGCGC GACCAGTtCG
301 AACGGATCTT TGACAAAGGC GCGGACGGG CAGATTGGC GGGCTTTTTT
351 TTCGCTTAAG TCGCACATGG CAGAAATACG GATTTCGCGC CCCAAGCGGC
401 GGGAAATTTT CTCTGCGTTG TCCCGCAACA CGGCAGCCGC ACCGCCGCCG
451 ACCgTACCTA AGCCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1466; ORF 520-1.ng>:

g520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSLRATSS
101 NGSLLKAADG QIWRAFSSLK SHMAEIRISR PKRREISSAL SRNTAAAPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1467>:

m520-1.seq

```

1  ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51  TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGCG CAGCGGGAAG
151 ATTTGCTTGC CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCCGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTACGTGTC GACCAGTTTC
301 AACGGATCTT TGACAAAGGC TGCGGACGGG CAGGTTGTGC GGGCTTTTTT
351 TTCACCTCAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTTT CTCCGCGTTG TCCCGCAACA CGGCAGCCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

```

This corresponds to the amino acid sequence <SEQ ID 1468; ORF 520-1>:

m520-1.pep

```

1  MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTFCFASGK
51  ISLPYSASSE LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS

```

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101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

g520-1/m520-1 97.1% identity in 173 aa overlap

	10	20	30	40	50	60
g520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
g520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSLR	ATSSNGSLTKA	ADGQIWRASF	SSLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
g520-1.pep	SHMAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1469>:

a520-1.seq

1 ATGAAGTTGC TGGTGCCGTT AATAATGCCG GCGATGGATT TAATCCTGTT
51 TGCCGCCAAA CCTTCGCGCA GGGCTTTGAT GATTGGGATA CCGCCCGCTA
101 CTGCCGCTTC AAATTGGACG ATGACGTTTT GTTTTCCGC CAGCGGGAAG
151 ATTCGTTGCG CGTATTCGGC GAGCAGTTTT TTGTTGGCGG TAACGATGTG
201 TTTGCCGTTT TCAATGGCTT TCAACACCGC ATCTTTGGCA ATGCCGGTAC
251 CGCCGAACAA TTCGACGACG ACATCGACGT CTTCACGTGC GACCAGTTCG
301 AACGGATCTT TGACAAAGGC TCGGACGGG CAGGTTTGTC GGGCTTTTTC
351 TTCACTCAAA TCGCACACGG CAGAAATACG GATTTCGCGC CCCAAGCGAC
401 GGGAAATTC CTCCGCGTTG TCCCGCAACA CGGCAGCGT ACCGCCGCCG
451 ACCGTACCCA AACCTAAAAG ACCGATGTTT ACTGGCTTCA TTGTGTCTCC
501 TTGTAAGCCG ACTGAAATGT AA

This corresponds to the amino acid sequence <SEQ ID 1470; ORF 520-1.a>:

a520-1.pep

1 MKLLVPLIMP AMDLILFAAK PSRRALMIGI PPATAASNWT MTCFCSASGK
51 ISLPYSASSF LLAVTMCLPF SMAFNTASLA MPVPPNNSTT TSTSSRATSS
101 NGSLTKAADG QVCRAFSSLK SHTAEIRISR PKRREISSAL SRNTAAVPPP
151 TVPKPKRPMF TGFIVSPCKP TEM*

m520-1/a520-1 100.0% identity in 173 aa overlap

	10	20	30	40	50	60
a520-1.pep	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
m520-1	MKLLVPLIMPAMD	LILFAAKPSRRAL	MIGIPPATAASN	WTMTCFCSASG	KISLPYSASSF	
	10	20	30	40	50	60
	70	80	90	100	110	120
a520-1.pep	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
m520-1	LLAVTMCLPFSMA	FNTASLAMPVPP	NNSTTTSTSSR	ATSSNGSLTKA	ADGQVCRAFSS	SLK
	70	80	90	100	110	120
	130	140	150	160	170	
a520-1.pep	SHTAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
m520-1	SHTAEIRISRPKR	REISSALSRNTA	AAVPPPTVPKPK	RPMFTGFI	VSPCKPTEMX	
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1471>:

g521.seq

1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACCTTTCCC TGATTTCAG
51 CCCATTGGGT GCGAATGCGG CAAAATCTA TACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCACCAAG CCGTCTAAAA GCTGCCACTC AACCGATTG

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```

151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCTGC CCCAAACTCC
201 CGAACCGGCA CCATCACCGT CAAACGGCGG ACAGGCTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCAATAC GCCGCCTCAA
301 CAAGCACCTG TAAATAACAG CAGACGCTCC ATTCTcgaag caGaattaag
351 cAatgaacgc aaagccctGa ctGaAGCCCA AAAAATGTTA TCACAagcac
401 gtCtGGCAAA AGGCGgcaAC AtcaaCCatc aaaAaatcaa cgcattgtaa
451 AGCAATGTTt tggacAGACA GCAAAATaTC Caagcactgc aaaGAgAATt
501 GGGACGTATG TAA

```

This corresponds to the amino acid sequence <SEQ ID 1472; ORF 521.ng>:

```

g521n.pep
  1 MKSKLPLILI NLSLISSPLG ANAAKIYTCT INGETVYTTK PSKSCHSTD
 51 PPIGNYSSER YILPQTPEPA PPSNGGQAV KYKAPVKTVS KPAKSNTTPQ
101 QAPVNSRRS ILEAELSNER KALTEAQKML SQARLAKGN INHQKINAL*
151 SNVLDQQNI QALQRELGRM *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1473>:

```

m521.seq
  1 ATGAAATCAA AACTCCTCTT AATCCTAATC AACTTTTCCC TGATTTCAG
 51 CCCATTGGGT GCGAATGCGG CCAAAATCTA sACCTGCACA ATCAACGGAG
101 AAACCGTTTA CACCAsCAAG CCGTCCAAAA GCTGCCACTC AACCGATTG
151 CCCCCAATCG GCAACTACAG CAGCGAACGC TATATCCCGC CCCAAACGCC
201 CGAACCGGTA TCATCACCGT CAAACGGCGG ACwGGTTGTC AAATATAAAG
251 CCCCAGTCAA AACAGTATCC AAGCCGGCAA AATCCArTAC GCCGCCGCCG
301 CAACAAGCAC CCTCAAACAA CAGCAGACGC TCCATTCTCG AACAGAATT
351 GAGCAACGAA CGCAAAGCAT TGGTTGAAGC CCAAAAAATG TTATCACAAG
401 CACGTCTGGC AAAGGGCGGC AACATCAACC ATCAAGAAAT AAATGCATTA
451 CAAAGCAATG TATTGGACAG GCAGCAAAAT ATTCAAGCCC TGCAAAGGGA
501 ACTGGGGCGT ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1474; ORF 521>:

```

m521.pep
  1 MKSKLLLLILI NLSLISSPLG ANAAKIXTCT INGETVYTXK PSKSCHSTD
 51 PPIGNYSSER YIPPQTPEPV SSPSNGGXVV KYKAPVKTVS KPAKSXTPPP
101 QQAPSNNRR SILETELSNE RKALVEAQKM LSQARLAKGG NINHQEINAL
151 QSNVLDQQN IQALQRELGR M*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 521 shows 90.6% identity over a 171 aa overlap with a predicted ORF (ORF 521.ng) from *N. gonorrhoeae*:

```

m521/g521
      10      20      30      40      50      60
m521.pep  MKSKLLLLILINFLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPIGNYSSER
          ||||| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g521      MKSKLPLILINLSLISSPLGANAAKIYTCTINGETVYTTKPSKSCHSTDLPPIGNYSSER
          10      20      30      40      50      60

      70      80      90      100     110     120
m521.pep  YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE
          || ||||| : ||||| : ||||| ||||| ||||| ||||| ||||| |||||
g521      YILPQTPEPAPSPSNGGQAVKYKAPVKTVSKPAKSNTTPP-QQAPVNSRRSILEAELSNE
          70      80      90      100     110

      130     140     150     160     170
m521.pep  RKALVEAQKMLSQARLAKGGINHQEINALQSNVLDQQNIQALQRELGRMX
          ||||| : ||||| ||||| ||||| ||||| ||||| ||||| |||||
g521      RKALTEAQKMLSQARLAKGGINHQKINALXSNVLDQQNIQALQRELGRMX
          120     130     140     150     160     170

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1475>:

```

a521.seq
  1 ATGAAATCAA AACTCCCCTT AATCCTAATC AACTTTTCCC TGATTTCAG

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```

51  CCCATTGGGT  GCGAATGCGG  CCAAATCTA  CACCTGCACA  ATCAACGGAG
101 AAACCGTTTA  CACCACCAAG  CCGTCCAAA  GCTGCCTCTC  AACCGATTG
151 CCCCCAATCG  GCAACTACAG  CAGCGAACGC  TATATCCCGC  CCCAAACATC
201 CGAACCGACA  CCATCACCGT  CAAACGGCGG  ACAGGCTGTC  AAATATAAAG
251 CCCCAGGTCAA  AACAGTATCC  AAGCCGGCAA  AATCCAATAC  GCCGCCGCCG
301 CAACAAGCAC  CCTCAAACAA  CAGCAGACGC  TCCATTCTCG  AAACAGAATT
351 GAGCAACGAA  CGCAAAGCAT  TGGTTGAAGC  CCAAAAAATG  TTATCACAAAG
401 CACGTCTGGC  AAAAGGCGGC  AACATCAACC  ATCAAGAAAT  CAACGCATTG
451 CAAAGCAATG  TATTGGACAG  GCAGCAAAT  ATCCAAGCAC  TGCAAAGAGA
501 ATTGGGACGT  ATGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1476; ORF 521.a>:

```

a521.pep
1  MKSKLPLILI  NFSLISSPLG  ANAAKIYTCT  INGETVYTTK  PSKSCLSTDL
51  PPIGNYSSER  YIPPQTSEPT  PSPSNGGQAV  KYKAPVKTVS  KPAKSNTPPP
101 QQAPSNNRR  SILETELSNE  RKALVEAQKM  LSQARLAKGG  NINHQEINAL
151 QSVLDRQON  IQALQRELGR  M*

```

m521/a521 94.2% identity in 171 aa overlap

	10	20	30	40	50	60
m521.pep	MKSLLLLILINFSLISSPLGANAAKIXTCTINGETVYTXKPSKSCHSTDLPPPIGNYSSER					
a521	MKSKLPLILINFSLISSPLGANAAKIYTCTINGETVYTTKPSKSCLSTDLPPPIGNYSSER					
	10	20	30	40	50	60
	70	80	90	100	110	120
m521.pep	YIPPQTPEPVSSPSNGGXVVKYKAPVKTVSKPAKSXTPPPQQAPSNNRRSILETELSNE					
	: :					
a521	YIPPQTSEPTSPSNGGQAVKYKAPVKTVSKPAKSNTPPPQQAPSNNRRSILETELSNE					
	70	80	90	100	110	120
	130	140	150	160	170	
m521.pep	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
a521	RKALVEAQKMLSQARLAKGGNINHQEINALQSNVLDROQNIQALQRELGRMX					
	130	140	150	160	170	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1477>:

```

g522.seq
1  atgactgagc  cgaaacacga  aacgccgacg  gaagagcagg  ttgccgcgcg
51  caaaaaagca  aaagccaaaa  tccgcaccat  ccgcatttgg  gcgtgggtca
101 ttttggcggt  gctcgcttca  accgccctgc  tctcccaatg  cgcgatgtcc
151 aaaccgcagg  caaaacagaa  aattgtcgag  tcttgcataa  aaaatattcc
201 gtttgcgtga  aaatggcaga  acgatttgaa  agcgcgcggc  ttggatgcgg
251 acaatacccg  tctcgccgct  gactactgca  aatgtatgtg  ggagcagcct
301 ttggacggat  tgagcgagaa  acagatcagc  tccttcggca  aactcgggtg
351 acaagaacag  cttgacctgc  tcggcggcgc  aaacgcgttt  gaaactcgag
401 acaaacaatg  tgtcgcggat  ttgaaagccg  attga

```

This corresponds to the amino acid sequence <SEQ ID 1478; ORF 522.ng>:

```

g522.pep
1  MTEPKHETPT  EEQVAARKKA  KAKIRTIRIW  AWVILALLAS  TALLSQCAMs
51  KPQAKQKIVE  SCMKNIPFAE  KWQNDLKARG  LDADNTRLAV  DYCKCMWEQP
101 LDGLSEKQIS  SFGKLGAQEQ  LDLLGGANAF  ETRDKQCVAD  LKAD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1479>:

```

m522.seq
1  ATGACTGAGC  CGAAACACGA  AATGCTGACG  AAAGAGCAGG  TTGCCGCGCG
51  CAAAAAAGCA  AAAGCCAAAA  TCCGCACCAT  CCGCATTGGA  GCGTGGGTCA
101 TTTTGGCGTT  GCTCGCTTTA  ACCGCCCTGC  TCTCCCAATG  CGCGATGTCC
151 AAACCGCAGG  CAAAACAGAA  AATTGTCGAG  TCTTGCGTGA  AGAATATTCC
201 GTTTGCCGAA  AAATGGCAAA  ACGATTGCG  GGCCCGCGGT  TTAGATTCAA
251 ACAATACCCG  CCTCGCCGTC  GACTACTGCA  AATGTATGTG  GGAGCAGCCT

```

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301 TTGGACAGAT TGAGCGAGAA ACAGATTAGA TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAGCACGTG
 401 ACAAGCAGTG TGTGCGCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1480; ORF 522>:

m522.pep

1 MTEPKHEMLT KEQVAARKKA KAKIRTIRIW AWVILALLAL TALLSQCAMSKPQAKQKIVE
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLAV DYCKCMWEQP
 101 LDRLSEKQIR SFGKLGAQEQ LDLLGGANAF EARDKQCVAD LKSE*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 522 shows 91.0% identity over a 144 aa overlap with a predicted ORF (ORF 522.ng) from *N. gonorrhoeae*:

m522/g522

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
g522	MTEPKHETPTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
	: : :					
g522	SCMKNIPFAEKWQNDLKARGLDADNTRLAVDYCKCMWEQPLDGLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120
	130	140				
m522.pep	LDLLGGANAFEARDKQCVADLKSEX					
	: :					
g522	LDLLGGANAFETRDKQCVADLKAD					
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1481>:

a522.seq

1 ATGACTGAGC CGAAACACGA AATGCCGACG GAAGAGCAGG TTGCCGCGCGG
 51 CAAAAAAGCA AAAGCCAAAA TCCGCACCAT CCGCATTTGG GCATGGGTCA
 101 TTTTGGCGTT GCTCGCTTCA ACCGCCCTGC TCTCCCAATG CGCGATGTCC
 151 AAACCGCAGG CAAAACAGAA AATTGTCTGAG TCTTGCGTGA AGAATATTCC
 201 GTTTGCCGAA AAATGGCAAA ACGATTTGCG GGCCCGCGGT TTAGATTCAA
 251 ACAATACCCG CCTTACCGTC GACTACTGCA AATGTATGTG GGAGCAGCCT
 301 TTGGACAGAT TGAGCGAGAA ACAGATTAGT TCCTTCGGCA AACTCGGCGC
 351 ACAAGAACAG CTTGACCTGC TCGGCGGCGC AAATGCCTTT GAAACGCGAG
 401 ACAAGCAGTG TGTGCGCGAT TTGAAATCAG AATAA

This corresponds to the amino acid sequence <SEQ ID 1482; ORF 522.a>:

a522.pep

1 MTEPKHEMPT EEQVAARKKA KAKIRTIRIW AWVILALLAS TALLSQCAMSKPQAKQKIVE
 51 KPQAKQKIVE SCVKNIPFAE KWQNDLRARG LDSNNTRLTV DYCKCMWEQP
 101 LDRLSEKQIS SFGKLGAQEQ LDLLGGANAF ETRDKQCVAD LKSE*

m522/a522 95.8% identity in 144 aa overlap

	10	20	30	40	50	60
m522.pep	MTEPKHEMLTKEQVAARKKAKAKIRTIRIWAWVILALLALTALLSQCAMSKPQAKQKIVE					
	:					
a522	MTEPKHEMPTTEEQVAARKKAKAKIRTIRIWAWVILALLASTALLSQCAMSKPQAKQKIVE					
	10	20	30	40	50	60
	70	80	90	100	110	120
m522.pep	SCVKNIPFAEKWQNDLRARGLDSNNTRLAVDYCKCMWEQPLDRLSEKQIRSFGLGAQEQ					
	:					
a522	SCVKNIPFAEKWQNDLRARGLDSNNTRLTVDYCKCMWEQPLDRLSEKQISSFGLGAQEQ					
	70	80	90	100	110	120

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```

                130      140
m522.pep      LDLLGGANAFEARDKQCVDLKSEX
                |||||
a522          LDLLGGANAFETRDKQCVDLKSEX
                130      140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1483>:

```

g523.seq
1  atgactgtat ggtttggtgc cgctggtgcc gtcttaatca tcgaattatt
51  gacgggaacg gtttatcttt tggttgtcag cgcggtttg gcgggttcgg
101 gcatcgcta cgggctgact ggcagcacgc ctgccgccgt cttgaccgcc
151 gcaactgctt ccgcgctggg catttggttc gtacatgcca aaaccgccgt
201 gggaaaagtt gaaacggatt catatcagga tttggatacc ggaaaatatg
251 ccgaaatcct ccgatacaca ggcggcaacc gttacgaagt tttttatcgc
301 ggtacgcact ggcaggcgca aaatacgggg caggaagtgt ttgaaccggg
351 aacgcgcgcc ctcacgtcc gcaaagaagg taaccttctt atcatcgcaa
401 acccttaa

```

This corresponds to the amino acid sequence <SEQ ID 1484; ORF 523.ng>:

```

g523.pep
1  MTVWFVAAVA VLIIELLTGT VYLLVVSAA AGSGIAYGLT GSTPAAVLTA
51  ALLSALGIWF VHAKTAVGKV ETDSYQDLDT GKYAEILRYT GGNRYEVFYR
101 GTHWQAQNTG QEVFEPGTRA LIVRKEGNLL IIANP*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1485>:

```

m523.seq (partial)
1  ..GCCGTCCTAA TCATCGAATT ATTGACGGGA ACGGTTTATC TTTTGGTTGT
51  nAGCGCGGCT TTGGCGGGTT CGGGCATTGC TTACGGGCTG ACCGGCAGTA
101 CGCCTGCCGC CGTCTTGACC GncGCTCTGC TTTCCGCGCT GGGTATTnG
151 TTCGTACACG CCAAACCCGC CGTTAGAAAA GTTGAAACGG ATTCATATCA
201 GGATTTGGAT GCCGACAAT ATGTCGAAAT CCTCCGACAC ACAGGCGGCA
251 ACCGTTACGA AGTTTTtTAT CGCGGTACGc ACTGGCAGGC TCAAATACG
301 GGGCAAGAAG AGCTTGAACC AGGAACTCGC GCCCTCATTG TCCGCAAGGA
351 AGGCAACCTT CTTATTATCA CACACCCTTA

```

This corresponds to the amino acid sequence <SEQ ID 1486; ORF 523>:

```

m523.pep (partial)
1  ..AVLIIELLTG TVYLLVVSAA LAGSGIAYGL TGSTPAAVLT XALLSALGIX
51  FVHAKTAVRK VETDSYQDLG AGQYVEILRH TGGNRYEVFY RGTWQAQNT
101 GQEELEPGTR ALIVRKEGNL LIITHP*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF523 shows 91.3% identity over a 126 aa overlap with a predicted ORF (ORF 523.ng) from *N. gonorrhoeae*:

m523/g523

```

                10      20      30      40      50
m523.pep      AVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTXALLSALGIXF
                |||||
g523          MTVWFVAAVAVLIIELLTGTVYLLVVSAA LAGSGIAYGLTGSTPAAVLTAALLSALGIWF
                10      20      30      40      50      60

                60      70      80      90      100     110
m523.pep      VHAKTAVRKVETDSYQDLGAGQYVEILRHTGGNRYEVFYRGTHWQAQNTGQEELEPGTRA
                |||||
g523          VHAKTAVGKVETDSYQDLDTGKYAEILRYTGGNRYEVFYRGTHWQAQNTGQEVFEPGTRA
                70      80      90      100     110     120

                120
m523.pep      LIVRKEGNLLIITHP
                |||||

```

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g523 LIVRKEGNLLIIANPX
130

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1487>:

a523.seq
1 ATGACTGTAT GGTTTGTGTC CGCTGTTGCC GTCTTAATCA TCGAATTATT
51 GACGGGAACG GTTTATCTTT TGGTTGTCAG CGCGGCTTTG GCGGGTTCGG
101 GCATTGCTTA CGGGCTGACC GGCAGCACGC CTGCCGCCGT CTTGACCGCC
151 GCTCTGCTTT CCGCGCTGGG TATTTGGTTC GTACACGCCA AAACCGCCGT
201 GGGAAAAGTT GAAACGGATT CATATCAGGA TTTGGATGCC GGGCAATATG
251 CCGAAATCCT CCGGCACGCA GCGGCAACC GTTACGAAGT TTTTATCGC
301 GGTACGCACT GGCAGGCTCA AAATACGGGG CAAGAAGAGC TTGAACCAGG
351 AACGCGCGCC CTAATCGTCC GCAAGGAAGG CAACCTTCTT ATCATCGCAA
401 AACCTTAA

This corresponds to the amino acid sequence <SEQ ID 1488; ORF 523.a>:

a523.pep
1 MTVWFVAAVA VLIIELLTGT VYLLVVSAAAL AGSGIAYGLT GSTPAAVLTA
51 ALLSALGIWF VHAKTAVGKV ETDSYQDLDA GOYAEILRHA GGNRYEVFVR
101 GTHWQAQNTG QEELEPGTRA LIVRKEGNLL IIAKP*

m523/a523 94.4% identity in 126 aa overlap

	10	20	30	40	50
m523.pep	AVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTXALLSALGIXF				
a523	MTVWFVAAVAVLIIELLTGTVYLLVVSAAALAGSGIAYGLTGSTPAAVLTAALLSALGIWF				
	10	20	30	40	50
	60	70	80	90	100
m523.pep	VHAKTAVRKVETDSYQDLDAQYVEILRHAGGNRYEVFVRGTHWQAQNTGQEELEPGTRA				
a523	VHAKTAVGKVETDSYQDLDAQYAEILRHAGGNRYEVFVRGTHWQAQNTGQEELEPGTRA				
	70	80	90	100	110
	120				
m523.pep	LIVRKEGNLLIIITHPX				
a523	LIVRKEGNLLIIAKPX				
	130				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1489>:

g525.seq
1 atgaagtacg tccggttatt tttcctcggc acggcactcg ccggcactca
51 agcggcggtt gccgaaatgg ttcaaactga aggcggcagc taccgcccgc
101 tttatctgaa aaaagatacc ggcttgatta aagtcaaacc gttcaaactg
151 gataaatatc ccgttaccaa tgccgagttt gccgaatttg tcaacagcca
201 cccccaatgg caaaaaggca ggatcggttc caaacaggca gaaccgctt
251 acctgaagca ttggatgaaa aacggcagcc gcagctatgc gccgaaggcg
301 ggcgaattga aacagccggt taccaatatt tcctgggttg ccgccaacgc
351 ctattgcgcc gcacaaggca aacgcctgcc gaccatcgac gaatgggaat
401 ttgccggact tgcttcgcc acgcagaaaa aacggctcaa acgaaccggg
451 ctacaaccgc actattctcg attggtatgc cgacggcgga cggaaaggcc
501 tgcacgatgt cggcaaagca ccgcccgaac tactgggggtg tttatgatat
551 gcacgggctg a

This corresponds to the amino acid sequence <SEQ ID 1490; ORF 525.ng>:

g525.pep
1 MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWMK NGSRSYAPKA
101 GELKQPVNTI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKKRLKRT
151 LQPHYSRLVC RRRTERPARC RQSTARTTGV FMICTG *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1491>:

790

m525.seq

```

1 ATGAAGTATG TCCGGTTATT TTWCCTCGGC GCGGCACTCG cCrrCACTCA
51 ArCGGCGGCT GcCGAAATGG TTCAAATCGA AGGCGGCAGc TACCGCCCrC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGc GCCGAAGgCG
301 GgCGAATTAA AACAACCGGT AACCAATGTT TCCTGGwTTG CCGCCAaCGC
351 CTAtTGC GCCAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAGAAAA A.CGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ATTGGTATGC CGACGGCGGA CGGAAAGGCC
501 TGCACGATGT CGGCA.AAGG CCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGGCTG A

```

This corresponds to the amino acid sequence <SEQ ID 1492; ORF 525>:

m525.pep

```

1 MKYVRLFXLG AALAXTQXAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHWK NGSRSYAPKA
101 GELKQPVNTV SWXAANAYCA AQGKRLPTID EWEFAGLASA TQKXRLKRTR
151 LQPHYSRLVC RRRTERPARC RXKAARTTGA FMICTG*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 525 shows 94.1% identity over a 186 aa overlap with a predicted ORF (ORF 525.ng) from *N. gonorrhoeae*:

m525/g525

	10	20	30	40	50	60
m525.pep	MKYVRLFXLGAALAXTQXAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
g525	MKYVRLFFLGTALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF					
	10	20	30	40	50	60
	70	80	90	100	110	120
m525.pep	AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVNTVSWXAANAYCA					
g525	AEFVNSHPQWQKGRIGSKQAEPAAYLKHWKNGSRSYAPKAGELKQPVNTISWFAANAYCA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m525.pep	AQGKRLPTIDWEFAGLASATQKXRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA					
g525	AQGKRLPTIDWEFAGLASATQKRLKRTRLQPHYSRLVCRRRTERPARCRQSTARTTGV					
	130	140	150	160	170	180
m525.pep	FMICTGX					
g525	FMICTGX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1493>:

a525.seq

```

1 ATGAAGTTTA CCCGGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCGC
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTCG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCCGCC ACGCAG.AAA AACGGCTCAA ACGAACCCGG
451 CTACAACCGC ACTATTCTCG ACTGGTATGC GGATGGCGAC CGGAAAGACC
501 TGCACGATGT CGGCAAAG.G TCGCCCGAAC TACTGGGGCG TTTATGATAT
551 GCACGGTCTG A

```


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This corresponds to the amino acid sequence <SEQ ID 1494; ORF 525.a>:

```
a525.pep
  1  MKFTRLLEFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101  GDLKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQXKRLKRTR
151  LQPHYSRLVC GWRPERPARC RQXVARTTGA FMICTV*
```

m525/a525 90.8% identity in 185 aa overlap

```

              10      20      30      40      50      60
m525.pep      MKYVRLFXLGAALAXTQXAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              ||::||: | |||| | ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525           MKFTRLLEFLCAALAGTQAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90      100     110     120
m525.pep      AEFVNSHPQWQKGRIGSKQAEPAYLKHHWMKNGSRSYAPKAGELKQPVTNVSWXAANAYCA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525           AEFVNSHPQWQKGRIGSKQAEPAYLKHHWMKNGSRSYAPKAGDLKQPVTNVSWFAANAYCA
              70      80      90      100     110     120

              130     140     150     160     170     180
m525.pep      AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCRRRTERPARCRXKAARTTGA
              ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
a525           AQGKRLPTIDWEFAGLASATQXKRLKRTRLQPHYSRLVCGWRPERPARCQXVARTTGA
              130     140     150     160     170     180

m525.pep      FMICTGX
              |||||
a525           FMICTVX
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1495>:

```
g525-1.seq
  1  ATGAAGTACG TCCGGTTATT TTTCCTCGGC ACGGCACTCG CCGGCACTCA
 51  AGCGGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGGCAGC TACCGCCCGC
101  TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151  GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201  CCCCCAATGG CAAAAGGCA GGATCGGTTT CAAACAGGCA GAACCCGCTT
251  ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301  GGCGAATTGA AACAGCCGGT TACCAATATT TCCTGGTTTG CCGCCAACGC
351  CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATCGAC GAATGGGAAT
401  TTGCCGGACT TGCTTCCGCC ACGCAGAAAA ACGGCTCAAA CGAACC CGGC
451  TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501  GCACGATGTC GGCAAAGACC GCCCGAACTA CTGGGGTGTT TATGATATGC
551  ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601  TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCAT CTGTGCGGGC
651  GAGCGACTCG TCCAACATATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701  GCCTGCAATC CAAATACGTC CTGCACAAC TGGGCTTCCG CTGCGCAAGC
751  CGATAA
```

This corresponds to the amino acid sequence <SEQ ID 1496; ORF 525-1.ng>:

```
g525-1.pep
  1  MKYVRLFFLG TALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
 51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101  GELKQPVTNI SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151  YNRTILDWYA DGGRKGLHDV GKDRPNYWG VYDMHGLIEW TEDFNSSLLS
201  SGNANQMFC SGASVGASDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCAS
251  R*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1497>:

```
m525-1.seq
  1  ATGAAGTATG TCCGGTTATT TTTCCTCGGC GCGGCACTCG CCGGCACTCA
 51  AGCGGGCGGCT GCCGAAATGG TTCAAATCGA AGCGGGCAGC TACCGCCCGC
101  TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
```

792

```

151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GGCGAATTAA AACAACCGGT AACCAATGTT TCCTGGTTTG CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA TTGGTATGCC GACGGCGGAC GGAAAGGCCT
501 GCACGATGTC GGCAAAGGCC GCCCGAACTA CTGGGGCGTT TATGATATGC
551 ACGGGCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGTACCA
701 GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1498; ORF 525-1>:

m525-1.pep

```

1 MKYVRLFFLG AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51 DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GELKQPVTNV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGGKRLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLSS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/g525-1 97.6% identity in 251 aa overlap

	10	20	30	40	50	60
m525-1.pep	MKYVRLFFLG	AALAGTQAAA	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL	DKYPVTNAEF
g525-1	MKYVRLFFLG	TALAGTQAAA	AEMVQIEGGS	YRPLYLKKDT	GLIKVKPFKL	DKYPVTNAEF
	70	80	90	100	110	120
m525-1.pep	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHHMK	NGSRSYAPKA	GELKQPVTNV	SWFAANAYCA
g525-1	AEFVNSHPQW	QKGRIGSKQA	EPAYLKHHMK	NGSRSYAPKA	GELKQPVTNI	SWFAANAYCA
	130	140	150	160	170	180
m525-1.pep	AQGKRLPTID	EWEFAGLASA	TQKNGSNEPG	YNRTILDWYA	DGGKRLHDV	GKGRPNYWGV
g525-1	AQGKRLPTID	EWEFAGLASA	TQKNGSNEPG	YNRTILDWYA	DGGKRLHDV	GKDRPNYWGV
	190	200	210	220	230	240
m525-1.pep	YDMHGLIEWE	TEDFNSSLSS	SGNANAQMFC	SGASIGSSDS	SNYAAFLRYG	IRTSLSQSKYV
g525-1	YDMHGLIEWE	TEDFNSSLSS	SGNANAQMFC	SGASVGSADS	SNYAAFLRYG	IRTSLSQSKYV
	250					
m525-1.pep	LHNLGFRCTS	RSX				
g525-1	LHNLGFRCS	RSX				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1499>:

a525-1.seq

```

1 ATGAAGTTTA CCCGTTACT CTTTCTCTGT GCGGCACTCG CCGGCACTCA
51 AGCGGCAGCT GCCGAAATGG TTCAAATCGA AGGCGGCAGC TACCGCCCCG
101 TTTATCTGAA AAAAGATACC GGCCTGATTA AAGTCAAACC GTTCAAACCTG
151 GATAAATATC CCGTTACCAA TGCCGAGTTT GCCGAATTG TCAACAGCCA
201 CCCCCAATGG CAAAAAGGCA GGATCGGTTC CAAACAGGCA GAACCCGCTT
251 ACCTGAAGCA TTGGATGAAA AACGGCAGCC GCAGCTATGC GCCGAAGGCG
301 GCGGATTTAA AACAACCGGT AACCAATGTT TCCTGGTTTC CCGCCAACGC
351 CTATTGCGCC GCACAAGGCA AACGCCTGCC GACCATTGAC GAATGGGAAT
401 TTGCCGGACT TGCTTCGGCC ACGCAGAAAA ACGGCTCAAA CGAACCCGGC
451 TACAACCGCA CTATTCTCGA CTGGTATGCG GATGGCGACC GGAAAGACCT
501 GCACGATGTC GGCAAAGGTC GCCCGAACTA CTGGGGCGTT TATGATATGC
551 ACGGTCTGAT TTGGGAATGG ACGGAAGATT TCAACAGCAG CCTGCTTTCT
601 TCCGGCAATG CCAACGCGCA AATGTTTTGC AGCGGCGCGT CTATCGGGTC
651 GAGCGACTCG TCCAACATG CCGCCTTCCT CCGCTACGGC ATCCGCACCA
701 GCCTGCAATC CAAATATGTC TTGCACAACT TGGGCTTCCG TTGCACAAGC
751 CGATAA

```

This corresponds to the amino acid sequence <SEQ ID 1500; ORF 525-1.a>:

a525-1.pep

```

1  MKFTRLFLC AALAGTQAAA AEMVQIEGGS YRPLYLKKDT GLIKVKPFKL
51  DKYPVTNAEF AEFVNSHPQW QKGRIGSKQA EPAYLKHHMK NGSRSYAPKA
101 GDLKQPVNTV SWFAANAYCA AQGKRLPTID EWEFAGLASA TQKNGSNEPG
151 YNRTILDWYA DGDRLDLHDV GKGRPNYWGV YDMHGLIEWE TEDFNSSLLS
201 SGNANAQMFC SGASIGSSDS SNYAAFLRYG IRTSLQSKYV LHNLGFRCTS
251 R*

```

m525-1/a525-1 97.2% identity in 251 aa overlap

```

              10      20      30      40      50      60
m525-1.pep  MKYVRLFFLGAALAGTQAAAAEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              ||::||::|| |||||
a525-1      MKFTRLFLC AALAGTQAAA AEMVQIEGGSYRPLYLKKDTGLIKVKPFKLDKYPVTNAEF
              10      20      30      40      50      60

              70      80      90     100     110     120
m525-1.pep  AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGELKQPVNTVSWFAANAYCA
              |||||
a525-1      AEFVNSHPQWQKGRIGSKQAEPAYLKHHMKNGSRSYAPKAGDLKQPVNTVSWFAANAYCA
              70      80      90     100     110     120

              130     140     150     160     170     180
m525-1.pep  AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGGRKGLHDVGKGRPNYWGV
              |||||
a525-1      AQGKRLPTID EWEFAGLASATQKNGSNEPGYNRTILDWYADGDRKDLHDVGKGRPNYWGV
              130     140     150     160     170     180

              190     200     210     220     230     240
m525-1.pep  YDMHGLIEWE TEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV
              |||||
a525-1      YDMHGLIEWE TEDFNSSLLSSGNANAQMFCSGASIGSSDSSNYAAFLRYGIRTSLQSKYV
              190     200     210     220     230     240

              250
m525-1.pep  LHNLGFRCTSRX
              |||||
a525-1      LHNLGFRCTSRX
              250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1501>:

g527.seq

```

1  atgggttttac cagtctcctt ttttcagcct gtccagttgg cggcgggtcgc
51  gcttggtcgg tctgccgtcg ggatgggagg aagtgatgcg gctcttcttc
101 tcgagctggt tgcactcttc cctcaatgct gccgttttcg cgtcttcttc
151 atacagaagc cgcgcctcgg gtgccgggag gcgttggtgg ttcaaacctt
201 taaccttgat tttatgggga aggaattga gcgtcaggtc gataatatcg
251 ccgatgtcta tgggttttact gtttttgact ttcgagccgt ttacttgaac
301 cctaccagct tcgatatgct tttgcgcaag ggaacggggtc ttgaaaaaac
351 gtgccgccca aagccatttg tccagccgca tggcggaaga atcgtgcttg
401 tctttcatatc gattttgttt gaaataattg aatttgtttc gagtttagca
451 taa

```

This corresponds to the amino acid sequence <SEQ ID 1502; ORF 527.ng>:

g527.pep

```

1  MVLPVSFFQP VOLAAVALGR SAVGMGGS DA AELVELFALF PQCCRFRVFF
51  IQKPRLCRA ALVVQTFNLD FMGKGIERQV DNIADVYGFT VFDFRAVYLN
101 PTQFDMLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1503>:

m527.seq

```

1  ATGGTTTTCAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
51  GCTTGGTCCG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTWTCG CGTCCTCTTC
151 ATACAGAAGC CGCGCTCCG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT

```

794

```

201 TAACCKTGAT TTTATAGGGA AGGG.AATtk AgCkTCaGTy GrTwATaTCG
251 CsGATGTmTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTtT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1504; ORF 527>:

```

m527.pep
  1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRXRVLf
 51 IQKPRXGCRA ALVVQTFNXD FIGKXNXASV XXIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 527 shows 90.0% identity over a 150 aa overlap with a predicted ORF (ORF 527.ng) from *N. gonorrhoeae*:

m527/g527

	10	20	30	40	50	60
m527 . pep	MVLPSVFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA					
	: : : : :					
g527	MVLPSVFFQPVQLAAVALGRSAVGMGGSDAAELVELFALFPQCCRFRVFFIQKPRLGCR					
	10	20	30	40	50	60
	70	80	90	100	110	120
m527 . pep	ALVVQTFNXDFIGKXNXASVXXIADVYGFTVFDLRAVYLNPTQFDVLLRKGTGLEKTCRP					
	: : : : : : : :					
g527	ALVVQTFNLD FMGKGI ERQVDNIADVYGFTVFDRAVYLNPTQFDMLLRKGTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527 . pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
	: : : : :					
g527	KPFVQPHGGRIVLVFHTILFEIIEFVSSLA					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1505>:

```

a527 . seq
  1 ATGGTTTTAC CAGTCTCCTT TTTTCAGCCT GTCCAGTTGG CGGCGGTCGC
 51 GCTTGGTCGG TCTGCCGTCG GGATAGGCGG AAGTGATGCG GCTGAATTGG
101 TCGAGCTGTT TGCGCTCTTC CCTCAATGTT GCCGTTTTCG CGTCCTCTTC
151 ATACAGAAGC CGGCGCTCGG ATGCCGGGCG GCGTTGGTGG TTCAAACCTT
201 TAACCTTGAT TTTATAGGGA AGGGAATTGA GCGTCAGGTC GATAATATCG
251 CCGATGTCTA TGGTTTTACT GTTTTTGACC TTCGAGCCGT TTA CTTGAAC
301 CCTACCCAGT TCGATGTGCT TTTGCGCAAG GGAACGGGTC TTGAAAAAAC
351 GTGCCGCCCA AAGCCATTTG TCCAGCCGCA TGGCGGAAGA ATCGTGCTTG
401 TCTTTCATAC GATTTTGTtT GAAATAATTG AATTTGTTTC GAGTTTAGCA
451 TAA

```

This corresponds to the amino acid sequence <SEQ ID 1506; ORF 527.a>:

```

a527 . pep
  1 MVLPSVFFQP VQLAAVALGR SAVGIGGSDA AELVELFALF PQCCRFRVLf
 51 IQKPRLGCRALVVQTFNLD FIGKGI ERQV DNIADVYGFT VFDLRAVYLN
101 PTQFDVLLRK GTGLEKTCRP KPFVQPHGGR IVLVFHTILF EIIEFVSSLA
151 *

```

m527/a527 93.3% identity in 150 aa overlap

	10	20	30	40	50	60
m527 . pep	MVLPSVFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRXRVLFIQKPRXGCRA					
	: : : : :					
a527	MVLPSVFFQPVQLAAVALGRSAVGIGGSDAAELVELFALFPQCCRFRVLFIQKPRLGCR					
	10	20	30	40	50	60

	70	80	90	100	110	120
m527.pep	ALVVQTFNXDFIGKXNXASVXXIADVYGFTVFDLRAYVLNPTQFDVLLRKGTTGLEKTCRP					
			:			
a527	ALVVQTFNLDFIGKGIERQVDNIADVYGFTVFDLRAYVLNPTQFDVLLRKGTTGLEKTCRP					
	70	80	90	100	110	120
	130	140	150			
m527.pep	KPFVQPHGGRIVLVFHTILFEIIEFVSSSLAX					
a527	KPFVQPHGGRIVLVFHTILFEIIEFVSSSLAX					
	130	140	150			

```
g528.seq
1  atggaaattc gggtaataaaa atatacggca acggctgcgt tgtttgcatt
51  tacggttgca ggctgccggc tggcggggcg gtatgagtggt ttgtccttgt
101 cccgctgggtg taagcccgaga aaacctggcg ccatcgattt ttgggatatt
151 ggcgcgcgaga gtccgctgtct ttagaggac tacgagatac cgctttcaga
201 cggcaatcgt tccgtcaggg caaacgaata tgaatccgcg caaaaatcct
251 acttttatag gaaaataggg aagtttgaag cctgcggggt ggattggcgt
301 acgcgtgacg gcaaaccctt gggttgagagg ttcaaacagg aaggtttcga
351 ctgtttggaa aagcaggggt tgcggcgcaa cggcctgtcc gagcgcgtcc
401 gatggttaa
```

g528.pep
1 MEIRVIKYTA TAALFAFTVA GCRLAGWYEC LSLSGWCKPR KPAAIDFWDI
51 GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```
m528.seq (partial)
1  ATGGAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCGCGG TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC GCCTTTCAGA
201 CGGCAATAGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAATATAGG AAGTTTGAAG C.TGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGAA AAG....
```

```
m528.pep      (partial)
      1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
     51  GGESPPSLGD YEIPLSDGNS SVRANEYESA QQSYFYRKIG KFEXCGLDWR
    101  TRDGKPLIET FKQGGFDCLE K....
```

ORF 528 shows 89.3% identity over a 121 aa overlap with a predicted ORF (ORF 528.ng) from *N. gonorrhoeae*:

```

m528/g528
      10      20      30      40      50      60
m528.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
          ||||:|||| |||:||||||| ||||| |||:||||||| ||| |||
g528      MEIRVIKYTATAALFAFTVAGCRLAGWYECLSLSGWCKPRKPAAIDFWDIGGESPLSLD
          10      20      30      40      50      60

      70      80      90      100     110     120
m528.pep  YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFQGGFDCLE
          ||||| ||||| |||||:||||||| ||||| ||||| ||||| |||||
g528      YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
          70      80      90      100     110     120

```

796

```

m528.pep      K
               |
g528           KQGLRRNGLSERVRW

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1511>:

```

a528.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCTCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1512; ORF 528.a>:

```

a528.pep
1   MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDGNR SVRANEYESA QQSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLK KQGLRRNGLS ERVRW*

```

m528/a528 95.0% identity in 121 aa overlap

```

              10      20      30      40      50      60
m528.pep      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
               |||||||
a528           MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLED
               10      20      30      40      50      60

              70      80      90     100     110     120
m528.pep      YEIPLSDGNSSVRANEYESAQQSYFYRKIGKFEXCGLDWRTRDGKPLIETFKQGGFDCLE
               |||||||
a528           YEIPLSDGNRSVRANEYESAQQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLK
               70      80      90     100     110     120

```

```

m528.pep      K
               |
a528           KQGLRRNGLSERVRW
               130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1513>:

```

g528-1.seq
1   ATGGAAATTC GGGTAATAAA ATATACGGCA ACGGCTGCGT TGTTTGCATT
51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GCGGCGGAGA GTCCGCTGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCG CAAAAATCTT
251 ACTTTTATAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGAGG TTCAAACAGG AAGGTTTCGA
351 CTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGCCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1514; ORF 528-1.ng>:

```

g528-1.pep
1   MEIRVIKYTA TAALFAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPLSLED YEIPLSDGNR SVRANEYESA QKSYFYRKIG KFEACGLDWR
101 TRDGKPLVER FKQEGFDCLE KQGLRRNGLS ERVRW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1515>:

```

m528-1.seq
1   ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCATT

```

797

```

51  TACGGTTGCA GGCTGCCGGC TGGCGGGGTG GTATGAGTGT TCGTCCCTCA
101 CCGGCTGGTG TAAGCCGAGA AAACCGGCTG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGGGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGCT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG GAGGATTTGA
351 CTGCTTGGA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1516; ORF 528-1>:

m528-1.pep..

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLTGWCKPR KPAAIDFWDI
51  GGESPPSLGD YEIPLSDG NR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQGGFDCLE KQGLRRNGLS ERVRW*

```

g528-1/m528-1 92.6% identity in 135 aa overlap

```

              10      20      30      40      50      60
g528-1.pep  MEIRVIKYTATAALFAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPLSLED
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90     100     110     120
g528-1.pep  YEIPLSDGNRSVRANEYESAQKSYFYRKIGKFEACGLDWRTRDGKPLVERFKQEGFDCLE
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90     100     110     120

              130
g528-1.pep  KQGLRRNGLSERVRWX
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1517>:

a528-1.seq

```

1  ATGGAAATTC GGGCAATAAA ATATACGGCA ATGGCTGCGT TGCTTGCAAT
51  TACGGTTGCA GGCTGCCGGT TGGCAGGTG GTATGAGTGT TCGTCCCTGT
101 CCGGCTGGTG TAAGCCGAGA AAACCTGCCG CCATCGATTT TTGGGATATT
151 GGCGGCGAGA GTCCGCCGTC TTTAGAGGAC TACGAGATAC CGCTTTCAGA
201 CGGCAATCGT TCCGTCAGGG CAAACGAATA TGAATCCGCA CAACAATCTT
251 ACTTTTACAG GAAAATAGGG AAGTTTGAAG CCTGCGGGTT GGATTGGCGT
301 ACGCGTGACG GCAAACCTTT GATTGAGACG TTCAAACAGG AAGGTTTTGA
351 TTGTTTGAAA AAGCAGGGGT TCGGCGCAA CGGTCTGTCC GAGCGCGTCC
401 GATGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1518; ORF 528-1.a>:

a528-1.pep

```

1  MEIRAIKYTA MAALLAFTVA GCRLAGWYEC SSLSGWCKPR KPAAIDFWDI
51  GGESPPSLED YEIPLSDG NR SVRANEYESA QSYFYRKIG KFEACGLDWR
101 TRDGKPLIET FKQEGFDCLE KQGLRRNGLS ERVRW*

```

a528-1/m528-1 97.0% identity in 135 aa overlap

```

              10      20      30      40      50      60
a528-1.pep  MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLSGWCKPRKPAAIDFWDIGGESPPSLED
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      MEIRAIKYTAMAALLAFTVAGCRLAGWYECSSLTGWCKPRKPAAIDFWDIGGESPPSLGD
              10      20      30      40      50      60

              70      80      90     100     110     120
a528-1.pep  YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQEGFDCLE
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      YEIPLSDGNRSVRANEYESAQSYFYRKIGKFEACGLDWRTRDGKPLIETFKQGGFDCLE
              70      80      90     100     110     120

              130
a528-1.pep  KQGLRRNGLSERVRWX
              |||::|||::|||::|||::|||::|||::|||::|||::|||::|||
m528-1      KQGLRRNGLSERVRWX
              130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1519>:

g529.seq (partial)

```

1 atgacccata tcaaaccctg cattgccgcg ctgcactca tggggcttgc
51 cgctgctcc ggcagcaaaa ccgaacagcc caagctcgac taccaaagcc
101 ggctgcaccg cctgatcaaa ctggaagtc cgctgattt gaacaacccc
151 gaccaaggca acctctaccg cctgcctgcc gggtcgggag ccgtccgcgc
201 cggggatttg gaaaaacgcc gcacaccgc cgtccaacag ccageggatg
251 ccggaagtat tgaaaagcgt caaaggcgtc cgcttcgagc ggcgacggca
301 gccaacgcct ggcttgctgt tgacggcaaa tcccccgccg aaatctccgc
351 cgctttctg.

```

This corresponds to the amino acid sequence <SEQ ID 1520; ORF 529.ng>:

g529.pep (partial)

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRAGDL EKRRTPAVQQ PADAGSIEKR QRRPLRAATA
101 ANAWLVVDGK SPAEISAAF.

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1521>:

m529.seq

```

1 ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51 CGCCTGCTCC GGCAGCAAAA CCGAACAGCC CAAGCTCGAC TACCAAAGCC
101 GGTGCGCACC CTTGATCAAA CTTGAAGTCC CACCTGATTG GAACAACCCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCGGGCG CCGTCCGCGC
201 CAGCGATTGT GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT GAAAGCGTCA AAAGTGTCGC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTCTG CCGCAAGTCT CCTGCCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAAA TCCGAAGAAC
401 CCGCCATCGG ACAATGGAA ACCGAGTGGG CGGAAAACCG CGCCAAATC
451 CCCAAGACA GCTTGGCGCG CCTCTTCGAC AAAGTCGGCT TGGGCGGCAT
501 CTACTCCACC GGCAGCGCG ACAATTCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAGCCAT GAAAGAAGTG
601 TACGGCGGCA AAGACAAAGA CACGACCGTA TGGCAGCCCT CCCCGTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTGGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAACC TACCCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACGGC AGAACTGGC GGCACCCGT GCTCGCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCCTT CCTGGTTCAA
901 AAAGCCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCAGAA CCTGTCGCCA ACGGCTCGCG CATCGTCCTG
1051 CTCAACAAAG ACGGCAGCGC ATATGCCGGC AAAGACGCAT CCGCATTATT
1101 GGGCAAACTC CATTCCGAAC TGCCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1522; ORF 529>:

m529.pep

```

1 MTHIKPVIAA LALIGLAACS GSKTEQPKLD YQSRSHRLIK LEVPPDLNNP
51 DQGNLYRLPA GSGAVRASDL EKRRTPAVQQ PADAEVLKSV KGVRLERDGS
101 QRWLVDGKS PAEIWPLLKA FWQENGFDIK SEEPAGQME TEWAENRAKI
151 PQDSLRLRFD KVGLGGIYST GERDKFIVRI EQGKNGVSDI FFAHKAMKEV
201 YGKDKDQTV WQSPSPDNL EAAFLTRFMQ YLGVGQQAE NASAKKPTLP
251 AANEMARIEG KSLIVFGDYG RNWRTVLAL DRIGLTVVGQ NTERHAFLVQ
301 KAPNESNAVT EQKPLFKRL LGKGKAEKPA EQPELIVYAE PVANGSRIVL
351 LNKDGSAYAG KDSALLGKL HSELR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 529 shows 83.5% identity over a 115 aa overlap with a predicted ORF (ORF 529.ng) from *N. gonorrhoeae*:

g529/m529

```

              10      20      30      40      50      60
g529.pep      MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNNPDQGNLYRLPA

```


m529	 MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLLPA 10 20 30 40 50 60
g529.pep	70 80 90 100 110 120 GSGAVRAGDLEKRRTPAVQQPADAGSIEKQRORPLRAATAANAWLVVDGKSPAEIFSAAFX : :: : : : ::
m529	GSGAVRASDLEKRRTPAVQQPADAЕVLKS VKGVRLER-DGSQRWL VVDGKSPA EIWPLLK 70 80 90 100 110
m529	AFWQENGFDIKSEEP AIGOMETEWAENRAKI PQDSL RRLRF DKVGLGGIYSTGERDKFIVR 120 130 140 150 160 170

```

a529.seq
1  ATGACCCATA TCAAACCCGT CATTGCCGCG CTCGCACTCA TCGGGCTTGC
51  CGCCTGCTCC GGCAGCAAAA CCGAACAGCG CAAGCTCGAC TACCAAAGCC
101 GCGTCGACCG CCGTATCAAA CTCGAAGTCC CACCTGATTT GAACAAACCC
151 GACCAAGGCA ACCTCTACCG CCTGCCTGCC GGTTCTGGGCG CCGTCCGCGC
201 CAGCGATTTG GAAAAACGCC GCACACCCGC CGTCCAACAG CCTGCCGATG
251 CCGAAGTATT TAAAGCGTCT AAAGGTGTCC GCCTCGAGCG CGACGGCAGC
301 CAACGCTGGC TCGTTGTGCA CGGCAAGTCT CATCGCGAAA TCTGGCCGCT
351 CCTGAAAGCC TTTTGGCAGG AAAACGGCTT CGACATCAA TCCGAAGAAC
401 CCGCCATCCG ACAAAATGAA ACCGAGTGGG CGGAAAAACG TGCCAAAATC
451 CCCCAGAACA GCTTGCGCCG CCTATTGCGA ACAGTCGGTT TGGGCGGGAT
501 CTACTCCACC GCGCAGCGCG ACAAAATCAT CGTCCGTATC GAACAGGGCA
551 AAAACGGCGT TTCCGACATC TTCTTCGCCC ACAAGCCAT GAAAGAAGTG
601 TACGGCGCGA AAGACAAGAA CACGACCCTA TGGCAGCCCT CCCCCTCCGA
651 TCCCAACCTC GAAGCCGCTT TCCTGACGCG CTTTATGCAA TATTTTGGCG
701 TTGACGGACA GCAGGCGGAA AACGCATCGG CAAAAAAACC TACCTTCCC
751 GCCGCCAACG AAATGGCGCG TATCGAAGGC AAAAGCCTGA TTGTCTTTGG
801 CGACTACCGC AGAAACGTGC GGCACACCGC GCTCGCCCTC GACCGCATCG
851 GGCTGACCGT CGTCGGTCAA AACACCGAAC GCCACGCTTT CCTGGTTCAA
901 AAAGCCCGA ACGAAAGCAA TGCAGTTACC GAACAAAAAC CCGGCTGTT
951 CAAACGCCTG CTGGGCAAAG GCAAAGCGGA GAAACCTGCC GAACAGCCGG
1001 AACTGATTGT CTATGCCGAG CCTGTGCGCA ACGGCTCGCG CATCGTCTTG
1051 CTCACAAAG ACGCGACCGC ATATGCGGCG AAAGACGCAT CCGCATTATT
1101 GGGCAAACTC CATTCCGAAC TGCCTTAA

```

a529.p	1	MTHIKPVIAA	LALIGLAACS	GSKTEQPKLD	YQSRSHRLIK	LEVPPDLNNP
	51	DQGNLYRLPA	GSQAVRASDL	EKRRTPAVQG	PADAEVLKSV	KGVRLERDGS
	101	QRWLVDGKS	HAEIFPLAKL	FWQENGFDIK	SEEPATGOME	TEWAENRAKI
	151	PQDSLRLRFD	TVGLGGIYST	GERDKFIVRI	EQGKNGVSDI	FFAHKAMKEV
	201	YGGKDKDTTV	WQPSPSDPNL	EAFLTRFMQ	YLGVDGQQA	NASAKKPTLP
	251	ANEMARIEG	KSLIVFGDYG	RNWRRTALAL	DRIGLTVVGQ	NTERHAFLVQ
	301	KAPNESNAV	EQKPGLFKRL	LGKGKAKEPA	EQPELIVYAE	PVANGSRIVL
	351	LNKDGSAAY	KDASALLGKL	HSELR*		

	10	20	30	40	50	60
m529.pep	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
a529	MTHIKPVIAALALIGLAACSGSKTEQPKLDYQSRSHRLIKLEVPPDLNPNPDQGNLYRLPA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m529.pep	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDVGKSPAEIWPLLKA					
a529	GSGAVRASDLEKRRTPAVQQPADAEVLKSVKGVRLERDGSQRWLVDVGKSHAEIWPLLKA					
	70	80	90	100	110	120
	130	140	150	160	170	180

800

```

m529.pep    FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDKVLGGIYSTGERDKFIVRI
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a529        FWQENGFDIKSEEPaIGQMETEWAENRAKIPQDSLRRLLFDTVLGGIYSTGERDKFIVRI
             130      140      150      160      170      180

             190      200      210      220      230      240
m529.pep    EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a529        EQGKNGVSDIFFAHKAMKEVYGGKDKDTTVWQPSDPNLEAAFLTRFMQYLGVDGQQAE
             190      200      210      220      230      240

             250      260      270      280      290      300
m529.pep    NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTVLALDRIGLTVVGQNTERHAFVQ
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a529        NASAKKPTLPAANEMARIEGKSLIVFGDYGRNWRRTALALDRIGLTVVGQNTERHAFVQ
             250      260      270      280      290      300

             310      320      330      340      350      360
m529.pep    KAPNESNAVTEQKPGFLFKRLLGKGAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
a529        KAPNESNAVTEQKPGFLFKRLLGKGAEKPAEQPELIVYAEPVANGSRIVLLNKDGSAYAG
             310      320      330      340      350      360

             370
m529.pep    KDASALLGKLHSELRX
             ||||||||||||||||
a529        KDASALLGKLHSELRX
             370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1525>:

```

g530.seq
1  atgagtgcga ggcgcggcaat gacgggtttg atatgggtca tctgtgtcatc
51 ctgtgtgatg gatattaaag tgtttgtcat gttatgccgt ccgaacgggtt
101 cagacggcat ggctatatat aaagtgtgcc tgaggcttcc agggcggcgc
151 ggacttttgc ctgtccgcct tccgtcagcg gaacgagcgg caggcgcacg
201 tgcggtccgc atccgccccaa ggcggatacc gccatttcg gtgcggcggg
251 actgggttcg cagaacatgg tgtcgtaa at cggaatcagc cggtcgttga

```

This corresponds to the amino acid sequence <SEQ ID 1526; ORF 530.ng>:

```

g530.pep
1  MSASAAMTGL IWVIVSSCVM DIKVFVMLCR PNGSDGMAIF KVVLRSLSGRR
51  GLLPVRLPSA ERAAGARAVR IRPRRIPIIS VRRDWVRRTW CRKSESAGR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1527>:

```

m530.seq
1  wTGAGTGCGA GCGCGGCAAT GACGGGTYTG ATATGGGTCA TCGTGTGCATC
51  sTGTGTGATG GATATTAAAG TGTyTGTTC GwTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGmTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGAckTTGC wTGTCGGTTT yCCGTcAGCG GAACGAGCGG CAGGCGGACG
201 TGCGGTTCGC ATCTGCCCAg GCGGATACC GCCCATTTCG GTGCGGCGGG
251 GCTGGGTTCG CAGAACATGG TGTCGTAAAT CGGAATCAGT CGGTCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1528; ORF 530>:

```

m530.pep
1  XSASAAMTGL IWVIVSSCVM DIKVXVAXCR PNGSDGMXIF KVVLRSLSGRR
51  GLLXVRFPSA ERAAGGRAVR ICPGRIPPIIS VRRGWVRRTW CRKSESVGR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 530 shows 88.8% identity over a 98 aa overlap with a predicted ORF (ORF 530.ng) from *N. gonorrhoeae*:

m530/g530

```

m530.pep    XSASAAMTGLIWVIVSSCVM DIKVXVAXCRPNGSDGMXIFKVVLRSLSGRRGLLXVRFPSA
             ||||||||||||||||||||| ||||||||| ||||||||||||| ||:||||

```

g530	MSASAAMTGLIWIVSSCVMEDIKVFVMLCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA	60
	10 20 30 40 50 60	
m530.pep	ERAAGGRAVRIICPGRIPIISVRRGWVRRTWCRKSESVGR	99
	: :	
q530	ERAAGARAVRIRPRRIPIISVRRDWVRRTWCRKSESAGR	99

```
a530.seq
1  ATGAGTGCGA GCGCGGCAAT GACGGGTTTG ATATGGGTCA TCGTGTATC
51  CTGTGTGATG GATATTAAG TGTTTGTTGC GTTATGCCGT CCGAACGGTT
101 CGGACGGCAT GGCTATATTT AAAGTTGTCC TGAGGCTTTC AGGGCGGCGC
151 GGACTTTTGC CTGTCCGCC TCCGTACAGC GAACGAGCGC CAGCGGACG
201 TGCGGTTCGC ATCTGCCCC GCGCGATACC GCCCATTCG GTGCGGCGGG
251 GCTGGGTTCC CAGAACATGG TGTCGTAAT CCGAATCAGC CGTTCGTTGA
```

a530.pep
1 MSASAAMTGL IWVIVSSCVM DIKVFVALCR PNGSDGMAIF KVVLRLSGRR
51 GLLPVRLPSA ERAAGGRAVR ICPGRIPPIS VRRGWVRTW CRKSESAGR*

```

          10          20          30          40          50          60
m530.pep  XSASAAMTGLIWVIVSSCVMDIKVXVAXCRPNGSDGMXIFKVVLRLSGRRGLLXVRFPSA
          |||||
a530       MSASAAMTGLIWVIVSSCVMDIKVFVALCRPNGSDGMAIFKVVLRLSGRRGLLPVRLPSA
          10          20          30          40          50          60

          70          80          90         100
m530.pep  ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESVGRX
          |||||
a530       ERAAGGRAVRICPGRIPPISVRRGWVRRTWCRKSESAGRX
          70          80          90         100

```

g531.seq	1	ATGACCGCCC	TACTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGTCGGCAC
51	GGCAGGCAGT	GTCTATCCCG	CCCTGCCCGG	CTTGGCATTG	ATGTTTGCCG	
101	GAACATGGCT	GCTTGCCAT	GCCGGCGGCT	ATCAAATCTA	CGGCGCAGGC	
151	ATCTTGTGGA	CGGTCGGACT	CATCAGCCTT	GGCGGCATAC	TGGCGGACTA	
201	TATGGCAGGC	ATGTTGGGGG	TAAATACAC	TGGGGCAGGC	AAACTCGCCG	
251	TCCGAGGTGC	ATTGGCCGGC	AGCATCATCG	GCATATTTT	CTCCCTTCCC	
301	GGACTAATAC	TCGGCCCCCT	TATCGGCGCG	GCGGCAGGCG	AACTGATCGA	
351	TCGGCGCAAT	ATGCTTCAGG	CAGGTAAGAG	GGGCTTGGGT	ACGCTGTTGG	
401	GGCTTGTCTT	CGGCACGGGC	TTCAAATCG	GCTGCGCGGT	ATCCATCTTG	
451	TTTATCCTGT	TGGTGAAATA	CATCGCATAC	CTGTTTTAA		

g531.pep

1	<u>MTALLVILAL</u>	<u>ALIAVGTAGI</u>	<u>VYPALPLAL</u>	<u>MFAGTWLLAY</u>	<u>AGGYQIYGAG</u>
51	<u>ILWTVGLISL</u>	<u>GGILADYMag</u>	<u>MLGVKYTGAG</u>	<u>KLAVRGALAG</u>	<u>SIIGIFFSLP</u>
101	<u>GLILGPFIGA</u>	<u>AAGELIDRRN</u>	<u>MLQAGKAGLG</u>	<u>TLLGLVVGTA</u>	<u>FKIGCAVSIL</u>
151	<u>FILLVKYIAY</u>	<u>AF</u>			

```
m531.seq
1  ATGACCGTAC TGACCGTCAT CCTCGCCCTC GCCCTGATAG CCGTCGGCAC
51  GGC GGGCATC GTTTACC CGCTGCCCG ATTGGCATG ATGTTTGCCG
101 GAACATGGCT GCTTGCC TAT GCGGGCGGCT ACCAAATCTA CGGCGCGGGC
151 GTTTGTGGA CGGTGGAGT CATCAGCCTT GCCGGCATA TGCGGAGTAA
201 TGTGGCAGC ATATGGGGGA CAAATATAC CGGAGCGGGC AAGCTCGCCG
251 TTCGCGCGCG ATTGGCGCG AGCATCATCG GCATATTTT TCCCTTCCC
301 GGACTAATAC TCGGTCCCTT TATCGGCGCG CGCGGAGCG AACTGATCGA
```

m531.pcp

```

1  MTLVTLVILAL ALIAVGTAGI VYPALPGLAL MFA GTWLLAY AGGYQIYGAG
51  VLWTVGLISL AGILADYVAG IWG TKYT GAG KLA VRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLVVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

```

Homology with a predicted ORF from *N. gonorrhoeae*

m531/q531

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGVLWTVGLISL					
	:					
g531	MTALLVILALALIAVGTAGIVYPALPGLALMFAGTWLLAYAGGYQIYGAGILWTVGLISL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTKYTGA GKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERN					
	: : : : :					
g531	GGILADYMAGMLGVKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIDRRN					
	70	80	90	100	110	120
	130	140	150	160		
m531.pep	MLQAGKAGLGTL LGLVVGTAFKIGCAVSILFILLVKYIAYLF					
g531	MLQAGKAGLGTL LGLVVGTAFKIGCAVSILFILLVKYIAYLF					
	130	140	150	160		

a531.seq

1	ATGACCGCCT	TGCTCGTCAT	CCTCGCCCTC	GCCCTGATAG	CCGCCGGTAC
51	GGCGGGCATC	GTTTACCCCG	CCCTGCCCGG	ATTGGCATTG	ATGTTTGCCG
101	GAACCTGGCT	GCTCGCCTAC	TCCGCGCGGT	ACCAAATCTA	CAGCGCGGGC
151	GTTTTGTGGA	CGGTGGACT	CTCAGCCCTT	CGCGGCATAC	TGGCGGACTA
201	TGTGGCAGGC	ATATGGGGGA	CAAAATATAC	CGGAGCGGGC	AAGCTGCGCC
251	TTCGCGGCGC	ATTGGCCGGC	AGCATCATCG	GCATATTTTT	CTCCCTTCCC
301	GGACTAATAC	TCGGTCCCTT	TATCGGCGCG	GCGCAGGGC	AACTGATCGA
351	ACGGCCCAAT	ATGCTTTCAG	CAGGTAAAGC	GGGCTTGGGT	ACGCTGTTGG
401	GGCTTATCGT	CGGTACGGCG	TTCAAAATCG	GCTGCGCCGT	ATCCATCTTG
451	TTTATCCTGT	TGGTGAATAA	CATCGCTAC	CTGTTTTTAA	

a531.pep

1 MTALLVILAL ALIAAGTAGI VYPALPGLAL MFACTWLLAY SGGYQIYGAG
51 VLWTVGLISL AGILADYVAG IWGTKYTGAG KLAVRGALAG SIIGIFFSLP
101 GLILGPFIGA AAGELIERN MLQAGKAGLG TLLGLIVGTA FKIGCAVSIL
151 FILLVKYIAY LF*

	10	20	30	40	50	60
m531.pep	MTVLTVILALALIAVGTAGIVYPALPLGLALMFAGTWLLAYAGGYQIYAGVLTWVGLISL					
	: : : : : : : : : :					
a531	MTALLVILALALIAAGTAGIVYPALPLGLALMFAGTWLLAYSGGYQIYAGVLTWVGLISL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m531.pep	AGILADYVAGIWGTKYTGACKLAVRGALAGSIIGIFFSLPLGLILGPFFIGAAAGELIERRN					

803

```

          |||
a531      AGILADYVAGIWGKYTGAGKLAVRGALAGSIIGIFFSLPGLILGPFFIGAAAGELIERN
          70      80      90      100      110      120

          130      140      150      160
m531.pep  MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          |||
a531      MLQAGKAGLGTLLGLVVGTAFAKIGCAVSILFILLVKYIAYLFX
          130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1537>:

g532.seq (partial)

```

1  atggctgaaa caatgaaaaa acagggcgat tcgcctgatt tgggtgtacgg
51  tttggaagac aggccgccgt tcggtaaatgc gctcttgagc gcggttacct
101 atcttttggc gattttcgtg ccgatgatta cgcccgcgct gattgtgggc
151 ggcgcgctgg aattgccggt ggagatgacg gcgtatctgg tgctgatggc
201 gatggttgcg tcgggtgtcg gcacttattt gcagggtcaac cgcttcgggt
251 cggtcggctc ggggatgctg tccatccagc gttaccgtca tgattgcgct
301 cggcgcgggg atgaaagagg gcggtttgag ...

```

This corresponds to the amino acid sequence <SEQ ID 1538; ORF 532.ng>:

g532.pep (partial)

```

1  MAETMKKQAD SPDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGYTLQVN RFGSVGSGML SIQRYRHDCA
101 RRGDERGRFE ...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1539>:

m532.seq

```

1  ATGAGCGGTC AGTTGGGCAA AGGTGCGGAT GCGCCTGATT TGGTGTACGG
51  TTTGGAAGAC AGGCCGCCGT TCGGTAATGC GCTCTTGAGC GCGGTTACCC
101 ATCTTTTGGC GATTTTGTG CCGATGATTA CGCCCGCGCT GATTGTGGGC
151 GGCGCGCTGG AATTGCCGGT GGAGATGACG GCGTATCTCG TGTCGATGGC
201 GATGGTTGCG TCGGGTGTG GCACTTATTT GCAGGTCAAC CGCTTCGGGC
251 CCGTCGGTTC GGGGATGCTG TCCATCCAGT CCGTGAATTT TTCGTTCTGT
301 ACCGTGATGA TTGCGCTGGG CGCGGGGATG AAAGAGGGCG GTTTGACTAA
351 GGATGCGATG ATTTGACGCG TCTTGGGCGT ATCGTTTGTC GGCGCGTTTT
401 TGGTGTGTTT CTCGGCGTGG CTTCTGCCGT ATTTGAAAAA AGTGATTACG
451 CCGACGGTCA GCGGCGTGGT CGTGATGCTC ATTGGTTTGA GTTTGGTACA
501 CGTCGGCATT ACCGATTTTC GCGGCGGCTT CGGCGCGAAG GCGGACGGCA
551 CGTTCGGCTC GATGGAAGAA TGGGGCTGG CATCGCTGGT GTTGCTGATT
601 GTGTTGGTGT TCAACTGCAT GAAAAACCG CTGTTGCGCA TGAGCGGCAT
651 TGCGGTGCGG CTGATTGCCG GCTATATCGT CGCGCTGTTT TTGGGCAAGG
701 TGGATTTTTC CGCGCTGCAA AACCTGCCGC TGGTTACGCT GCGCGTACCG
751 TTAAATACG GTTTTGCTTT CCACTGGCAC GCGTTTATTG TGGCGGGCGC
801 GATTTTCTTG TTGAGCGTGT TTGAGCGGGT CGGCGATTTA ACCGCGACGG
851 CAATGGTGTG CGACCAGCCG ATTGAAGGCG AGGAATACAC CAAACGCCTG
901 CGCGGCGGCG GTTGGCTGA CGGCTTGGTG TCGGTGATTG CGACGGCTTT
951 GGGTTGCTG CCGCTGACGA CGTTTGC GCA AAACAACGGC GTGATTGAGA
1001 TGACCGGCGT GGCTTCGCGC CATGTGGGCA AATATATTGC CGTGATTTTG
1051 GTGCTGTTGG GTCTGTTCCC CGTTGTCGGT CGCGCGTTTA CGACGATTCC
1101 GAGTCCGGTG TTGGGCGGCG CGATGGTTT GATGTTTCGGC TTAATTGCGA
1151 TTGCGGGCGT GCGGATTTTG GTCAGTCACG GCATCCGCAG GCGCGAAGCG
1201 GTGATTGCGG CAACGTCGGT CGGTTTGGGC TTGGGTGTCG CGTTTGAGCC
1251 GGAAGTGTTC AAAAACCTGC CCGTCTTGT CCAAACTCT ATTTCCGCCG
1301 GCGGCATTAC GGCAGTCTTG CTGAATTTGG TCTTGCCCGA AGATAAAACC
1351 GAGGCGGCGG TCAAGTTTGA TACCGACCAC TTGGAACACT GA

```

This corresponds to the amino acid sequence <SEQ ID 1540; ORF 532>:

m532.pep

```

1  MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51  GALELPVEMT AYLVSMAMVA SGVGYTLQVN RFGPVGSGML SIQSVNFSFV
101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI

```

201	<u>VLVFNCKMKNP</u>	<u>LLRMSGIAVG</u>	<u>LIAGYIVALF</u>	LGKVDFSALQ	NLPLVTLVPV
251	FKYGFAFDWH	AFIVAGAIFL	<u>LSVF</u> EAVGDL	TATAMVSDQP	IEGEYTKRL
301	RGGLADGLV	<u>SVIAT</u> ALGSL	PLTTFAQNGG	VIQMTGVASR	HVGKYIAVIL
351	VLLGLSPVVG	RAFTTIPSPV	<u>LGGAMVLMFG</u>	<u>LIAIAGVRIL</u>	VSHGIRREA
401	<u>VIAAT</u> SPVVG	LGVAFEPEVF	KNLPVLFQNS	ISAGGITAVL	LNVLVPEDKT
451	EEAVKFDTDH	LEH*			

ORF532 shows 91.4% identity over a 93 aa overlap with a predicted ORF (ORF 532.ng) from *N. gonorrhoeae*:

	10	20	30	40	50	60
g532.pep	MAETMKQADSPDLVYGLEDPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	: : :					
m532	MSGQLGKGADAPDLVYGLEDPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT					
	10	20	30	40	50	60
	70	80	90	100	110	
g532.pep	AYLVSMAMVASGVGTYLQVNRFGSVGSGMLSIQRYRHDCARRGDERGRFEX					
m532	AYLVSMAMVASGVGTYLQVNRFGPVGSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM					
	70	80	90	100	110	120

1	ATGAGCGGTC	AGTTGGGCAA	AGGTGCGGAT	GCGCCTGATT	TGGTGTACGG
51	TTTGGAGGAT	AGGCCGCCGT	TCGGTAATGC	GCTCTTGAGC	GCGGTTACCC
101	ATCTTTTGGC	GATTTTTTGTG	CCGATGATTA	CGCCCGCGCT	GATTGTGGGC
151	GGCGCGCTGG	AATTGCCGGT	GGAGATGACG	GCGTATCTCG	TGTCGATGGC
201	GATGGTTGCG	TCGGGTGCTG	GCACTTATT	GCAGTCAAC	CGCTTCGGGC
251	CGGTGCGTTC	GGGGATGCTG	TCCATCCAGT	CGGTGAATT	CTCGTTCGTT
301	ACCGTCATGA	TTGCGCTCGG	CGCGGGGATG	AAAGAGGGCG	GTTTGACTAA
351	GGATGCGATG	ATTTGACGCG	TCTTGGGCGT	ATCGTTTGTG	GGCGCGTTTT
401	TGGTGTGTTT	TTCGGCGTGG	CTTCTGCCGT	ATTTGAAAAA	AGTGATTACG
451	CCGACGGTCA	GCGGTGTGGT	GGTGATGCTG	ATCGGCTTGA	GTTTGGTACA
501	CGTCGGTATT	ACCGATTTCG	GCGGCGGCTT	CGGCGCAAAG	GCGGACGGCA
551	CGTTGCGCTC	GATGAAAAAC	TTGGGGCTGG	CATCGTGGT	GCTGCTGATT
601	GTGCTGGTGT	TCAATTGCAT	GAAAAACCCG	CTGCTGCGGA	TGAGCGGCGAT
651	TGCGGTGCGT	CTGATTGCCG	GCTATATCGT	CGCGCTGTTT	TTGGGCAAGG
701	TGGATTTTTT	GGCACTGCAA	AACCTGCCGC	TGGTTACGCT	GCCCGTACCG
751	TTTAAATATG	GTTTTGCTTT	TGACTGGCAC	GCATTTATTG	TGGCGGGTGC
801	GATTTTCTTG	TTGAGCGTGT	TTGAGGCGGT	CGGCGATTG	ACGGCGACGG
851	CAATGGGTGTC	CGACCAGCCG	ATTGAAGGCG	AGGAATACAC	CAAACGCTTG
901	CGCGGCGGCG	TGTTGGCGGA	CGGCTTGGTG	TCGGTGATTG	CGACGGCTTT
951	GGGTTGCTG	CCGCTGACGA	CGTTTGACA	AAACAACGGC	GTGATTTCAGA
1001	TGACCGGCGT	GGCTTCGCGC	CATGTGGGCA	AATATATTGC	CGTGATTTTG
1051	GTGCTGTTGG	GTCTGTTCCC	CGTTGTCGGA	CGCGCGTTTA	CGACGATTCC
1101	GAGTCCGGTG	TTGGGCGGCG	CGATGGTTTT	GATGTTGCGC	TTGATTGCGA
1151	TTGCGGGCGT	GCGGATTTTG	GTCAGCCACG	GCATCCGCAG	GCGCGAAGCG
1201	GTAATTGCGG	CAACGTCCGT	CGGTTTGGGC	TTGGGTGTCG	CGTTTGAGCC
1251	GGAAGTGTTT	AAAAACCTGC	CCGTCTTGTT	CCAAAACTCT	ATTTCCGCCG
1301	GCGGCATTAC	GGCAGTCTTG	CTGAATTTGG	TCTTGCCCGA	AGATAAAACC
1351	GAGGCGGCGG	TCAAGTTTGA	TACCGACCAC	TTGGAACACT	GA

1 MSGQLGKGAD APDLVYGLED RPPFGNALLS AVTHLLAIFV PMITPALIVG
51 GALELPVEMT AYLVSMMAMVA SGVGTYLQVN RFGPVGSGML SIQSVNFSFV

805

```

101 TVMIALGAGM KEGGLTKDAM ISTLLGVSFV GAFLVCFSAW LLPYLKKVIT
151 PTVSGVVVML IGLSLVHVGI TDFGGGFGAK ADGTFGSMEN LGLASLVLLI
201 VLVFNCMKNP LLRMSGIAVG LIAGYIVALF LGKVDFSALQ NLPLVTLPPV
251 FKYGFAFDWH AFIVAGAIFL LSVFEAVGDL TATAMVSDQP IEGEEYTKRL
301 RGGVLADGLV SVIATALGSL PLTTFAQNNG VIQMTGVASR HVGKYIAVIL
351 VLLGLFPVVG RAFTTIPSPV LGGAMVLMFG LIAIAGVRIL VSHGIRRREA
401 VIAATSVGLG LGVAFEPEVF KNLPVLFQNS ISAGGITAVL LNLVLPEDKT
451 EAAVKFDTDH LEH*

```

m532/a532 100.0% identity in 463 aa overlap

	10	20	30	40	50	60
m532.pep	MSGQLGKGADAPDLVYGLED	RRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT				
a532	MSGQLGKGADAPDLVYGLED	RRPPFGNALLSAVTHLLAIFVPMITPALIVGGALELPVEMT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m532.pep	AYLVSMAMVASGVGTYLQVNRFG	PGVSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM				
a532	AYLVSMAMVASGVGTYLQVNRFG	PGVSGMLSIQSVNFSFVTVMIALGAGMKEGGLTKDAM				
	70	80	90	100	110	120
	130	140	150	160	170	180
m532.pep	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
a532	ISTLLGVSFVGAFLVCFSAWLLPYLKKVITPTVSGVVVMLIGLSLVHVGITDFGGGFGAK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m532.pep	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRMSGIAVG	LIAGYIVALFLGKVDFSALQ				
a532	ADGTFGSMENLGLASLVLLIVLVFNCMKNPLLRMSGIAVG	LIAGYIVALFLGKVDFSALQ				
	190	200	210	220	230	240
	250	260	270	280	290	300
m532.pep	NLPLVTLPPVPFKYGFADFWDHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
a532	NLPLVTLPPVPFKYGFADFWDHAFIVAGAIFLLSVFEAVGDLTATAMVSDQPIEGEEYTKRL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m532.pep	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASR	HVGKYIAVILVLLGLFPVVG				
a532	RGGVLADGLVSVIATALGSLPLTTFAQNNGVIQMTGVASR	HVGKYIAVILVLLGLFPVVG				
	310	320	330	340	350	360
	370	380	390	400	410	420
m532.pep	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRRREAVIAATSVGLGLGVAFEPEVF					
a532	RAFTTIPSPVLGGAMVLMFGLIAIAGVRILVSHGIRRREAVIAATSVGLGLGVAFEPEVF					
	370	380	390	400	410	420
	430	440	450	460		
m532.pep	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
a532	KNLPVLFQNSISAGGITAVLLNLVLPEDKTEAAVKFDTDHLEHX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1543>:

```

g535.seq
1  atgccctttc ccgttttcag acaantatatt gcttngtcct tgctacggtt
51  ttttgccgta ggtcggattc tcgaatccga catttccaac agcggttttt
101 cggaaacgat aaacgcgtca aatgtttttt ttgtcggata cgaatatccg
151 gcctgcattt caaatttaca tcgcttccaa ttctgcaaac ttggtatcca
201 gttctttcac gccctgtttg ccgaagttag ttggtcagtcg ggcggattcg
251 cctttgtctg cggcatcgat aatcacgccg gtgccgaatt tggcgtgacg
301 gacgttttgt ccgatgcgga agcctgcgta ggtttgcggc tgtttgaagt

```

806

```

351 catcgatgat tttgtcccggt tgtacgggtgg tttggcgcggt gttgccgtag
401 ctgtcgaagg cgggtttttt gacggacagg tagtgcaata cttctggcgg
451 gatttcttcg acgaagcggg atgcgatgcc gaattgggtt tgtccgtgca
501 gcatgcgctg ctgtgccatg gtgatgtaga ggcgtttgcg ggcgcgggtg
551 atggcgacgt acatgaggcg gcgttcttct tgcaggccgc cgcgctcggc
601 aaggctcatt tcgctgggga aacgccctc ttccataaccg gtgaggaaga
651 cggcgctgaa ttccaagcct ttggcgcggt ggacggtcat cagttggacg
701 gctttttcgc ctgccctgc ttggttttcg ccggattcga gggcgcggtt
751 gctcaagaag gcgaggatgg ggaaggcggg atcgtctga

```

This corresponds to the amino acid sequence <SEQ ID 1544; ORF 535.ng>:

g535.pep

```

1 MPFPVFRQXF AXSLLRFFAV GRILESDISN SGFSETINAS NVFFVGYEYP
51 ACISNLHRFQ FRKLGIQFFH ALFAEVDGQS GGFAFVCGID NHAGAEFGVT
101 DVLSDAEACV GLRLFVEIDD FVPLYGGLAR VAVAVEGGFF DGQVVQYFWR
151 DFFDEAGCDA ELGLSVQHAL LCHGDVEAFA GAGDGDVHEA AFFFEAAALG
201 KAHFAGETPL FHTGEEDGVE FQAFGGVDGH QLDGFFACPC LVFAGFEGGV
251 AQEGEDGEGG IV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1545>:

m535.seq

```

1 aTGCCCTTtC CCGTTTTCAG ACGGCCTTTT GCTTTGTCCT TACTtACGTT
51 TTTTGCCGTA AGTCAGATTC TTGTATCCGA CATTCCAAC AGCGGTGTTT
101 CGGAAACAAT AGACCGCTCA AATGTTTTTG TCGGATACGA ATATCCGACC
151 TACATTTCAA ATTTACATCT CTCCAATTT CGCAAATTTG GTGTCCAAC
201 CTTTCACGCC CTGTTTGCCG AAATTGATGG TCAGTCGGGC GGATTGCGCT
251 TTATCTGCGG CATCGATAAT CACGCCGGTG CCGAATTTGG CGTGGCGGAC
301 GTTTTGTCCG ATACGGAAAC CTGCGTAGGT TTGGGGCTGT TTGTAGTCGT
351 CGATGATTTT ATCTTTGGAT GCGGCGGTTT GGCGCGTGTT GCCGTAAC
401 TCGTAGGCAG GCTTTTTGAC GGACAGGTAG TGCAATACTT CGGGTGGGAT
451 CTCTTCGACG AAGCGGGAGA CGATGCCGAA TTGGGTTTGT CCGTGCAGCA
501 TGCGTTGTTG CGCCATGGTG ATGTAGAGGC GTTTCGGGC GCGGGTGATG
551 GCGACGTACA TGAGGCGGCG TTCTTCTTCG AGGCCGCCGC GTTCGGCAAG
601 GCTCATTTTC CTGGGAAGC GGCCTTCTTC CATGCCGGTG AGGAAGACGG
651 CGTTAAATTC CAAGCCTTTG GCGGCGTGGA CGTCATGAG TTGGACGGCC
701 TTTTCGCCTG CGCCTGCCTG GTTTTCACCG GATTCGAGGG CGGCATTGCT
751 TAGGAAGGCG AGAATGGGGA AGGCGGGGTC GTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1546; ORF 535>:

m535.pep

```

1 MPFPVFRFRPF ALSLLTFFAV SQILVSDISN SGVSETIDAS NVFVGYEYPT
51 YISNLHLFQF RKLGVQLFHA LFAEIDGQSG GFAPICGIDN HAGAEEFGVAD
101 VLSDTETCVG LGLFVVVDDF IFGCGGLARV AVTVVGRFLD GQVVQYFGWD
151 LFDEAGDDAE LGLSVQHALL RHGDVEAFAG AGDGDVHEAA FFEEAAAFGK
201 AHFAGEAAFF HAGEEDGVKF QAFGGVDGHE LDGLFACACL VFTGFEGGIA
251 XEGENGEGBV V*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 535 shows 80.9% identity over a 262 aa overlap with a predicted ORF (ORF 535.ng) from *N. gonorrhoeae*:

m535/g535

```

          10      20      30      40      50      59
m535.pep  MPFPVFRFRPFALSLLTFFAVSQILVSDISNSGVSETIDASNVF-VGYEYPTYISNLHLFQ
          |||||: || || | |||: || ||||| |||||: ||||| ||
g535      MPFPVFRQXFAXSLLRFFAVGRILESDISNSGFSETINASNVFFVGYEYPACISNLHRFQ
          10      20      30      40      50      60

          60      70      80      90      100     110     119
m535.pep  FRKLGVLFLHALFAEIDGQSGGFAPICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDD
          |||||: ||||| |||||: ||||| |||||: ||||| || |||
g535      FRKLGIQFFHALFAEVDGQSGGFVFCGIDNHAGAEFGVTDVLSDAEACVGLRLFVEIDD
          70      80      90      100     110     120

```


	120	130	140	150	160	170	179
m535.pep	FIFGCGGLARVAVTVVGRFLFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFA						
	: : : :						
g535	FVPLYGGLARVAVAVEGGFFDGQVVQYFWRDFFDEAGCDAELGLSVQHALLCHGDVEAFA						
	130	140	150	160	170	180	
	180	190	200	210	220	230	239
m535.pep	GAGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKFQAFGGVDGHELDGLFACAC						
	: : : : : : :						
g535	GAGDGDVHEAAFFFEAAALGKAHFAGETPLFHTGEEDGVFQAFGGVDGHQLDGGFFACPC						
	190	200	210	220	230	240	
	240	250	260				
m535.pep	LVFTGFEGGIAXEGENGEGGVV						
	: : : :						
g535	LVFAGFEGGVAQEGEDGEGGIV						
	250	260					

```

a535.seq (partial)
1 TTCAGACGGC CTTTTCGCTT GTCTTGCTA CAGTTTTTTG CCATAGGTCG
51 GATTCTCGAA TCCGACATT CCAACAGCGC TTTTTCGGAA ACGTAAAGCG
101 CGTCAAATAT TTTTGTGCGA TACGAGTATC CAGCCTGCAT ACAGAAATTTA
151 CATCGCTTCC AATTTCGCAA ACTTGGTGTC CAACTCTTTC ACGCCCTGTT
201 TGCCGAAATT GATGGTCAGT CGGGCGGATT CGCTTTTATC TGCGGCATCG
251 ATAATCACGC CGGTGCCGAA TTTGGCGTGG CGGACGTTTT GTCCGATAACG
301 GAAACCTGCG TAGTTTGGG GCTGTTGTA GTCTGTCGAT ATTTTGTCTT
351 TGGGCGCGGC GAGTTTGGCG GTGTTGCCAT AGCGTCTGTA GGGGGGTTTT
401 TTGACGGACA GGTAGTGCAA TACTTCGGGC GGGATTTCCT CGACGAAGCG
451 GGAGACGATG CCGAATTGGG TTTGTCCGTG CAGCATGCGT TGTTGCGCCA
501 TGGTGATGTA GAGGCGTTTG CGGGCGCGGG TGTATGGCGAC GTACATCAGG
551 CGGCGTTCTT CTTTCGAGGCC CGCGCGTTCG GCAAGGCTCA TTTCGCTGGG
601 GAAGCGGCCT TCTTCCATGC CGGTGAGGAA TACGGCGTTA AATTCCAAGC
651 CTTTGGCGGC GTGCACGCTC ATGAGTTGTA CGGCTTTTTT GCCGCGCCT
701 GCTTGGTTTT GCCTGGATTC GAGAGCAGCA TTGCTTAGGA AAGCGAGGAT
751 GGGGAAGGCG GGGTCGTCTG A

```

```

a535.pep      (partial)
  1  FRRPFALSLL QFFAIGRILE SDISNSGFSE TIDASNIFVG YEYPACISNL
  51  HRFQFRKLGV QLFHALFAEI DGQSGGFAFI CGIDNHAGAE FGVADVLSDT
101  ETCVGLGLFV VVDDFVFGRG GLARVAIAVV GGFEDGQVVQ YFGRDFFDEA
151  GDDAELGLSV QHALLRHGDV EAFAGAGDGD VHQAFFFEEA AAFGKAHFAG
201  EAAFFVHAGEE YGVKQFAFGG VHGHELYGFF ARACLVFAGF ESSIA*ESED
251  GEGGVV*

```

	10	20	30	40	50	60
m535.pep	MPFPVFRFPFALSLLTFFAVSQILVSDISNSGVSETIDASN VFVG YEYP TYISNLHLFQF					
	: : : : : :					
a535	FRRPFALSLLQFFAIGRILES DISNSGFSETIDASN IFVG YEYPACISNLHRFQF					
	10	20	30	40	50	
	70	80	90	100	110	120
m535.pep	RKLGVQLFHALFAEIDGQSGGF AFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	: : : : : :					
a535	RKLGVQLFHALFAEIDGQSGGF AFICGIDNHAGAEFGVADVLSDTETCVGLGLFVVVDDF					
	60	70	80	90	100	110
	130	140	150	160	170	180
m535.pep	IFGCGGLARVA VTVVGR LFDGQVVQYFGWDLFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	: : : : : : : : :					
a535	VFGRGGLARVA IAVVGGFFDGQVVQYFGRDFFDEAGDDAELGLSVQHALLRHGDVEAFAG					
	120	130	140	150	160	170

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	190	200	210	220	230	240
m535.pep	AGDGDVHEAAFFFEAAAFGKAHFAGEAAFFHAGEEDGVKQAFGGVDGHELDGLFACACL					
	:					:
a535	AGDGDVHQAAFFFEAAAFGKAHFAGEAAFFHAGEEYGVKQAFGGVHGHELYGFFARACL					
	180	190	200	210	220	230
	250	260				
m535.pep	VFTGFEGGIAXEGENEGGVVX					
	: : :					
a535	VFAGFESSIAXESEDGEGGVVX					
	240	250				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1549>:

g537.seq

```

1  atgaaatccc tttttatttg gctgcttcta ttgggctcgg cggcaggcgt
51  tttctaccat acccaaaacc aatccctgcc cgcgggcgaa cttgtctatc
101 cgtccgcacc gcaaatcagg gacggcgggc atgcgctgca ctacctcaac
151 cgcacccgca cacaatcggg ttgacgcgct ctggcacacg cgccggtttt
201 ggaaaattcc gcccgcaggc acgcacgcta tctcacgctc aatcccgaag
251 acggacacgg cgaacacccat cccgacaatc cgcactacac cgcacaaaag
301 ctgaccgaac gcacacgcct tgccgggtat ctctacaacg gcgtgcatga
351 aaacatcagc acggaagagg aagccgccga atcgtccgac agcgacatcc
401 gcacgcagca acgccaagtg gacgctttga tgagcgcaat ctaccaccgc
451 ctttcgctgc ttgaccgcca taccgacgaa gcagggtcgg catttgtgctg
501 cgaaaacggc aaaaccgtcc tcgtattcaa tcagggcaac ggcagcttcg
551 agcgcgcctg tgcaaaagga aggcggcgagc cggaagcagg acggaatat
601 taccgcaacg cttgccacaa cgggtgcggc gtttatgctg acgaagccat
651 gcccgtaacg gaattgcttt ataccgccta tccggttggc ggcggcgctc
701 tgccttattt ttacggggaa cgtcccgacc cgtgcccga atatgaaatc
751 acaggcaatc ctgccagcat tgatttttcc gaggcggcag gcaaaattgc
801 gatgaaaagt ttcaagctgt atcagggtaa aaacgaaatc cgccccgtca
851 ggggttttaac cgcgggcaac gaccctaacg gcaggctgac cgcgcaccaa
901 ttccgccttt tcccgtcaa acctttggaa tacggcacgc tttatacggc
951 ggtattcgac tatgtccgca acggacggca cgcgcaggcg aaatggcagt
1001 ttagaaccgg aaaaccgat tacccttatt ttgaggtaaa cggcgcgag
1051 acacttgctg ttagaaaagg cgaaaaatat ttcattccact ggcgcggacg
1101 ctggtgtctg gaagcgtgta cccgttatac ctaccggcgg cagttcggca
1151 acagcctgtc catactccgg caggaagcgg gcggcattgt cttcagcgtc
1201 agcggaatgg cgggaagccg catcaggctt actccggaag acagcccgga
1251 acgcggtgta accctttatt tgaggattg a

```

This corresponds to the amino acid sequence <SEQ ID 1550; ORF 537.ng>:

g537.pep

```

1  MKSLFIWLLL LGSAGVFIYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
51  RIRTQIGLHA LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
101 LTERTRLAGY LYNVHENIS TEEEAESSD SDIRTQQRQV DALMSAIYHR
151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GSFERACAKG RROPEAGRKY
201 YRNACHNGAA VYADEAMPVT ELLYTAYPVG GGALPYFYGE RPDPVPEYEI
251 TGNPASIDFS EAAGKIAMKS FKLYQGKNEI RPVRVLTAGN DPNGRLTAHQ
301 FALFPLKPLE YGTLYTAVFD YVRNGRHAQA KWQFRTRKPD YPYFEVNGGE
351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRR QFGNSLSILR HEAGGIVFSV
401 SGMAGSRIRL TPEDSPERGV TLYLQD *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1551>:

m537.seq (partial)

```

1  ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCAGGCGT
51  TTTCTACCAT ACCCAAaMCC AATCCCTGCC CGCGGCGGAA CTTGTCTATC
101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
151 CGCATCCGAG CCCAAATCGG TTTGCACAAG CTGGCACACG CGCCGTTTTT
201 GGAAAACTCC GCCCGCAGGC ACGCAAGCTA CCTCACGCTC AATCCCGAAG
251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG

```

809

301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAAG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCTAC TTGACCGCCA TACGGATGAG TCAGGAGCGG CATT...

This corresponds to the amino acid sequence <SEQ ID 1552; ORF 537>:

m537.pep (partial)
 1 MKSLFIRLLL LGSAAGVFYH TQXQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHASYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDRHTDE SGAA...

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 537 shows 95.7% identity over a 164 aa overlap with a predicted ORF (ORF 537.ng) from *N. gonorrhoeae*:

m537/g537

m537.pep	10	20	30	40	50	60
	MKSLFIRLLL LGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN RIRAQIGLHK					
g537	MKSLFIWLLL LGSAAGVFYHTQNQSLPAGELVYPSAPQIRDGGDALHYLN RIRITQIGLHA					
	10	20	30	40	50	60
m537.pep	70	80	90	100	110	120
	LAHAPVLENSARRHASYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
g537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
m537.pep	130	140	150	160		
	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDRHTDESGAA					
g537	TEEEAESSDSDIRTQQRQVDALMSAIYHRLSLDRHTDEAGAAVRENGKTVLVFNQGN					
	130	140	150	160	170	180
g537	GSFERACAKGRRQPEAGRKYRNACHNGAAVYADEAMPVTELLYTAYPVGGGALPYFYGE					
	190	200	210	220	230	240

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1553>:

a537.seq
 1 ATGAAATCCC TTTTATTTCG GCTGCTCCTG TTGGGTTCGG CGGCCGGCGT
 51 TTTCTATCAT ACCCAAAACC AATCCCTGCC CGCGGGCGAA CTTGTCTATC
 101 CGTCCGCACC GCAAATCAGG GACGGCGGCG ATGCGCTGCA CTACCTCAAC
 151 CGCATCCGCG CCCAATCGG TTTGCACAAG CTGGCACACG CGCCGTTT
 201 GGAAAATTCC GCGCGCAGGC ACGCACGCTA TCTCAGCTC AATCCCGAAG
 251 ACGGACACGG CGAACACCAT CCCGACAATC CGCACTACAC CGCACAAAAG
 301 CTGACCGAAC GCACACGCCT TGCCGGGTAT CTCTACAACG GCGTGCATGA
 351 AAACATCAGC ACGGAAGAGG AAGCCGCCGA ATCGTCCGAC AGCGACATCC
 401 GCACGCAGCA ACGCCAAGTG GACGGATTAA TGAGCGCAAT CTACCACCGC
 451 CTTTCCTAC TTGACCGCCA TACGGATGAG GCAGGAGCGG CATTGTGCG
 501 CGAAAACGGT AAAACCGTTC TCGTATTCAA TCAGGCAAC GGCAGTTT
 551 AGCGGCATTG CGCCCAAGGC AGAAATCAGC CGGAAGCAGG ACGGAAATAT
 601 TACCGCAACG CCTGCCATAA CGGTGCGGTC GTGTACACG ACGAAGCCAT
 651 GCCCGCACAG GAGCTGCTCT ATACAGCCTA TCCCGTCGGC AACGGCGCAC
 701 TGCCTTATTT CCACGGCGAG CGTCCAGACC CCGTGCCGGA ATATGAAATC
 751 ACGGGCAATC CTGCCAGCAT TGATTTTCC GAGGCGCGAG GCAAATATAC
 801 GATGAAAAGT TTCAAGCTGT ATCAGGGTAA AAACGAAATC CGCCCCGTCA
 851 GGGTTTAAAC CGCCGGCAAC GACCCCAACG GCAGGCTGAC CGCGTACCAA
 901 TTCGCGCTTT TCCCGCTCAA GCCTTTGGAA TACGGTACGC TTTATACGGC
 951 GGTATTCGAC TATGTCCGCA ACGGACGGCG CGCGCAGGCG AAATGGCAGT
 1001 TTAGAACCGG AAAACCCGAT TACCCTTATT TTGAGGTAAA CGGCGCGCAG
 1051 ACACTTGCGG TTAGAAAAGG CGAAAAATAT TTCATCCACT GGC GCGGACG
 1101 CTGGTGTTTG GAAGCGTGA CCCGTTATAC CTACCGGCAG CGACCCGGCA

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1151 GCCGCCTGTC CATAGGAAGG CACAAGGCGG GCGGCATCGT CTTACAGCGTT
 1201 GACGGAATGG CGGGCAGCCG CATCACGCTT GCACCGGAAG GAGAAACGGA
 1251 ACGAGGCGTA ACCCTTTATT TACAGGATTG A

This corresponds to the amino acid sequence <SEQ ID 1554; ORF 537.a>:

a537.pep
 1 MKSLFIRLLLL LGSAAGVFYH TQNQSLPAGE LVYPSAPQIR DGGDALHYLN
 51 RIRAQIGLHK LAHAPVLENS ARRHARYLTL NPEDGHGEHH PDNPHYTAQK
 101 LTERTRLAGY LYNGVHENIS TEEEAESSD SDIRTQQRQV DGLMSAIYHR
 151 LSLDDRHTDE AGAAFVRENG KTVLVFNQGN GRFERHCAQG RNQPEAGRKY
 201 YRNACHNGAV VYTDEAMPAQ ELLYTAYPVG NGALPYFHGE RPDVPVEYEI
 251 TGNPASIDFS EAAGKITMKS FKLYQGKNEI RPYRVLTAGN DPNGRLTAYQ
 301 FALFPLKPLE YGTLYTAVFD YVRNGRRAQA KWQFRTRKPD YPYFEVNGGE
 351 TLAVRKGEKY FIHWRGRWCL EACTRYTYRQ RPSRLSISR HKAGGIVFSV
 401 DGMAGSRITL APEGETERGV TLYLQD*

m537/a537 98.2% identity in 164 aa overlap

	10	20	30	40	50	60
m537.pep	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN					
a537	MKSLFIRLLLLGSAAGVFYHTQXQSLPAGELVYPSAPQIRDGGDALHYLN					
	10	20	30	40	50	60
	70	80	90	100	110	120
m537.pep	LAHAPVLENSARRHASLYTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
a537	LAHAPVLENSARRHARYLTLNPEDGHGEHHPDNPHYTAQKLTERTRLAGYLYNGVHENIS					
	70	80	90	100	110	120
	130	140	150	160		
m537.pep	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDDRHTDESGAA					
a537	TEEEAESSDSDIRTQQRQVDGLMSAIYHRLSLDDRHTDEAGAAFVRENGKTVLVFNQGN					
	130	140	150	160	170	180
	190	200	210	220	230	240
a537	GRFERHCAQGRNQPEAGRKYRNACHNGAVVYTDEAMPAQELLYTAYPVGNGALPYFHGE					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1555>:

g538.seq
 1 atgtcaggta gaacaggacg gaacagtgcc actcaggcgc aaccggaacg
 51 cgtcatgctg gtgggcgtaa tgttgataa agatgatacg ggcagcaatg
 101 ccgccgctct gaacgggtttt cagacggcat tggcggaaagc cgtcagagctg
 151 gtcaaagcgg cgggcggcga ttccgtacgc gtggagactg ccaaacgcga
 201 ccgccgcac actgcgctgt ttgtcggcac gggcaaggcg gcggagctgt
 251 cggaagcagt tgccgcagac ggcattgatt tggctgtatt caaccacgaa
 301 cttactcca cgcaggaacg caatttgga aaaatcctcc aatgccgcgt
 351 attggacaga gtggggctga ttctggcgat ttctgcccgc cgcgccgcga
 401 cgcaggaaag caggctgcaa gtcgagttgg cgcaattgag ccatttggcg
 451 ggacgcttga tacgcggtta cggacatttg caaagccagc gcggcggtat
 501 cggcatgaaa gggccgggag aaaccaaact ggaaaccgac cgccgattaa
 551 ccgcccatcg gatcaacgcc ttgaaaaaac agcttgccaa cctcaaaaaa
 601 cagcgcgccc tgcgcgcgaa gtcccgcgag tcgggcagaa tcaaaacggt
 651 tgcgctggtc ggctatacca atgtcggcaa atccagcctg ttcaaccggc
 701 tgaccaagtc gggcatatat gcgaaagacc agcttttcgc cactctcgac
 751 acgacggcgc ggcggctgta catcagtcgc gcatgcagca ttatcctgac
 801 cgataccgct ggattcgtca gcgatctgcc gcacaaactg atttccgcct
 851 tttccgccac cttggaagaa accgtgcaag ccgatgtgct gctgcacgct
 901 gtcgatgctg ccgccgggaa cagcgggag cagattgaag acgtggaaaa
 951 cgtactgcaa gaaatccatg cccacgatat tccgtgcata aagggtgtaca
 1001 acaaaaccga cctgctgccg tctgaagaac aaaacacggg catatggcgc
 1051 gacgctgcgg gaaaaattgc cgccgtccgc atttccgttg ctgaaaaatac

This corresponds to the amino acid sequence <SEQ ID 1556; ORF 538.ng>:

```
g538.pep
  1  MSGRTGRNSA TQAQPERVML VGVMLDKDDT GSNAARLNGF QTALAEAVEL
 51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101  LTPTQERNLE KILQCRVLDL RGLILAIFAR RARTQEGRLQ VELAQLSHLA
151  GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLTAHRINA LKKQLANLKK
201  QRALRRKSRE SGRIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
251  TTARRLYISP ACSIIITDTV GFVSDLPKHL ISAFSATLEE TVQADVLLHV
301  VDAAARNNGQ QIEDVENVLQ EIHADIPCI KVYNKTDLLP SEEQNTGIWR
351  DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1557>:

```
m538.seq
  1  ATGACAGGCA GAACAGGCGG CAACGGCAGT ACCCAAGCGC AACCCGAACG
 51  CGTCATGCTG GTGGGCGTAA TGTTGGACAA AGATGGTACG GGCAGTAGTG
101  CCGCCCGTCT GAACGGTTTT CAGACGGCAT TGGCGGAAGC TGTCGAGCTG
151  GTCAAAGCGG CGGGCGGCGA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201  CCGTCCGCAC ACCGCGCTGT TTGTCCGCAC GGGCAAGGCG GCGGAGCTGT
251  CAGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301  CTCACGCCCA CGCAGGAACG CAACCTTGAA AAAGAACTsA AATGCCGCGT
351  ATTGACAGAG GTAGGGCTGA TTCTGGCGAT TTTCGCTCGC CGCGCCCGCA
401  CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CGCAATTGAG CCATTTGGCG
451  GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501  CGGCATGAAA GGCCCGGCGG AAACCAAACG GGAAACCGAC CGCCGATTGA
551  TCGCCCATCG GATCAATGCC TTGATAAAAC AGCTTGCCAA CCTCAAAAAA
601  CAGCGCGCCC TCGCGCCGAA GTChCGCGAA TCGGGCACAA TCAAAACGTT
651  TCGCTGGTGC GGCTATACAA ATGTCGAAA ATCCAGCCTG TTCAACCGGC
701  TGACAAAGTC GGGCATATAT GCAAAGGACA AGCTTAGTCC CGAATGCAGC
751  ATTATCCTGA CCGATACCGT CGGATTCGTn AGCGATCTGC CGCacAAACT
801  GATTTCGGCC TTTTCgCC.A CGCTGGAAGA AACCGCGCAA GCCGATGTGC
851  TGCTGCACGT CGTCGATGCC GCCGCTCCGA ACAGCGGACA GCAGATTGAA
901  GACGTGGAAA ACGTACTGCA AGAAATCCAT GCCGGCGATA TTCCGTGCAT
951  cAAGGTGTAC AACAAAACCG ACCTGCTGCC GTCTGAAGAA CAAAACACGG
1001 GCATATGGCG CGACGCTGCG GGAAAAATTG CCGCCGTCCG CATTTCGGTT
1051 GCTGAAAATA CCGGTATAGA CGCACTGCGC GAAGCcATTG CCGAGTCTTG
1101 TGCCGCCGCA CCAAACACAG ACGAAACCGA AATGCCATGA
```

This corresponds to the amino acid sequence <SEQ ID 1558; ORF 538>:

```
m538.pep
  1  MTGRTGGNGS TQAQPERVML VGVMLDKDGT GSSAARLNGF QTALAEAVEL
 51  VKAAGGDSVR VETAKRDRPH TALFVGTGKA AELSEAVAAD GIDL VVFNHE
101  LTPTQERNLE KELKCRVLDL RGLILAIFAR RARTQEGRLQ VELAQLSHLA
151  GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LIKQLANLKK
201  QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDKLSPECS
251  IILTDIVGFV SDLPKHLISA FSXTLEETAQ ADVLLHV VDA AAPNSGQQIE
301  DVENVLQEIH AGDIPCIKVY NKTDLLPSEE QNTGIWRDAA GKIAAVRISV
351  AENTGIDALR EAIAESCAAA PNTDETEMP*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 538 shows 92.1% identity over a 392 aa overlap with a predicted ORF (ORF 538.ng) from *N. gonorrhoeae*:

```
m538/g538

          10      20      30      40      50      60
m538.pep  MTGRTGGNGSTQAQPERVMLVGVMLDKDGTGSSAARLNGFQTALAEAVELVKAAGGDSVR
          |::||| |::| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g538       MSGRTGRNSATQAQPERVMLVGVMLDKDDTGSNAARLNGFQTALAEAVELVKAAGGDSVR
          10      20      30      40      50      60

          70      80      90     100     110     120
m538.pep  VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPPTQERNLEKELKCRVLDL
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g538       VETAKRDRPHTALFVGTGKAAELSEAVAADGIDL VVFNHELTPPTQERNLEKI LQCRVLDL
```

812

	70	80	90	100	110	120
	130	140	150	160	170	180
m538.pep	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
g538	VGLILAI FARRARTQEGRLQVELAQLSHLAGRLIRGYGHLQSQRGGIGMKGPGETKLETD					
	190	200	210	220	230	240
m538.pep	RRLIAHRINALIKQLANLKKQALRRKSRESGRIKTFALVGYNVGVKSSLFNRLTKSGIY					
g538	RRLTAHRINALKKQLANLKKQALRRKSRESGRIKTFALVGYNVGVKSSLFNRLTKSGIY					
	190	200	210	220	230	240
	250	260	270	280		
m538.pep	AKDKL-----SPECSIILTDTVGVFVSDLPKHLISAFSXTLEETAQADVLLHV					
	:					
g538	AKDQLFATLDTTARRLYISPACSIILTDTVGVFVSDLPKHLISAFSATLEETVQADVLLHV					
	:					
	250	260	270	280	290	300
	290	300	310	320	330	340
m538.pep	VDAAAPNSGQOIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
g538	VDAAARNSGQOIEDVENVLQEIHAHDIPCIKVYNKTDLLPSEEQNTGIWRDAAGKIAAVR					
	310	320	330	340	350	360
	350	360	370	380		
m538.pep	ISVAENTGIDALREAIAESCAAPNTDETEMPX					
g538	ISVAENTGIDALREAIAEYCAAPNTDETEMPX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1559>:

```

a538.seq
1   ATGACAGGCA GAACAGGCCG CAACGGCAGT ACCCAAGCGC AACCCGAACG
51  CGTCATGCTG GTGGGCGTAA TGTGGACAA AGATGGTACG GGCAGCAGTG
101 CCACCCGCTC GAACGGTTT CAGACGGCAT TGGCGGAAGC TGTTCGAGCTG
151 GTCAAAGCGG CGGGCGGCCA TTCCGTGCGC GTGGAGACTG CCAAACGCGA
201 CCGTCCGCAC ACCGCGCTGT TTGTCGGCAC GGGCAAGGCG GCGGAGCTGT
251 CGGAAGCAGT TGCCGCAGAC GGCATCGATT TGGTCGTATT CAACCACGAA
301 CTTACGCCCA CGCAGGAACG CAATTTGGAA AAAATCCTCC AATGCCGCGT
351 ATTGGACAGA GTGGGGCTGA TTCTGGCGAT TTTCCGCCGC CGCGCCCGCA
401 CGCAGGAAGG CAGGCTGCAA GTCGAGTTGG CACAATTGAG CCATTGCGCG
451 GGACGCTTGA TACGCGGTTA CGGCCATCTG CAGAGCCAGC GCGGCGGTAT
501 CGGCATGAAA GGCCCCGGCG AAACCAAACT GGAAACCGAC CGCCGATTGA
551 TCGCCCATCG GATCAATGCC TTGAAAAAAC AGCTTGCCAA CCTCAAAAAA
601 CAGCGCGCCC TCGCGCGCAA GTCCCGCGAA TCGGGCACAA TCAAACGTT
651 TGCGCTGGTC GGCTATACCA ATGTCGGCAA ATCCAGTCTG TTCAACCGGC
701 TGACCAAGTC GGCATATAT GCGAAAGACC AGCTTTTCGC CACACTCGAC
751 ACGACGGCGC GCGGCTGTA CATCAGTCCC GAATGCAGCA TTATCCTGAC
801 CGATACCGTC GGATTCTCA GCGATCTGCC GCACAACTG ATTTCCGCCT
851 TTTCCGCCAC GCTGGAAGAA ACCGCGCAAG CCGATGTGCT GCTGCACGTC
901 GTCGATGCCG CCGCTCCGAA CAGCGGACAG CAGATTGAAG ACGTGGAAAA
951 CGTACTGCAA GAAATCCATG CCGGCGATAT TCCGTGCATC AAGGTGTACA
1001 ACAAACCGA CCTGCTGCCG TCTGAAGAAC AAAACACGGG CATATGGCGC
1051 GACGCTGCGG GAAAAATTGC CGCCGTCCGC ATTTCCGTG CTGAAAATAC
1101 CGGTATAGAC GCACTGCGCG AAGCCATTGC CGAGTATTGT GCCGCCGCAC
1151 CAAACACAGA CGAAACCGAA ATGCCATGA

```

This corresponds to the amino acid sequence <SEQ ID 1560; ORF 538.a>:

```

a538.pep
1   MTGRTGRNGS TQAQPERVML VGVMLDKDGT GSSATRLNGF QTALAEAVEL
51  VKAAGDSVR VETAKRDRPH TALFVGTKA AELSEAVALD GIDLVFNFHE
101 LTPTQERNLE KILQCRVLDL VGLILAI FAR RTQEGRLQ VELAQLSHA
151 GRLIRGYGHL QSQRGGIGMK GPGETKLETD RRLIAHRINA LKKQLANLKK

```

813

201 QRALRRKSRE SGTIKTFALV GYTNVGKSSL FNRLTKSGIY AKDQLFATLD
 251 TTARRLYISP ECSIILTDTV GFVSDLPKHL ISAFSATLEE TAQADVLLHV
 301 VDAAAPNSGQ QIEDVENVLQ EIHAGDIPCI KVYNKTDLLP SEEQNTGIWR
 351 DAAGKIAAVR ISVAENTGID ALREAIAEYC AAPNTDETE MP*

m538/a538 94.6% identity in 392 aa overlap

m538.pep	10	20	30	40	50	60
	MTGRTGGNGSTQAQPERV	MLGVMLDKDGTGSSAAR	LNQFQTALAEAVELVKA	AGGDSVR		
a538	10	20	30	40	50	60
	MTGRTGRNGSTQAQPERV	MLGVMLDKDGTGSSATRL	NQFQTALAEAVELVKA	AGGDSVR		
m538.pep	70	80	90	100	110	120
	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VVFNHETPTQERNLEKE	LKCRVLD		
a538	70	80	90	100	110	120
	VETAKRDRPHTALFVGTG	KAAELSEAVAADGIDL	VVFNHETPTQERNLEK	ILQCRVLD		
m538.pep	130	140	150	160	170	180
	VGLILAI FARRARTQEGRL	QVELAQLSHLAGRLIRG	YGHLSQRGGIGMKGPGE	TKLETD		
a538	130	140	150	160	170	180
	VGLILAI FARRARTQEGRL	QVELAQLSHLAGRLIRG	YGHLSQRGGIGMKGPGE	TKLETD		
m538.pep	190	200	210	220	230	240
	RRLIAHRINALIKQLANL	KKQRALRRKSRESGTIK	TFALVGYTNVGKSSLFN	RRLTKSGIY		
a538	190	200	210	220	230	240
	RRLIAHRINALIKQLANL	KKQRALRRKSRESGTIK	TFALVGYTNVGKSSLFN	RRLTKSGIY		
m538.pep	250	260	270	280		
	AKDKL-----SPECSI	IILTDTVGFVSDLPKHL	ISAFSXTLEETAQADVLL	HV		
a538	250	260	270	280	290	300
	AKDQLFATLDTTARRLYI	SPECSIILTDTVGFVSD	LPHKLISAFSATLEETAQ	ADVLLHV		
m538.pep	290	300	310	320	330	340
	VDAAAPNSGQQIEDVENV	LQEIHAGDIPCIKVYNK	TDLLPSEEQNTGIWRDA	AGKIAAVR		
a538	290	300	310	320	330	340
	VDAAAPNSGQQIEDVENV	LQEIHAGDIPCIKVYNK	TDLLPSEEQNTGIWRDA	AGKIAAVR		
m538.pep	350	360	370	380		
	ISVAENTGIDALREAIAE	SCAAAPNTDETEMPX				
a538	350	360	370	380	390	
	ISVAENTGIDALREAIAE	YCAAAPNTDETEMPX				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1561>:

g539.seq

1	atggaggatc	tgcaggaaat	cgggttcgat	gtcgccgccg	taaaggtagg
51	tcggcagcgc	gaacatcatc	gtctgcatca	taccagttcc	ggcaacggca
101	aggcggacga	tgtattgttt	gcgttctttt	tggttggcgg	cttcgatttt
151	ttgcgcgtca	taggggtcgg	cgggtgtagc	tgtctgccgg	attttcaaca
201	gaatgtcga	gaggcggatt	ttgccgtcgt	cccagacgac	gcggcagcgg
251	tgcgtgctgt	aattgaggtc	gatgcggacg	atgccgtctg	tgcgcaaaag
301	ctgctgttcg	atcagccaga	cgcaggcggc	gcaggtaatg	ccgctgagca
351	tcagcactgc	ttcgtgcgtg	ccattatggg	tttcacaaa	gtcggattgg
401	acttcgggca	ggctgtacag	gcggatttgg	tcgaggattt	cttggggcgg
451	cagttcgggt	tttttcgcgt	cggcgggtcg	tcgtttgtaa	taactgccca
501	agccggaatc	gatgatgctt	tgtgcgactg	cctgacagcc	gacgcagcag
551	gtttcgcgg	cttcgccttc	gtagcggacg	gtcagatgca	ggttttcggg
601	aacgtccagc	ccgcagtggg	aacaggtttt	tttcatggca	tttcggtttc

814

```

651 gtctgtgttt ggtgcggcgg cacaatactc ggcaatggct tcgcgagtg
701 cgtctatacc ggtattttca gcaacggaaa tgcggacggc ggcaattttt
751 cccgcagcgt cgcgccatat gcccggtgtt tgttcttcag acggcagcag
801 gtcgggtttt ttgtacacct tgatgcacgg aatatcgtgg gcatggattt
851 cttgcagtac gttttccacg tcttcaatct gctgcccgtt gttccgggag
901 gcagcatcga cgacgtgcag cagcacatcg gcttgcacgg tttcttccaa
951 ggtggcgga aaggcgga aagcgtttgt cggcagatcg ctgacgaatc
1001 cgacgggtat ggtcaggata atgctgcatg cgggactgat gtacagccgc
1051 cgcgccgtcg tgcgagagt ggcgaaaagc tggctcttcg catatatgcc
1101 cgacttggtc agccggttga acaggttga tttgccgaca ttggtatag

```

This corresponds to the amino acid sequence <SEQ ID 1562; ORF 539.ng>:

```

g539.pep
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHTQS GNGKADDVLF AFFLVGGFDF
51 LRVIGCGGVA CLPDFQQNVG EADFAVVPDD AAARAVIEV DADDAVCAQK
101 LLFDQPDAGG AGNAAEHQHC FVRAIMGPHK VGLDFGQVVQ ADLVEDFLGR
151 QGFFFRVGGG SFVITAQAGI DDALCDCLTA DAAGFAVFVF VADGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISW AWISCSTFST SSICPLFRA
301 AASTTCSSTS ACTVSSKVAE KAEISLCGRS LTNPVSVRI MLHAGLMYSR
351 RAVVSRVAKS WSFAYPDLV SRLNRLDLPT LV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1563>:

```

m539.seq (partial)
1 ATGGAGGATT TGCAGGAAAT CGGGTTCGAT GTCGCCGCCG TAAAGGTAGG
51 TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCTTTT TGGTTGGCGG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCAG CGGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCgG
251 TCGGTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCTG TACGCAAAAG
301 CTGCTGTTCT ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTTAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGGACTGG
401 ACTTCGGGCA GGTCTGACAG CGCGATTGGG TCGAGGATTT CTTGGGGCGG
451 CAgCTCGGTT TTTTGCAGCT CGGCGGTGCG TTGTTTGTA TAACTGCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACCG CCTGACAGCC GGCGCaCAGG
551 GTTTCGCGGT CTTCGTTTTT GTAACGGACA GTCAGGTGGA GGTGTTCCGG
601 AACATCCAGA CCGCAGTGGA AACAGGTTTT TTTCATGGCA TTTCCGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAAGACTC GGCAATgGCT TCGCGCAGTG
701 GCTCTATACC GGTATTTTCA GCAACGGAAA TCGCGACGGC GGCAATTTTT
751 CCCGCAGCGT CGCGCCATAT GCGCGTGTTC TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTTG TTGTACACCT TgATGCACGG AATATCGCCG GCATGGATTT
851 CTTGCAGTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGCAG CAGCACATCG GCTTGCGCGG TTTCTTCCAG
951 CGTGGcG.AA AAGGCGGAAA TCAGTTTgTG CGGCAGATCG CTnACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGAC...

```

This corresponds to the amino acid sequence <SEQ ID 1564; ORF 539>:

```

m539.pep (partial)
1 MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGFDF
51 LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVFHK VGLDFGQVVQ ADLVEDFLGR
151 QLGLFRVGGG LfVITAQARV NNALCDRLTA GAQGFVFVF VTDSQVEVFG
201 NIQTAVETGF FHGISVSSVF GAAAQDSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICPLFLGA
301 AASTTCSSTS ACAVSSSVAX KAEISLCGRS LTNPVSVRI MLHSG...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 539 shows 89% identity over a 345 aa overlap with a predicted ORF (ORF 539.ng) from *N. gonorrhoeae*:

```

m539/g539
10 20 30 40 50 60
m539.pep MEDLQEIGFDVAAVKVGRQREHHRLHHPQPNGEADDVLF AFFLVGGFDFLRVIGCGGVA
|||||
g539 MEDLQEIGFDVAAVKVGRQREHHRLHHTQSGNGKADDVLF AFFLVGGFDFLRVIGCGGVA

```


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	10	20	30	40	50	60
m539.pep	70	80	90	100	110	120
	YLPDFQQNVGKADFAVVPDDAAAVRAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHKNR					
g539	70	80	90	100	110	120
	CLPDFQQNVGEADFAVVPDDAAAVRAVIEVDADDAVCAQKLLFDQPDAGGAGNAAEHQHC					
m539.pep	130	140	150	160	170	180
	LARAAVGFHKVGLDFGQVVQADLVEDEFGRQLGFLRVGGALFVITAQARVNNALCDRLTA					
g539	130	140	150	160	170	180
	FVRAIMGFHKVGLDFGQVVQADLVEDEFGRQFGFFRVGGASFVITAQAGIDDALCDCLTA					
m539.pep	190	200	210	220	230	240
	GAQGFVAVFVFTDSQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
g539	190	200	210	220	230	240
	DAAGFAVFAFVADGQMVFVFGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
m539.pep	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMVFVCSSDGRSVLLYTLMHGISPAWISCSFTSTSSICCPLEGA					
g539	250	260	270	280	290	300
	ATEMRTAAIFPAASRHMVFVCSSDGRSVLLYTLMHGISPAWISCSFTSTSSICCPLEGA					
m539.pep	310	320	330	340		
	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
g539	310	320	330	340	350	360
	AASTTCSSTSACTVSSKVAEKAEISLCGRSLTNPTVSVRIMLHAGLMYSRRRAVVSRAKS					
g539						
	WSFAYMPDLVSRLNRLDLPTLV					
	370	380				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1565>:

```

a539.seq
1  ATGGAGGATT TGCAGGAAAT CGGTTTCGAT GTCGCCGCCG TAAAGGTAGG
51  TCGGCAGCGC GAACATCATC GTCTGCATCA TCCCCAGCCC GGCAACGGCG
101 AGGCGGACGA TGTATTGTTT GCGTTCCTTT TGGTTGCGCG CTTCGATTTT
151 TTGCGCGTCA TAGGGTGCGG CCGTGTAGCC TATCTGCCTG ATTTTCAACA
201 GAATGTCGGA AAGGCGGATT TTGCCGTCGT CCCAGACGAC GCGGCAGCGG
251 TGCCTGCTGT AATTGAGGTC GATGCGGACG ATGCCGTCGT TACGCAAAAG
301 CTGCTGTTCT ATCAGCCAGA CGCAGGCGGC GCAGGTGATG CCGCCGAGCA
351 TTAAAACCGC CTCGCGCGTG CCGCCGTGGG TTTCCACAAA GTCGGACTGG
401 ACTTCGGGCA GGTCGTACAG GCGGATTGG TCGAGGATTT CTGGGGCGG
451 CAGCTCGGTT TTTTGCGCGT CGGCGGTGCG TTGTTGTAA TAAGTCCCA
501 AGCCCGCGTC AATAATGCTT TGTGCGACTG CCTGACAACC GGCGCAGCAG
551 GTTTCGCGGT CTTCTGTTTC GTAACGGACG GTCAGATGCA GGTTTTCGGG
601 AACGTCCAGC CCGCAGTGGA AACAGGTTT TTTCATGGCA TTTCGGTTTC
651 GTCTGTGTTT GGTGCGGCGG CACAATACTC GGCAATGGCT TCGCGCAGTG
701 CGTCTATACC GGTATTTTCA GCAACGGAAA TGCGGACGGC GGCAATTTT
751 CCCGCGCGT CGCGCCATAT GCGCGTGT TGTCTTCAG ACGGCAGCAG
801 GTCGGTTTGT TTGTACACCT TGATGCACGG AATATCGCG GCATGGATTT
851 CTTGCACTAC GTTTTCCACG TCTTCAATCT GCTGTCCGCT GTTCGGAGCG
901 GCGGCATCGA CGACGTGACG CAGCACATCG GCTTGCAGCG TTTCTTCCAG
951 CGTGGCGGAA AAGGCGGAAA TCAGTTTGTG CCGCAGATCG CTGACGAATC
1001 CGACGGTATC GGTCAGGATA ATGCTGCATT CGGGACTGAT GTACAGCCGC
1051 CGCGCCGTCG TGTCGAGTGT GGCGAAAAGC TGGTCTTCG CATATATGCC
1101 CGACTTGGTC AGCCGGTTGA ACAGACTGGA TTTGCCGACA TTGGTATAG

```

This corresponds to the amino acid sequence <SEQ ID 1566; ORF 539.a>:

```

a539.pep
1  MEDLQEIGFD VAAVKVGRQR EHHRLHHPQP GNGEADDVLF AFFLVGGGDF

```

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```

51  LRVIGCGGVA YLPDFQQNVG KADFAVVPDD AAARAVIEV DADDAVCTQK
101 LLFDQPDAGG AGDAAEH*NR LARAAGVGHK VGLDFGQVVQ ADLVEDFLGR
151 QLGFLRVGGA LFFVITAQARV NNALCDCLTT GAAGFAVEFE VTDGQMVFVG
201 NVQPAVETGF FHGISVSSVF GAAAQYSAMA SRSASIPVFS ATEMRTAAIF
251 PAASRHMPVF CSSDGSRSVL LYTLMHGISP AWISCSTFST SSICCPLFGA
301 AASTTCSSTS ACAVSSSSVAE KAEISLCGRS LTNPVSVRI MLHSGLMYSR
351 RAVVSSVAKS WSFAYMPDLV SRLNRLDLPT LV*

```

m539/a539 97.1% identity in 345 aa overlap

	10	20	30	40	50	60
m539.pep	MEDLQEI IGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA					
a539	MEDLQEI IGFDVAAVKVGRQREHRLHHPQPGNGEADDVLFAFFLVGGFDFLRVIGCGGVA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m539.pep	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
a539	YLPDFQQNVGKADFAVVPDDAAARAVIEVDADDAVCTQKLLFDQPDAGGAGDAAEHXNR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m539.pep	LARAAGVGHKVGGLDFGQVVQADLVEDFLGRQLGLFLRVGGALFVITAQARVNNALCDRLTA					
a539	LARAAGVGHKVGGLDFGQVVQADLVEDFLGRQLGLFLRVGGALFVITAQARVNNALCDCLTT					
	130	140	150	160	170	180
	190	200	210	220	230	240
m539.pep	GAQGF AVFVFVTD SQVEVFGNIQTAVETGFFHGISVSSVFGAAAQDSAMASRSASIPVFS					
a539	GAAGF AVFVFVTD GQM QVFGNVQPAVETGFFHGISVSSVFGAAAQYSAMASRSASIPVFS					
	190	200	210	220	230	240
	250	260	270	280	290	300
m539.pep	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPLFGA					
a539	ATEMRTAAIFPAASRHMPVFCSSDGSRSVLLYTLMHGISP AWISCSTFSTSSICCPLFGA					
	250	260	270	280	290	300
	310	320	330	340		
m539.pep	AASTTCSSTSACAVSSSVAXKAEISLCGRSLTNPTVSVRIMLHSG					
a539	AASTTCSSTSACAVSSSVAEKAEISLCGRSLTNPTVSVRIMLHSGLMYSRR AVVSSVAKS					
	310	320	330	340	350	360
a539	WSFAYMPDLVSRLNRLDLPTLVX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1567>:

g540.seq

```

1  atgccgccct cccgacgcgg caacgggggtg ttttatcaaa acggcaaact
51  tgccaatgcg gtttccgctt gccgattgcc aaaccggcaa acctttcccg
101  tgccgggtgcc gaacccgatg ccgtctgaac cttcagacgg catcgggtgt
151  ttattttgtcc actcggacgg gtgcagggtc gtattgtgtc gattcgtcgc
201  cgtataacag cagccgagt ttgacgggga tgcgtccctg cgatttgagg
251  tgggcgttgg aatcgcgcaa ggaatacgcg cagccgagc attcctgctg
301  gtagaagttt tcgcgtttgc tgatttcaat catacgcgcg ccgccgcgcg
351  ctttgcgcca gttgaagtcc caataggcca catcatcgta aggcgcggcg
401  gcacgggtgtc cgcagtcgtt gatttgcgcc atatttttcc agcgtga

```

This corresponds to the amino acid sequence <SEQ ID 1568; ORF 540.ng>:

g540.pep

```

1  MPPSRRGNV FYQNGKLANA VSACRLPNRQ TFPVPVPNPM PSEPSDGIGC

```

```
m540.seq (partial)
1    ..CCGAACCCGA TGCCGTCTGA ACCTTCAGAC GGCATCGGGT GTTTATTTGT
51   CCACCCGGAT GGGGGCAGGT TCGTATTGTG TCGATTCTGC GCCGTAATAC
101  AGCACGCCGA GTTTGATGGG GATTCTGCCC TGTGATTTCG GGTGGGCATT
151  GGAATCCCTC AGGGAATAGG CACAACCGCA ATATTCCTGC TGGTAGAAGT
201  TTTCACGTTT GCTGATTICA ATCATGCGCG CGCTGCCGCG GCCTTTGCGC
251  CAGTTGAAAT CCCAATACAC CACATCATCG TAAGGCGCGG CGGCGCGGTG
301  TCCGTGACGTC TTGATTTGCG CCATATTTTT CCAGCGTGA
```

m540.pep (partial)

1 ..PNMPSEPSD GIGCLFVHPD GGRFVLCRFV AVIQHAEDFG DSAL*FAVGI

51 GI PQGIGTTA IFLLVEVTFE ADFNHARAAA AFAPVEIPIH HIIVRRGGAV

101 SAVVDLRHIF PA*

```

m540/g540
                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGFRFVLCRFV
                                |||||
g540      GNGVIFYQNGKLANAVSACRLPNRQTFPVVPNPMPSEPSDGIGCLFVHSDGCRFVLCRFV
                10      20      30      40      50      60

                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQGIGTTAIFLLVEVFTFADFNHARAAAFAFAPVEIPIH
                |||||:| |||:| |||:| |||||:| |||||:| |||||:| |||||:|
g540      AVIQHAEFDGDASLRFAVGVGIAQGIRAAAVFLLVEVFADFNHTRAAAFAFAPVEVPIG
                70      80      90      100     110     120

                100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
                |||||:| |||||
g540      HIIVRRGGTVSAVVDLRHIFPAX
                130     140

```

```

a540.seq
1  ATGCCGTCCT CCCGACGCGG CAACGGGGTG TTTTATCAAA ACGGCAAAC
51  TGCCAATGCG GTTTCCGATT GCAGATTGCC AAACCGGCAA ACCTTTCCCG
101 TGCCGATGCC GAACCCGATG CCGTCTGAAC CTTCAGACGG CATCGGGTGT
151 TTATTTGTCC ACCCGGATGG GTGCAGGTTT GTATTGTGTC GATTCGTCGC
201 CGTAATACAG CACGCCGAGT TTGATGGGGA TTCTGCCCTG TGATTTGCGG
251 TGGGCGTTGG AATCCCTCAG GGAATAGGCA CAACCGCAAT ATTCCTGCTG
301 GTAGAAGTTT TCACGTTTGC TGATTTCAAT CATACGCGCG CTGCCGCCGC
351 CTTTGCGCCA GTTGAATACC CAATACACCA CATCATCGTA AGCGCGGGCG
401 CGCGCGCGGC CGCAGATCGT AATCTGGTTC ATGTTTTTCC A

```

```
a540.pep (partial)
1  MPSSRRGNGV FYQNGKLANA VSDCRLPNRQ TFPVMPNPM PSEPSDGIGC
51  LFWHPDGC RF VLCRFVAVIQ HAEFDGDSAL *FAVGVGIPQ GIGTTAIFLL
101 VEFTEADFN HTRAAAAFAP VEIPIHHIIV RRGAAAAAVV NLVHVFP
```

818

m540/a540 92.8% identity in 111 aa overlap

```

                                10      20      30
m540.pep                      PNPMPSEPSDGIGCLFVHPDGGRFVLCRFV
                                |||||
a540      GNGVFYQNGKLANAVSDCRLPNRQTFVPMPNPNMPSEPSDGIGCLFVHPDGCREFVLCRFV
                                10      20      30      40      50      60

                                40      50      60      70      80      90
m540.pep      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHARAAAAFAPVEIPIH
                                |||||:|||||:|||||:|||||:|||||:|||||
a540      AVIQHAEFDGDSALXFAVGIGIPQIGIGTTAIFLLVEVFTFADFNHTRAAAAFAPVEIPIH
                                70      80      90      100     110     120

                                100     110
m540.pep      HIIVRRGGAVSAVVDLRHIFPAX
                                |||||:|:|
a540      HIIVRRGGAAAAVNLVHVFP
                                130     140

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1573>:

```

g542.seq
1  atgccgaat ggtcgcgcac acggcggttc agcgctcctt cgctgatggt
51 cagcgcggtc gtcagccggt tgacttggtg tgcgcccgcg tcgaacgcgg
101 cattcagggt gcggtgaag tcttcagacg gcatagcgtc tgcttcgcc
151 gtttgccccg ccgcccgcgc gatgccgtct gaaaccgtgt cccacaaatc
201 cgacagcagc cgcaacacgt ccgcctcgcg gcgcaatggt tcgccccaat
251 gccctttgg gacggttgc aggcaggatg ccgccaagcc gcgcagggtt
301 gggggcaaat cccatatcct gaccggttcg cggttaa

```

This corresponds to the amino acid sequence <SEQ ID 1574; ORF 542.ng>:

```

g542.pep
1  MPKWSRIRRC SVLSLMFSAA VSRLTWCAPP SNAAFRVRLK SSDGIASASA
51  VCPAAGSMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTVC RQDAAKPRRF
101 GGKSHILTGS R*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1575>:

```

m542.seq
1  ATGCCGAAAT GGTGCGGCAT ACGGCGTTGC AGCGTCCTTT CACTGATGTT
51  CAGCGGTCT GTCAGCCGGT TGA CTGTTGGT TGCGCCGTCG GCAAACGCGG
101 CATTTAGGGT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCGG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG .CGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTT
301 GGGGGCAAAT CCCATATCCT GACCGGTTTC CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1576; ORF 542>:

```

m542.pep
1  MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASA
51  VCPAAGFMPS ETVSHKSDSS RNTSASRAMF RPNAPLGRNV SPKCPFGTAF
101 RQDAAKPRRF GGKSHILTGS R*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 542 shows 93.7% identity over a 111 aa overlap with a predicted ORF (ORF 542.ng) from *N. gonorrhoeae*:

```

m542/g542

                                10      20      30      40      50      60
m542.pep      MPKWSRIRRC SVLSLMFSAS VSRLTWCAPS ANAAFRVRLK SSDGIASASAVCPAAGPMPS
                                |||||:|||||:|||||:|||||:|||||
g542      MPKWSRIRRC SVLSLMFSAAVSRLTWCAPP SNAAFRVRLK SSDGIASASAVCPAAGSMPS
                                10      20      30      40      50      60

                                70      80      90      100     110
m542.pep      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRF GGKSHILTGSRX

```

819

```

|||||
g542  ETVSHKSDSSRNTSASRRNVSPKCPFGTVCRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1577>:

```

a542.seq
1   ATGCCGAAAT GGTGCGGCAT ACGGCGTTGC AGCGTCCTTT CGCTGATGTT
51  CAGCGTGTCT GCCAGCCGGT TGACTTGATG TGCGCCGCCG GCAAACGCGG
101 CATTGAGGAT GCGGCTGAAG TCTTCAGACG GCATAGCGTC TGCTTCCGCC
151 GTTTGCCCCG CCGCCGGCCC GATGCCGTCT GAAACCGTGT CCCACAAGTC
201 CGACAGCAGC CGCAACACGT CCGCCTCGCG GCGCAATGTT TCGCCCAAAT
251 GCCCCTTTGG GACGGCTTTC AGGCAGGATG CCGCCAAGCC GCGCAGGTTC
301 GGGGGCAAAT CCCATATCCT GACCGTTTCG CGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1578; ORF 542.a>:

```

a542.pep
1   MPKWSRIRRC SVLSLMFSVS ASRLT*CAPP ANAAFRMLK SSDGIASASA
51  VCPAAGPMPS ETVSHKSDSS RNTSASRRNV SPKCPFGTAF RQDAAKPRRF
101 GGKSHILTGS R*

```

m542/a542 94.6% identity in 111 aa overlap

```

              10      20      30      40      50      60
m542.pep  MPKWSRIRRC SVLSLMFSVSASRLTWCAPSANAAFRVRLKSSDGIASASAVCPAAGPMPS
          |||||
a542      MPKWSRIRRC SVLSLMFSVSASRLTXCAPPANAAFRMLKSSDGIASASAVCPAAGPMPS
              10      20      30      40      50      60

              70      80      90      100     110
m542.pep  ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
          |||||
a542      ETVSHKSDSSRNTSASRRNVSPKCPFGTAFRQDAAKPRRFGGKSHILTGSRX
              70      80      90      100     110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1579>:

```

g543.seq
1   atggtttgtc ggttatttgc cgccgttttt ggctttcaac tcggcaatca
51  gcccgctgat gcctttggct ttgatgattt cgccgaattg gttgcggtac
101 acggttaacca ggctcgtgcc ttcgatggcg acgttgtagg tacggtattt
151 gccgccgctt tggtaggttg taaagtccat attgacgggc ttctgaccgg
201 ggatgccgac ttcggcacgg acgacgattt ccttgccgcc cttattgacg
251 atgggattgt ctttgacgtt gacggtcgcg tttttgaatt tcagcatcgt
301 gccggaatag gtgcggatca gcagggtttg aaattccttg gccaacgctt
351 gtttttgcgc gtcggacgcg gtacgccaag ggttgccgac cgccaatgcg
401 gtcatacgtt ggaaatcgaa atagggaacc gcataggctt cggcttttgg
451 gcgtgcagaa gccgcgtcgc cgcttttgag gatggc aaa acctgtgtgg
501 cgttttggcg gatttgtccc actgcgtcgg ccggggaggc aaatgccatg
551 ccgatgctca aaataccgat gcccaatgcg ctgatgaagg aggatttttt
601 cacgatgtct ttcctgaaaa tggatgtgta tgtttattct gcggcttttt
651 ccgcattgcc gccctcagcg tttttctcgg cgaagctggt catgaattta
701 ccgatcaggt tttccagaac cattgcagaa ctggttacgg agatggtgtc
751 gccgpcagca aggttttccg tatcgccgcc ctgctgcagc ccgatgtact
801 gttcgcccaa aagtcgccga gtcaggattt gcgcggaaac gtcactgctg
851 aactgatact tgccgtccaa atcaaggcgc accctcgcct gataggattt
901 cgggtcaagc ccgatagcgc cgacgcgcc gaccaatacg cctgcggatt
951 tgacgggggc attgacctc aaaccgccga tgcgcgcgaa atcggcataa
1001 acggcgtaag ttttgtccga accgccgaac gccgcgcgc ccgccacgcg
1051 gaaagcgaga aaggcaaccg ccgcccgcgc gatcaagacg aacagtccga
1101 cccaaaattc caatatgttc tttttcatta a

```

This corresponds to the amino acid sequence <SEQ ID 1580; ORF 543.ng>:

```

g543.pep
1   MVCRLFAAVF GFQLGNQPVDF AFGFDDFAEL VAVHGNQARA FDGDVVGTVF

```

820

```

51  AAALVGGKVH IDGLLTGDAD FGTDDDFLAA LIDDGIVFDV DGRVFEFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGTPRVAD RQCGHTLEIE IGNRIGFGFW
151 ACRSRVAAFE DGQNLGCVLA DLSHCVGRGG KCHADAQNTD AQCADEGGFF
201 HDVFPENGCV CLFCGFFRIA ALSVFLGEAG HEFTDQVFQN HCRTGYGDGV
251 AGSKVFRIAA LLQPDVLFQA KRSRQDLRGN VTAEILAVQ IKAHPRLIGF
301 RVKPDSDADAP DQYACGFDGG IDLQADVAE IGINGVSFVR TAERRAARHA
351 ESEKGNRRRA DQDEQSDPKF QYVLFH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1581>:

```

m543.seq
1  ATGGTTTGTC GGTATTGTC CGCCGTTTTT GGCTTTC AAC TCGGCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTTGCCCGG
201 GTACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCCGC TTTATTGACG
251 ATGGGATTGT CTTTGACGTT GACGTGGCG TTTTAAATT TCAGCATCGT
301 GCCGAATAG GTGCGGATCA GCAGGGTTTG AAATCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCAAG GGTGCGGAC CGCCAATCGG
401 GTCATACGTT GAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTTG
451 GCGAGCGGTG TTGGCATCGC CGTTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTGACG GATTTGGCTT ACCCGGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAGGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGCGCG
651 CTTTTTCGCG ATTGCCGCG TCGGCATTTT TCTCGGCAAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCGC GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAAGT CCCGAAGTCA GGATTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTGCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATCCAAT ATGTTCTTCT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1582; ORF 543>:

```

m543.pep
1  MVCRLFAAVF GFQLGNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGGEVH VDGFPLGYAD FGADDDFFAA FIDDGIVFDV DVGVFQFQHR
101 AGIGADQOGL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 ASGVGIAXFX DAQYLSGVL TDLAYRVGRGG KCHADAQNTD AQCADEGGFF
201 HDXVSXFEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRGTGYD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQADV AEINGVSF VRTAERRTAG
351 HAESEKGNRR RANQDEQSDP KFQYVLLH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 543 shows 84.2% identity over a 379 aa overlap with a predicted ORF (ORF 543.ng) from *N. gonorrhoeae*:

```

m543/g543
10 20 30 40 50 60
m543.pep MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNQARAFDGDVVGTVFTAALVGGEVH
|||||
g543 MVCRLFAAVFGFQLGNQPVDAFGFDDFAELVAVHGNQARAFDGDVVGTVFAALVGGKVH
10 20 30 40 50 60
70 80 90 100 110 120
m543.pep VDGFPLGYADFGADDDFFAAFIIDDGIVFDVDVGVFQFQHRAGIGADQOGLKFFGQRLFLR
:|:|:|
g543 IDGLLTGDADFGTDDDFLAALIDDGIVFDVDGRVFEFQHRAGIGADQOGLKFFGQRLFLR
70 80 90 100 110 120
130 140 150 160 170 180

```

821

```

m543.pep  VGRGAPRVADRQCGHTLEIEIGNRIGFGFLASGVGIAVFXDAQYLSGVLTDLAYRVGRGG
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      VGRGTPRVADRQCGHTLEIEIGNRIGFGFWACRSRVAAFEDGQNLGCVLADLSHCVGRGG
          130      140      150      160      170      180

          190      200      210      220      230      239
m543.pep  KCHADAQNTDAQCADEGGFFHDXVSXFEYDG-IRLFGGFFRIA AVGIFLGKTRHEFADKV
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      KCHADAQNTDAQCADEGGFFHDXV---FPENGCVCLFCGFFRIAALSVFLGEAGHEFTDQV
          190      200      210      220      230

          240      250      260      270      280      290      299
m543.pep  FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLAQKRSQDLRGNVAAELILAVQIEAHPRL
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      FQNHCRITGYGDGVAGSKVFRVAALLQPDVLLFAQKRSQDLRGNVTAELILAVQIKAHPR
          240      250      260      270      280      290

          300      310      320      330      340      350      359
m543.pep  IGFRVKSDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRTAGHAESEKGNR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      IGFRVKPDSADAPDQYACGFDGGIDLQTDVAEIGINGVSFVRTAERRAARHAESEKGNR
          300      310      320      330      340      350

          360      370      379
m543.pep  RRANQDEQSDPKFQYVLLHX
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g543      RRADQDEQSDPKFQYVLFHX
          360      370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1583>:

```

a543.seq
1  ATGGCTTATG GATTACTTGC TGCCGTTTNT AGCCTTCAAC TCGNCAATCA
51  GTCCGTCCAC GCCTTTCGCT TTGATAATTT CGCCGAATTG GTTGCGGTAC
101 ACGGTAACCA GGCTCGCGCC TTCGATGGCG ACGTTGTAGG TACGGTATTT
151 ACCGCCGCTT TGGTAGGTGG TGAAGTCCAT GTTGACGGGT TTTGCCCGG
201 NNACGCCGAC TTCGGCGCGG ACGATGATTT CTTTGCCGCC TTTATTGACG
251 ATNGGATTGT CTTTGACGTT GACGTTGGCG TTTTAAATT TCAGCATCGT
301 GCCGGAATAG GTGCGGATCA GCAGGGTTTG AAATTCTTTG GCCAACGCTT
351 GTTTTTCGCG GTCGGACGCG GTGCGCCAAG GGTGCGGAC CGCCAATGCG
401 GTCATACGTT GGAAATCGAA ATAGGGAATC GCATAGGCTT CGGCTTTTGT
451 GCGGGCGGTG TTGGCATCAC CGCTTTTAA GATGCTCAAT ACTTGAGTGG
501 CGTTTTCGCG GATTTGGTTT ACCGCGTCGG CAGGGGCGGC AAATGCCATG
551 CCGATGCTCA AAATACCGAT GCCCAATGCG CTGATGAAGG AGGATTTTTT
601 CATGATTAAG TGTCTAGTT TGAATATGAT GGCATACGTT TATTCGGCGG
651 CTTTTTCCGC ATTGCCGCGC TCGGCATTTT TCTCGGCAA ACTCGTCATG
701 AATTTGCCGA TAAGGTTTTT CAGAACCATT GCAGAACTGG TTACGGAGAT
751 GGTGTCGCCG GCAGCAAGGT TTTCCGTGTC GCCGCCCTGC TGCAGCCCGA
801 TGTACTGCTC GCCCAAAGT CCCGAAGTCA GGATTTGCGC GGAAACGTCG
851 CTGCTGAAC TACTTTGCC GTCCAAATCG AGGCGCACCC TCGCCTGATA
901 GGATTTCCGG TCAAGTCCGA TAGCGCCGAC GCGCCCGACC AATACGCCCTG
951 CGGATTTGAC GGGGGCATTG ACCTTCAAAC CGCCGATGTC GCCGAAATCG
1001 GCATAAACGG CGTAAGTTT GTCCGAACCG CCGAACGCCG CACCGCCGGC
1051 CACGCGGAAA GCGAGAAAGG CAACCGCCGC CGCGCCAATC AGGACGAACA
1101 GTCCGACCCA AAATTCCAAT ATGTTCTTTT TCATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1584; ORF 543.a>:

```

a543.pep
1  MAYGLLA AVX SLQLXNQSVH AFRFDNFAEL VAVHGNQARA FDGDVVGTVF
51  TAALVGG EVH VDGFLPGXAD FGADDDFFAA FIDDXIVFDV DVGVF*FQHR
101 AGIGADQO GL KFFGQRLFLR VGRGAPRVAD RQCGHTLEIE IGNRIGFGFL
151 AGGVGITA F* DAQYLSGVLT DLVYRVGRGG KCHADAQNTD AQCADEGGFF
201 HD*VS*FEYD GIRLFGGFFR IAAVGIFLGK TRHEFADKVF QNHCRITGYGD
251 GVAGSKVFRV AALLQPDVLL AQKRSQDLR GNVAELILA VQIEAHPRLI
301 GFRVKSDSAD APDQYACGFD GGIDLQTDV AEIGINGVSF VRTAERRTAG

```

	10	20	30	40	50	60
m543.pep	MVCRLFAAVFGFQLGNQSVHAFRFDNFAELVAVHGNGARAFDGDGVGTVFTAALVGGEVH : : :					
a543	MAYGLLA AVXSLQLXNQSVHAFRFDNFAELVAVHGNGARAFDGDGVGTVFTAALVGGEVH					
	10	20	30	40	50	60
	70	80	90	100	110	120
m543.pep	VDFGLPGYADFGADDFFAAFI DDGI VDV DVGVFX FQH RAGIG ADQQ GLK FF GQR LFL R 					
a543	VDFGLPG XAD FGADDFF AA FI DDX IVD VD VG VF XF QHR AGI GAD QQ GL KFF G QR LF LR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m543.pep	VGR GAP RVADRQC GHTLE IE IG NR IF GF FL AS GV GI A V FX DA QYL SG VL TD LA YRV GR GG : :					
a543	VGR GAP RVADR QC GH T LE I E I GN RI GF FL AG GV GIT AF XD AQ YL S G V LT DL V Y RV GR GG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m543.pep	KCHADAQN TDAQCADEGGFF HDXSXF EYDGIRLF GGFFRIAAVGIFLGKTRHEFADKV F 					
a543	KCHADAQN TDAQ CA DEGG FF H DX SX FEY DG IR LF GG FF RI AA VG IF LG KT RH EF AD KV F					
	190	200	210	220	230	240
	250	260	270	280	290	300
m543.pep	QNH CRTGY GDGVAGSKVF RVAALLQP DVL LAQKS RSQDL RG NVA AE LI LAVQIEAHP RL I 					
a543	QNH CRTGY GDGVAGSKVF RVA ALLQP DVL LAQ KSRSQDLRG NVAE ELI LAVQIEAH PRLI					
	250	260	270	280	290	300
	310	320	330	340	350	360
m543.pep	GFRVKSDSADAPDQYACGFDDGGIDLTQTADV AEIGIN GVSFVRTA ERRTAGHAES EKGNRR 					
a543	GFRVKSD SAD APDQYA CG FD GG ID LT QT ADV AE IG IN GS FVR TAER RTAG HA ES EK GN RR					
	310	320	330	340	350	360
	370	379				
m543.pep	RANQE QS DP KFQYV LLHX :					
a543	RAN QEQS DPKFQYVLFHX					
	370					

```

g544.seq
  1  atgaaaaaaaa tactcaccgc cgccgcccgtc gcactgatcg gcatcctcct
 51  cgccaccgtc ctcatcccg acagtaaac cgcgcccgcc ttctccctgc
101  ccgacctgca cggaaaaacc gtttccaacg ccgacctgca aggcaaagtc
151  accctgatta atttttggtt tccctcctgt ccgggttggtg tgagcgaaat
201  gcccaaagtc accaaaacgg caaacgacta caaaaataaa gatttccaag
251  tctctcgccgt tgcccagccc atcgatccga tagaaagcgt ccgccaatac
301  gtcaaagact acggaactgcc gtttaccgtc atttatgatg cggacaagtc
351  cgctcggacag gcattcgcca cacaggttta tccgacttcc gtccttatcg
401  gcaaaaaagg cgaaatcctc aaaacttatg tcggcggaacc cgatttcggc
451  aaactctacc aagaaatcga taccgcgctg gcgcaatag

```

g544.pep

1	MKKILTA	AAV	ALIGILL	ATV	LIPDSKT	TAPA	FSLPDL	HGKT	VSNADL	QGKV
51	TLINFW	PSC	PGCVSE	MPKV	TKTAND	YKNK	DFQVLA	VAAQP	IDPIES	VRQY
101	VKDYGL	PFTV	IYDADK	AVGQ	AFGTQV	YPTS	VLIGKK	GEIL	KTYVGE	PDEG

m544.seq

MS	1	ATG	AAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
	51	TGCCATCGTC	CTCmTCCCG	ACAGCAAAC	CGCGCCCGCC	TTCTCCmTGC	
	101	CCGACCTGCA	CGGAAAAACC	GTTTCCAACG	CCGACCTGCA	AGGCAAAGTA	
	151	ACCTGATTA	ATTTTTGGTT	TCCCTCCTGT	CCGGTGTGTG	TGAGCGAwAT	
	201	GCCCCAAATC	ATTA AACCG	CAATGACTA	TAAAwCAAA	AACTTCCAAG	
	251	TACTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT	
	301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC	
	351	TGTCGGACAG	CGCTTTCGGA	CACAGGTTTA	TCCGACTTCC	GTCTTATATC	
	401	GCAAAATAAG	GAAATCTTC	AAAACCTACG	TCGGCGAACC	CGATTTCGGC	
	451	AAACTCTACC	AAGAAATCGA	TACGCGCGTG	GCgCAATAG		

m544 . pep

1 MXKILTAAVV ALIGILLAIV LXPDSKTAPA FSXPDLHGKT VSNADLQGV
51 TLINFWFPC PGCVSXMPKI IKTANDYKXK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGQ AFGTQVYPTS VLIK*GEIF KTYVGEPDFG
151 KLYOEIDTRV AQ*

from *N. gonorrhoeae*:

m544/g544

	10	20	30	40	50	60
m544 . pep	MXKILTA	AAVVALIGILL	AIVLXPDSKT	APAFSXPDL	HGKTVSNADL	QGKVTLINFWFPSC
g544	MKKILTA	AAVVALIGILL	ATVLI	PDPSKT	APAFSLPDL	HGKTVSNADL
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 . pep	PGCVSXMPK	IIKTANDYK	KKNFQVL	AVAQPIDP	IESVRQY	VKDYG
g544	PGCVSEMP	KVTKTANDY	KKNKDFQ	VLAVAQ	PIDP	IESVRQY
	70	80	90	100	110	120
	130	140	150	160		
m544 . pep	AFGTQVYPT	SVLIGKXGE	IFKTYVGE	PDFGKLYQE	IDTRVAQX	
g544	AFGTQVYPT	SVLIGKXGE	ILKTYVGE	PDFGKLYQE	IDTALAQX	
	130	140	150	160		

a544.seq

1	ATGAAAAAAA	TACTCACCGC	CGCCGTCGTC	GCACTGATCG	GCATCCTCCT
51	TGCCATCGTC	CTCATCCCCG	ACAGCAAAAC	CGCGCCCGCT	TTCTCCCTGT
101	CCGANCTGCA	CGGAAAAANC	GTTTNCAACG	CCGACCTGCA	AGGCNAAAGT
151	ANCTGTATTA	ANTTTTGGTT	TCCCTCCTGT	CCGGGTGTGA	TAGCGGAAAT
201	GNCCANAATC	ATTAATAACG	CAACTGACTA	TAAAAACAAA	AAGTCCAAG
251	TCCTTGCCGT	CGCCCAGCCC	ATCGATCCGA	TAGAAAGCGT	CCGCCAATAT
301	GTCAAAGACT	ACGGTTTGCC	GTTTACCGTC	ATGTATGATG	CGGACAAAGC
351	TGTCGGACAG	GCGTTCGGCA	CACAGGTTTA	TCCGACTTCC	GTCCTTATCG
401	GCAAAAAAGG	CGAAATCCTC	AAAAGTTATG	TCGGCGAACC	CGATTTCGGC
451	AAACTCTACC	AAGAAATCGA	TACCGCGCTG	GCACAATAG	

a544.pcp

1 MKKILTAADV ALIGILLAIV LIPDSKTAPA FSLSLHGKX VVNADLQGXV
51 XLIXFWFPSC PGCVSEMXXI IKTANDYKNK NFQVLAVAQP IDPIESVRQY
101 VKDYGLPFTV MYDADKAVGO AFGTOVYPTS VLIGKKGEIL KTYVGEPEFG

824

151 KLYQEIDTAL AQ*

m544/a544 88.9% identity in 162 aa overlap

	10	20	30	40	50	60
m544 .pep	MXKILTA	AVVALIG	ILLAIVL	XPDSKT	APAFSXP	DLHGKT
a544	MKKILTA	AVVALIG	ILLAIVL	IPDSKT	APAFSLS	XLHGKX
	10	20	30	40	50	60
	70	80	90	100	110	120
m544 .pep	PGCVSX	MPKIIK	TANDYK	XKNFQV	LAVAQPI	DIPIES
a544	PGCVSEM	XXIIK	TANDYK	NKNFQV	LAVAQPI	DIPIES
	70	80	90	100	110	120
	130	140	150	160		
m544 .pep	AFGTQV	YPTSVL	IGKXGE	IFKTYV	GEPDFG	KLYQEID
a544	AFGTQV	YPTSVL	IGKKGE	ILKTYV	GEPDFG	KLYQEID
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1591>:

g547 .seq

```

1  atgttcgtag ataacggatt taataaaacg gtagcgagtt ttgccccaaat
51  cgtcgaaact ttcgacgtat tcttcttttag gaacgattgc gccttttttta
101 cgcagatgaa acagcgggtgc ggttgggtct gctcgttggt atatctcggt
151 gatatatatta caagatgctgc cttcgagatt ccgaaccgct cctttaaaga
201 gcttgggctt ttgatacaga taagtctgtc ggaacgtttt aggactaatg
251 ccgaagtcga gatggatgcc cattacttcc ccttactcag aaaatattta
301 aaatttataa tgttacatat agttacaaat attagagttt tttgtgtgtg
351 cgtcaaggaa ttgttgacaa ttttagttaa aaatttgtct ccaaacggaa
401 aaaagcgggt tgttttttgt tgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1592; ORF 547.ng>:

g547 .pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFTRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIVTN IRVFCVCVKE LLTILVKNLS PNGKKRFVFC C*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1593>:

m547 .seq

```

1  ATGTTTCGTAG ATAACGGATT TAATAAAACG GTAGCGAGTT TTGCCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACGATTGC GCCTTTTTTA
101 CGCAGATGAA ACAGCGGTGC GGTGCGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG ATTCGAGATT CCGAACCCTC CTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTTT AGGACTAATG
251 CCGAAGTCGA GATGGATGCT CATTACTTCC CCTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTWTGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT TAAAAATTG TCTCCAAACG
401 GAAAAAAGCG GTTTGTTTTT TGTGTGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1594; ORF 547>:

m547 .pep

```

1  MFVDNGFNKT VASFAQIVET FDVFFFRNDC AFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEMDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXCVCKV ELLTILVKNL SPNGKKRFVF CC*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 547 shows 97.2% identity over a 142 aa overlap with a predicted ORF (ORF 547.ng) from *N. gonorrhoeae*:

m547/g547

825

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
g547	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFTRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLFIMLHIFTNIKVFXCVCVK					
g547	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLFIMLHIVTNIRVF-CVCVK					
	70	80	90	100	110	
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
g547	ELLTILVKNLSPNGKKRFVFCCX					
	120	130	140			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1595>:

```
a547.seq
1  ATGTCGTAG ATAACGGATT TAATAAACG GTAGCGAGTT TTGCCCAAAT
51  CGTCGAAACT TTCGACGTAT TCTTCTTTAG GAACAATTGC ACCTTTTSTA
101 CGCAGATGAA ACAGCGGTGC GGTGGGTCT GCTCGTTGGT ATATCTCGTT
151 GATATCTTTC CAAGATGCGG CTTCGAGATT CCGAACCGCT CCTTTAAAGA
201 GCTTGGGCTT TTGATACAGA TAAGTCTGTC GGAACGTTT AGGACTAATG
251 CCGAAGTCGA GATAGATGCT CATTACTTCC CTTACTCAG AAAATATTTA
301 AAATTTATAA TGTTACATAT ATTTACAAAT ATTAAAGTTT TTTT.TGTGT
351 GTGCGTCAAG GAATTGTTGA CAATTTTAGT T
```

This corresponds to the amino acid sequence <SEQ ID 1596; ORF 547.a>:

```
a547.pep
1  MFVDNGFNKT VASFAQIVET FDVFFFRNNC TFFTQMKQRC GWVCSLVYLV
51  DIFPRCGFEI PNRSFKELGL LIQISLSERF RTNAEVEIDA HYFPLLRKYL
101 KFIMLHIFTN IKVFXCVCVK ELLTILV
```

m547/a547 97.6% identity in 127 aa overlap

	10	20	30	40	50	60
m547.pep	MFVDNGFNKTVASFAQIVETFDVFFFRNDCAFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
a547	MFVDNGFNKTVASFAQIVETFDVFFFRNNTFFTQMKQRCGWVCSLVYLVDIFPRCGFEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m547.pep	PNRSFKELGLLIQISLSERFRTNAEVEMDAHYPLLRKYLFIMLHIFTNIKVFXCVCVK					
a547	PNRSFKELGLLIQISLSERFRTNAEVEIDAHYPLLRKYLFIMLHIFTNIKVFXCVCVK					
	70	80	90	100	110	120
	130	140				
m547.pep	ELLTILVKNLSPNGKKRFVFCCX					
a547	ELLTILV					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1597>:

```
g548.seq
1  atgttttccg taccgcgttc ctttttgccg ggcgttttcg tacttgccgc
51  gcttgccgcc tgcaaacctc aagacaacag tgcggcgcaa gccgcttctt
101 caagtgcacg cgcgcgggct gcggaataat cggcaaaagg gcaaacgcgc
151 ggtacggata tgcgtaagga agacatcggc ggcgatttca cactgaccga
201 cggcgaaggc aagcctttca gcctgagcga tttgaaaggc aaggtcgtga
251 ttctgtcttt cggcttttac cactgtcccg atgtctgccc gacagggctt
```

826

```

301  ttgacgtaca gcgacacttt gaagcagttg ggcgggcagg ctaaggacgt
351  gaaagtgggtg ttcgtcagca tcgatccgga acgcgacacg cctgaaatca
401  tcggcaagta tgccaaacag ttcaatccgg actttatcgg tctgacggca
451  acgggcggcc aaaacctgcc ggtcatcaag cagcaatacc gcgtggtttc
501  tgccaaaatc aatcaaaaag acgacagcga aaactatttg gtcgaccact
551  cttccggtgc gtatcttatc gataaaaacg gtgaggttgc cattttctcg
601  ccttacggaa gcgagccgga aacgattgct gccgatgtaa ggaccctgct
651  ctga

```

This corresponds to the amino acid sequence <SEQ ID 1598; ORF 548.ng>:

g548.pep

```

1  MFSVPRSFLP GVFLAALAA CKPQDNSAAQ AASSSASAPA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFSLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV VFSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGGQNLPIVK QQYRVVSAKI NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1599>:

m548.seq

```

1  ATGTTTTCCG TACCGCGTTC CTTTTTGCCG GCGGTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TGCGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAATG CGGCAAAGCA AnACACGCGC
151 GGTACGGATA TCGGTAAGGA AGACATCGGC GGCGATTTC ACGTGACCGA
201 CGGCGAAGGC AAGCCTTTCA ACCTGAGCGA TTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GGCGGCGAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCAAACAG TTCAATCCGG ACTTTATCGs TCTGACGGCA
451 ACGGGCGGCC AAAACCTGCC GGTCATCAAG CAGCAATACc GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAmG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1600; ORF 548>:

m548.pep

```

1  MFSVPRSFLP GVFLAALAA CKPQDNSAAQ VASSSASASA AENAAKQXTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTGL
101 LTYSDTLKQL GGQAKDVKV VFSIDPERDT PEIIGKYAKQ FNPDFIXLTA
151 TGGQNLPIVK QQYRVVSAKV NQXDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTLL*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 548 shows 95.9% identity over a 217 aa overlap with a predicted ORF (ORF 548.ng) from *N. gonorrhoeae*:

m548/g548

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFLAALAAACKPQDNSAAQVASSSASASAAENAAKQXTRGTD					
g548	MFSVPRSFLPGVFLAALAAACKPQDNSAAQAASSSASAPAAENAAKPQTRGTD					
	10	20	30	40	50	60
	70 80 90 100 110 120					
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTPELLTYSDTLKQLGGQAKDVKV					
g548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTGLLTYSIDLKQLGGQAKDVKV					
	70	80	90	100	110	120
	130 140 150 160 170 180					
m548.pep	FVSIIDPERDTPEIIGKYAKQFNPDFIXLTATGGQNLPIVKQQYRVVSAKVNQXDDSENYL					
g548	FVSIIDPERDTPEIIGKYAKQFNPDFIGLTATGGQNLPIVKQQYRVVSAKINQKDDSENYL					
	130	140	150	160	170	180

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	190	200	210
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
g548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX		
	190	200	210

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1601>:

```

a548.seq
1  ATGTTTTCCTG TACCGCGTTC CTTTTTGCCG GCGGTTTTTCG TACTTGCCGC
51  GCTTGCCGCC TGCAAACCTC AAGACAACAG TCGGGCGCAA GTCGCTTCTT
101 CAAGTGCATC CGCGTCGGCT GCGGAAAATG CGGCAAAGCC GCAAACGCGC
151 GGTACGGATA TCGTAAGGA AGACATCGGC GGCATTTCAT CGCTGACCGA
201 CGGCGAAGGC AAGCCTTCA ACCTGAGCGA TTTGAAAGGC AAGGTCGTGA
251 TTCTGTCTTT CGGCTTTACG CACTGTCCCG ATGTCTGCCC GACAGAGCTT
301 TTGACGTACA GCGACACGTT GAAGCAGTTG GCGGGCAGG CTAAGGACGT
351 GAAAGTGGTG TTCGTCAGCA TCGATCCGGA ACGCGACACG CCTGAAATCA
401 TCGGCAAGTA TGCCAAACAG TTCAATCCGG ACTTTATCGG TCTGACGGCA
451 ACGGGCGACC AAAACCTGCC GGTCAATCAAG CAGCAATACC GCGTGGTTTC
501 TGCCAAAGTC AATCAAAAAG ACGACAGCGA AAACATTTTG GTCGACCACT
551 CTTCCGGTGC GTATCTCATC GACAAAAACG GTGAGGTTGC CATTTTCTCG
601 CCTTACGGAA GCGAGCCGGA AACGATTGCT GCCGATGTAA GGACCCTGCT
651 CTGA

```

This corresponds to the amino acid sequence <SEQ ID 1602; ORF 548.a>:

```

a548.pep
1  MFSVPRSFLP GVFVLAALAA CKPQDNSAAQ VASSSASASA AENAAKPQTR
51  GTDMRKEDIG GDFLTLDGEG KPFNLSDLKG KVVILSFGFT HCPDVCPTL
101 LTYSDTLKQL GGQAKDVKV VFSIDPERDT PEIIGKYAKQ FNPDFIGLTA
151 TGDQNLPIVK QQYRVVSAKV NQKDDSENYL VDHSSGAYLI DKNGEVAIFS
201 PYGSEPETIA ADVRTL*

```

m548/a548 97.7% identity in 217 aa overlap

	10	20	30	40	50	60
m548.pep	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASA	AENAAKQXTRGTDMRKEDIG				
a548	MFSVPRSFLPGVFVLAALAAACKPQDNSAAQVASSSASASA	AENAAKQXTRGTDMRKEDIG				
	10	20	30	40	50	60
m548.pep	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELL	TYSDTLKQLGGQAKDVKV				
a548	GDFLTLDGEGKPFNLSDLKGKVVILSFGFTHCPDVCPTELL	TYSDTLKQLGGQAKDVKV				
	70	80	90	100	110	120
m548.pep	FVSIDPERDTP	PEIIGKYAKQFNP	DFIXLTATGGQNL	PVIKQQYRVV	SAKVNQXDD	SENYL
a548	FVSIDPERDTP	PEIIGKYAKQFNP	DFIGLTATGDQNL	PVIKQQYRVV	SAKVNQXDD	SENYL
	130	140	150	160	170	180
m548.pep	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
a548	VDHSSGAYLIDKNGEVAIFSPYGSEPETIAADVRTLTX					
	190	200	210			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1603>:

```

g550.seq
1  atgataacgg acaggtttca tctctttcat tttccagtat ctttcattta
51  tcaatctgac aacaaaatgc cgcctgaaaa cagttcagac ggcatthtaa
101 ccacaaacgg cttacagctt ccattcgccc aacttggcag cgtaagcttc

```

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```

151 caaatctgca atcggacggg ttgccacgcc gctttccatc gctgcttttg
201 cggcagccgt agcgacgcga ggcagcaggc ggaatcgaa cggagtagga
251 atcaggtatt ccgcgccgaa ttcgaatttc ttaccgtaag cggcaaccac
301 ttcttcgggt acttcttcca tcgccaaatc tgccaaagca tacacgcagg
351 cgcgtttcat ttcttcggtt atggtgggtt cgccgacatc caacgcgccc
401 cggaagatga acgggaagca caatacgttg ttcacttggt tcgggaagtc
451 ggagcgcccg gtaccgataa ccacgtcccg acgggtttct ttcgccagcg
501 gcggcaggat ttccggattc gggttggcca tggcgaacac gatggggttt
551 tcgttcacgt tgttcaacat ttcaggcgct agcagggttg cgccggagag
601 gcccaagaag atgtctttgc cttaaacgc atcggaagt acgcgccggc
651 cggtgtcttc aacggcgtag aatttttttg attcgtccat gcggtctttg
701 tcttcgcggg tttggtaaat cagcctttg gagttgcaa cggttacgtt
751 ttcacgtttc aagcccaaat ccagcagttg gttcaggcag gcaatcgcg
801 cggcacctgc gccggagcac accaaagtcg cttcttcgat tttacggccg
851 gtataacgca gggcggtcaa tacggcggcg gcggtaatga tggccgtgcc
901 gtgctggtca tcatgaaata cggggatttt gcagcgtttg cgtaa

```

This corresponds to the amino acid sequence <SEQ ID 1604; ORF 550.ng>:

```

g550.pep
  1 MITDRFHLFH FVPSFIYQSD NKMPPENSSD GILTTNGLQL PFAQLGSVSF
 51 QICNRTGCHA AFHRCFGSSR SDARQQAGIE RSRNQVFRAE FEFLTVSGNH
101 FFGYFFHRQI CQSIHAGAFH FFVDGGCADI QRAPEDEREA QYVHLVREV
151 GAAGTDNHVR TGFFRQRQD FRIRVGHGEH DGFFVHRVQH FRRQQVCAGE
201 AQEDVFAFNR IGKYAPAVVF NGVEFFGFVH AVFVFAGLVN HAFGVANGYV
251 FTFQAQIQQL VQAGNRGGTC AGAHQSRFFD FTAGITQGVQ YGGGGNDGRA
301 VLVIMKYGDF AAFA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1605>:

```

m550.seq (partial)
  1 ..GACGGCATCG GCAAGCACGC GCTGGCCGTT GTCTTCAATG GCGTAGAACT
 51 GTTTGGACTC GTCCATACGG TCTTTGTCTT CGCGGGTTTG GTAAATCACG
101 CCTTTGGAGT CGCAAACGGT CACGTTTTCG CGTTTCAAGC CCAAATCCAG
151 CAATTGGwTC AAGCAGGCAA TCGCGGCCG ACCTGCGCCG GAACACACCA
201 AAGTCGCTTC TTCGATTTTA CGGCCGGTAA AACGCAkGGC GTTCAATACG
251 GCGGCGGCCG TAATGATGGC CGTGCCGTGC TGGTCGTCGT GGAATACGGG
301 GATTTTGCAG CGTTTGCCTA A

```

This corresponds to the amino acid sequence <SEQ ID 1606; ORF 550>:

```

m550.pep (partial)
  1 ..DGIGKHALAV VFNGVELFGL VHTVFVFAGL VNHAFGVANG HVFAFQAQIQ
 51 QLXQAGNRGR TCAGTHQSRF FDFTAGKTXG VOYGGGGNDG RAVLVVVEYG
101 DFAAFA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 550 shows ___% identity over a ___ aa overlap with a predicted ORF (ORF 550.ng) from *N. gonorrhoeae*:

```

m550/g550

m550.pep
          10      20      30
          DGIGKHALAVVFNGVELFGLVHTVFVFAGLVN
          |||:| ||||| |||:| |||:| |||||
g550      DGFFVHRVQHFRROQVCAGEAQEDVFAFNRIGKYAPAVVFNGVEFFGFVHAVFVFAGLVN
          190      200      210      220      230      240

          40      50      60      70      80      90
m550.pep  HAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDGRA
          ||||| |||:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g550      HAFGVANGYVFTFQAQIQQLVQAGNRGGTCAGAHQSRFFDFTAGITQGVQYGGGGNDGRA
          250      260      270      280      290      300

          100
m550.pep  VLVVVEYGDFAAFAFAX
          |||:| ||||| |||
g550      VLVIMKYGDFAAFAFAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1607>:

```
a550.seq
1   CTATATCAAT CTGACAGCAA AATGCCGCCT GAAAACAGTT CAGACGGCAT
51  TTTAACCGCA AACGGCTTAC AGCTTCCATT CGCTCAGCTT GGCAGCGTAA
101 GCTTCCAAAT CTGCAATCGG ACGGGTTGCC ACGCCGCTTT CCATCGCTGC
151 TTTGGCGGCA GCCGTAGCAA CGCGCGGCAG CAGGCGGGAA TCGAACGGAG
201 TCGGAATCAG GTATTCCGCG CCGAATTCAA ATTTCTTACC GTAAGCGGCA
251 ACCACTTCTT CGGTTACCTC TTCCATCGCC AAATCCGCCA AAGCATACAC
301 GCAGGCGCGT TTCATTTCTT CGTTGATGGT CGTCGCGCCG ACATCCAACG
351 CACCGCGGAA GATGAACGGG AAGCACAATA CATTGTTTAC TTGGTTCGGG
401 AAGTCGGAGC GGCCGGTACC GATAACCACG TCCGGACGGG TTTCTTTTCG
451 CAGCGGCGGC AGGATTTCGG GATTTCGGTT GCCCATAGCG AACACGATGG
501 GTTTTTTCGT CATGGTGTTT AGTATTTTCA GCGTCAGCAG GTTCGCGCCG
551 GAGAGGCCCA AGAAGATGTC TTTGCCTTTG ACGGCATCGG CAAGCACGCG
601 CTGGCCGTTG TCTTCAATGG CGTAGAACTG TTTGGACTCG TCCATACGGT
651 CTTTGTCTTC GCGGGTTTGG TAAATCACGC CTTTGGAGTC GCAAACGGTC
701 ACGTTTTCGC GTTTCAAGCC CAAATCCAGC AATTGGTTCA AGCAGGCAAT
751 CGCGGCCGCA CCTGCGCCGG AACACACCAA AGTCGCTTCT TCGATTTTAC
801 GGCCGGTAAA ACGCAGGGCG TTCAATACGG CAGCGGCGGT AATGATGGCC
851 GTGCCGTGCT GGTGCTGCTG GAATACGGGG ATTTTGCAGC GTTTGCGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1608; ORF 550.a>:

```
a550.pep
1   LYQSDSKMPP ENSSDGILTA NGLQLPFAQL GSVSFQICNR TGCHAAFHRC
51  FGGSRSNARQ QAGIERSRNQ VFRAEFKFLT VSGNHFFGYL FHRQIRQSIH
101 AGAFHFFVDG RRADIQRTAE DEREAYIVH LVREVGAAGT DNHVRTGFFER
151 QRRQDFRIRV GHSEHDGFFV HGVQYFRRQQ VRAGEAQEDV FAFDGIGKHA
201 LAVVFNGVEL FGLVHTVFEV AGLVNHAFGV ANGHVFAFQA QIQQLVQAGN
251 RGRTCAGTHQ SRFFDFTAGK TQGVQYGS GG NDGRAVLVVV EYGDFAAFA*
```

m550/a550 97.2% identity in 106 aa overlap

				10	20	30
m550.pep				DGIGKHALAVVFNGVELFGLVHTVVFV	FAGL	
a550	EHDGFFVHGVQYFRRQQVRAGEAQEDVFAFDGIGKHALAVVFNGVELFGLVHTVVFV	FAGL				
	170	180	190	200	210	220
		40	50	60	70	80
m550.pep	VNHAFGVANGHVFAFQAQIQQLXQAGNRGRTCAGTHQSRFFDFTAGKTXGVQYGGGGNDG					
a550	VNHAFGVANGHVFAFQAQIQQLVQAGNRGRTCAGTHQSRFFDFTAGKTQGVQYGS GGNDG					
	230	240	250	260	270	280
		100				
m550.pep	RAVLVVVEYGDFAAFAX					
a550	RAVLVVVEYGDFAAFAX					
	290	300				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1609>:

```
g552.seq
1   atgaagctga aaaccttggt attgcccttc gccgcactgg cattgtgtgc
51  caacgcattt gccgccccgc ccggcgacgc gtcgttggca cgttggtcgg
101 atacgcagaa tttcgaccgg gatatagaaa aaaatatgat tgaaggcttt
151 aatgccggat ttaaaccgta tgcggacaaa gcccttgccg aaatgccgga
201 agcgaaaaaa gatcaggcgg cagaagcctt taatcgttat cgtgagaatg
251 ttttgaaaga tttgattacg cccgaagtga aacaggctgt ccgcaatacc
301 ttattgaaga atgcccggtg aatatacacg caagaagaaa ttgacggcat
351 gattgccttt tacggttcgc ctgtcgggtc gtccgtcgtt gccaaaaatc
401 cgcgcctaat caagaaatcg atgagtgaat tagcggatc ttggactgca
```

830

451 ttgtcagggg aaatcgcgcg acatcatctg cccgagttta cggaagagtt
 501 acggcgcatc atctgcggcg gtatagtggg ttaa

This corresponds to the amino acid sequence <SEQ ID 1610; ORF552.ng>:

g552.pep

1 MKLKTLLLPF AALALCANAF AAPPGDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIARHHL PEFTEELRRI ICGGIVD*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1611>:

m552.seq (partial)

1 ..ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAAACCGTA TCGCGACAAA GCCCTTGCCG AAATGCCGGA
 201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
 251 TTTTGAAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
 301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
 351 GATTGCCTTT TACGGTTCGC CTGTCGGTCA GTCCGTCGTT GCCAAAAATC
 401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAG TAGCGGTATC TTGGACTGCA
 451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
 501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
 551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

This corresponds to the amino acid sequence <SEQ ID 1612; ORF 552>:

m552.pep (partial)

1 ..IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
 101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
 151 LSGKIAQHHL PEFTEELRRI ICGKPNPDAG CKQAGQVGKR HQK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 552 shows 97.1% identity over a 174 aa overlap with a predicted ORF (ORF 552.ng) from *N. gonorrhoeae*:

m552/g552

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
g552	MKLKTLLLPFAALALCANAFAPPGDASLARWLDTQNFDRDIEKNMIEGFNAGFKPYADK					
	10	20	30	40	50	60
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
g552	ALAEMPEAKKDQAAEAFNRYRENVLKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF					
	70	80	90	100	110	120
m552.pep	YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIAQHHLPEFTEELRRIICGGKPNPDAG					
g552	YGSPVGQSVVAKNPRLIKKSMEIAVSWTALSGKIARHHLPEFTEELRRIICGGIVDX					
	130	140	150	160	170	
m552.pep	CKQAGQVGKRHQKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1613>:

a552.seq

1 ATTAACTGA AAACCTTGTT ATTGCCCTTC GCCACGCTGG CATTGTGCAC
 51 CAATGCTTTT GCCGCCCCGC CCAGCGACGC GTCGTTGGCG CGTTGGCTGG
 101 ATACGCAGAA TTTTGACCGG GATATAGAAA AAAATATGAT TGAGGGCTTT
 151 AATGCCGGAT TTAAACCGTA TCGCGACAAA GCCCTTGCCG AAATGCCGGA

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```

201 AGCGAAAAAA GATCAGGCGG CAGAAGCCTT TAACCGTTAT CGTGAGAATG
251 TTTTGAAGA TTTGATTACG CCCGAAGTGA AACAGGCTGT CCGCAATACT
301 TTATTGAAGA ATGCCCGTGA GATATACACG CAAGAAGAAA TTGACGGCAT
351 GATTGCCTTT TACGGTTTCG CTTGTCGGTCA GTCCGTCGTT GCCAAAAATC
401 CGCGCTTAAT CAAGAAATCG ATGAGTGAAA TAGCGGTATC TTGGACTGCA
451 TTGTCAGGGA AAATCGCGCA ACATCATCTG CCCGAGTTTA CGGAAGAGTT
501 GCGGCGCATC ATCTGCGGCG GTAAAAATCC CGATGCGGGC TGTAACAACG
551 CCGGACAGGT TGGGAAAAGG CATCAGAAAT AA

```

This corresponds to the amino acid sequence <SEQ ID 1614; ORF 552.a>:

```

a552.pep
  1 IKLKTLLLPF ATLALCTNAF AAPPSDASLA RWLDTQNFDR DIEKNMIEGF
 51 NAGFKPYADK ALAEMPEAKK DQAAEAFNRY RENVLKDLIT PEVKQAVRNT
101 LLKNAREIYT QEEIDGMIAF YGSPVGQSVV AKNPRLIKKS MSEIAVSWTA
151 LSGKIAQHHL PEFTEELRRI ICGKKNPDAG CKQAGQVGKR HQK*

```

m552/a552 100.0% identity in 193 aa overlap

	10	20	30	40	50	60
m552.pep	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
a552	IKLKTLLLPFATLALCTNAFAAPPSDASLARWLD	TQNFDRDIEKNMIEGFNAGFKPYADK				
	10	20	30	40	50	60
	70	80	90	100	110	120
m552.pep	ALAEMPEAKKDQAAEAFNRYRENV	LKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
a552	ALAEMPEAKKDQAAEAFNRYRENV	LKDLITPEVKQAVRNTLLKNAREIYTQEEIDGMIAF				
	70	80	90	100	110	120
	130	140	150	160	170	180
m552.pep	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHL	PEFTEELRRIICGKKNPDAG				
a552	YGSPVGQSVVAKNPRLIKSMSEIAVSWTALSGKIAQHHL	PEFTEELRRIICGKKNPDAG				
	130	140	150	160	170	180
	190					
m552.pep	CKQAGQVGKRHQKX					
a552	CKQAGQVGKRHQKX					
	190					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1615>:

```

m552-1.seq
  1 TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
 51 GTGCACCAAT GCTTTTGCCG CCCCGCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAGCCCG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1616; ORF 552-1>:

```

m552-1.pep
  1 LNIKLTLLL PFATLALCTN AFAAPPSDAS LARWLDQNF DRDIEKNMIE
 51 GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVKDL ITPEVKQAVR
101 NTLLKNAREI YTQEEIDGMI AFYGVSPVQS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGKKNPD AGCKQAGQVG KRHQK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1617>:

a552-1.seq

832

```

1  TTGAATATTA AACTGAAAAC CTTGTTATTG CCCTTCGCCA CGCTGGCATT
51  GTGCACCAAT GCTTTTGCCG CCCC GCCCAG CGACGCGTCG TTGGCGCGTT
101 GGCTGGATAC GCAGAATTTT GACCGGGATA TAGAAAAAAA TATGATTGAG
151 GGCTTTAATG CCGGATTAA ACCGTATGCG GACAAAGCCC TTGCCGAAAT
201 GCCGGAAGCG AAAAAAGATC AGGCGGCAGA AGCCTTTAAC CGTTATCGTG
251 AGAATGTTTT GAAAGATTG ATTACGCCCG AAGTGAAACA GGCTGTCCGC
301 AATACTTTAT TGAAGAATGC CCGTGAGATA TACACGCAAG AAGAAATTGA
351 CGGCATGATT GCCTTTTACG GTTCGCCTGT CGGTCAGTCC GTCGTTGCCA
401 AAAATCCGCG CTTAATCAAG AAATCGATGA GTGAAATAGC GGTATCTTGG
451 ACTGCATTGT CAGGGAAAAT CGCGCAACAT CATCTGCCCG AGTTTACGGA
501 AGAGTTGCGG CGCATCATCT GCGGCGGTAA AAATCCCGAT GCGGGCTGTA
551 AACAAGCCGG ACAGGTTGGG AAAAGGCATC AGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1618; ORF 552-1.a>:

a552-1.pep

```

1  LNIKLKTL LL PFATLALCTN AFAAPPSDAS LARWLDTONF DRDIEKNMIE
51  GFNAGFKPYA DKALAEMPEA KKDQAAEAFN RYRENVLKDL ITPEVKQAVR
101 NTLLKNAREI YTOEEIDGMI AFYGSPVQGS VVAKNPRLIK KSMSEIAVSW
151 TALSGKIAQH HLPEFTEELR RIICGGKNPD AGCKQAGQVG KRHQK*

```

a552-1/m552-1 100.0% identity in 195 aa overlap

	10	20	30	40	50	60
a552-1.pep	LNIKLKTL	LLPFATLALCTN	AFAAPPSDAS	LARWLDTONF	DRDIEKNMIE	GFNAGFKPYA
m552-1	LNIKLKTL	LLPFATLALCTN	AFAAPPSDAS	LARWLDTONF	DRDIEKNMIE	GFNAGFKPYA
	70	80	90	100	110	120
a552-1.pep	DKALAEMPEAK	DKDQAAEAFN	RYRENVLKDL	ITPEVKQAVR	NTLLKNAREI	YTOEEIDGMI
m552-1	DKALAEMPEAK	DKDQAAEAFN	RYRENVLKDL	ITPEVKQAVR	NTLLKNAREI	YTOEEIDGMI
	130	140	150	160	170	180
a552-1.pep	AFYGSPVQGS	VVAKNPRLIK	KSMSEIAVSW	TALSGKIAQH	HLPEFTEELR	RIICGGKNPD
m552-1	AFYGSPVQGS	VVAKNPRLIK	KSMSEIAVSW	TALSGKIAQH	HLPEFTEELR	RIICGGKNPD
	190					
a552-1.pep	AGCKQAGQVG	KRHQKX				
m552-1	AGCKQAGQVG	KRHQKX				
	190					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1619>:

g553.seq

```

1  atggattatc tgcaaaacct gtctttgggc ttgacaaaaa agctgcccgt
51  tatactgcaa acagaagtag cggagtgtgg ctggcatgtg ctagcggctg
101 tggccgggatt ttatggtttc tatacggatt tgcgcgcact gcgttcaaaa
151 tactgtctgt cacttaaggg tgagaatttg gcagatattg ttcgttttgc
201 tgatgatatg gggctgacgg gacgggctgt gaggtggat ttagacgaat
251 tgggcagttt gcgcctgccc tgtattctac attgggattt gaatcatttt
301 gtggtgctgg aatcggtatc ttcggacggg gctgccgtca tggatccggc
351 ttcggggacga cgcaaagtca agacggagga aatatcgcg c aagtttacgg
401 gaattgtctt ggaactgtgg ccaaacacgc gtctcgaggc aggggaagaa
451 aagcaggaaa tccgcatact acccatgttg cgcgggattt ctgggctggg
501 gcggacattg tttcagcttt tggctttggc agcagcaatg gaagtgtttg
551 cttttttaca aaacgtcagc ttcaagatcg gacgtggtga atcgcttgcg
601 ttaatcggac gatcgggctg cggtaaactg acacttttgg atattttaag
651 cggcaatcta cctcccgaat caggcaaatg catgataaat gggcacgcaca
701 ttacagctt accgccacct ttattccgc aatttgagtg cgatggtcaa
751 ggcaggacga tgttttatag tggattaaat ttaaacgggt ag

```

This corresponds to the amino acid sequence <SEQ ID 1620; ORF 553.ng>:

g553.pep

833

```

1 MDYLQNLSLG LTKKLPVILQ TEVAECGLAC LAAVAGFYGF YTDLRALRSK
51 YCLSLKGENL ADIVRFADDM GLTGRALRLD LDELGSLRLP CILHWDNLNHF
101 VVLESVSSDG AAVMDPASGR RKVKTEEISR KFTGIALELW PNTRFEAGEE
151 KQEIRILPML RGISGLGRTL FOLLALAAAM EVFAFLQNVS FKIGRGESLA
201 LIGRSGCGKS TLLDILSGNL PPESGKVMIN GHDIYSLPPP FIPQFECDGQ
251 GRTMFYSLN LNR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1621>:

```

m553.seq (partial)
1 ATGGATTATT TATCAAGACT GTCCTTTGGA TTTAACAAAA AGCTACCTGT
51 CATTCTGCAA ACAGAAAGTTG CTGAATGTGG TTTAGCATGC CTGACATCCA
101 TCTTGTCTTA TTATGGCTTT CACACTGATT TAAGAACGTT ACGCCAAAAA
151 TACACCCTGT CATTAAAGGG CGCAAATCTT GCAGACATCA TGAGATTGG
201 CAATGAAATG AATTTAACGC CACGAGCTTT GCGTTTAGAG TTAGATGAGC
251 TGTCAAATTT ACAACTACCC TGCATTCTCC ATTGGAACCT AAACCATTTT
301 GTTGTACTTT GTTCCATTTC CAAAGACAGT ATCGTCATTA TGGACCCTGC
351 TGTGCGTATG CGAAAAATCA AAATGGACGA AGTTTCACAA AAATTCACAG
401 GGATTGCCCT AGAATTATTC CCAATACCC ATTTTGAAGA GAAAAAGAA
451 ACAAAGAAAA TCAAATATT ATCTCTATTA AGGGGGGG.T CAGGCTTAAA
501 ACGCTCTTTA ATTCAAATGC TTATATTAGC TATTTCTTTG GAAGTCTTTG
551 CATTG...

```

This corresponds to the amino acid sequence <SEQ ID 1622; ORF 553>:

```

m553.pep (partial)
1 MDYLSRLSFG FNKKLPVILQ TEVAECGLAC LTSILSYYG FHTDLRLRQK
51 YTLCLKGANL ADIMRFGNEM NLTPRALRLE LDELNLQLP CILHWNLNHF
101 VVLCISKDS IVIMDPAVGM RKIKMDEVSQ KFTGIALELF PNTHFEKKKE
151 TKKIKILSL RGSXGLKRSL IQMLILAI SL EVFAL...

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 553 shows 65.5% identity over a 185 aa overlap with a predicted ORF (ORF 553.ng) from *N. gonorrhoeae*:

m553/g553

	10	20	30	40	50	60
g553.pep	MDYLQNLSLGLTKKLPVILQTEVAECGLACLA	AAVAGFYGFYTDLRALRSKYCLSLKGENL				
m553	MDYLSRLSFGFNKKLPVILQTEVAECGLACL	TLSILSYYG FHTDLRLRQKYTLCLKGANL				
	10	20	30	40	50	60
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLP	CILHWDNLNHFVVLESVSSDGA	AVMDPASGR			
m553	ADIMRFGNEMNLTPRALRLELDELNLQLP	CILHWNLNHFVVLCISKDSIVIMDPAVGM				
	70	80	90	100	110	120
g553.pep	ADIVRFADDMGLTGRALRLDLDELGSLRLP	CILHWDNLNHFVVLESVSSDGA	AVMDPASGR			
m553	ADIMRFGNEMNLTPRALRLELDELNLQLP	CILHWNLNHFVVLCISKDSIVIMDPAVGM				
	70	80	90	100	110	120
g553.pep	RKVKTEEISRKFTGIALELWPNTRFEAGEEK	QEIRILPMLRGISGLGRTL	FOLLALAAAM			
m553	RKIKMDEVSQKFTGIALELFNTHFEKKET	KKIKILSLLRGSXGLKRSLIQMLILAI	SL			
	130	140	150	160	170	180
g553.pep	RKVKTEEISRKFTGIALELWPNTRFEAGEEK	QEIRILPMLRGISGLGRTL	FOLLALAAAM			
m553	RKIKMDEVSQKFTGIALELFNTHFEKKET	KKIKILSLLRGSXGLKRSLIQMLILAI	SL			
	130	140	150	160	170	180
g553.pep	EVFAFLQNVSFKIGRGESLALIGRSGCGKST	LDDILSGNLPPESGKVMINGHDIYSLPPP				
m553	EVFAL					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1623>:

```

a553.seq
1 ATGCCCCATC TGCAAAACCT GTCTTTGGGC TTAAAGAAAA AGCTGCCTGT
51 TATCCTGCAA ACAGAAATAT CAGAATGCGG CTGCGCATGT CTGGCGGCTG
101 TGGCGGGATT TCATGGTTTC CATACGAATT TACGCGCACT GCGTTCAAAA
151 TAC

```

This corresponds to the amino acid sequence <SEQ ID 1624; ORF 553.a>:

```
a553.pep
      1  MPHQLQNLSLG LKKKLPVILQ TEISECGLAC LAAVAGFHGF HTNLRALRSK
     51  Y
```

m553/a553 62.7% identity in 51 aa overlap

	10	20	30	40	50	60
m553.pep	MDYLSRSL	SFGFNKKLPVILQ	TEVAECGLAC	LSILSYGFHTDLR	TLRQKYTL	SLKGANL
	: :	: :	: :	: :	: :	: :
a553	MPHQLQNLS	LG LKKKLPVILQ	TEISECGLAC	LAAVAGFHGF	HTNLRALRSK	
	10	20	30	40	50	
	70	80	90	100	110	120
m553.pep	ADIMRFGNEMNLT	PRALRLELDEL	SNLQLPCILHWN	LNHFVVLCSISK	DSIVIMDPAVGM	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1625>:

```
g554.seq..
      1  atgacagcac ataaaatcct gcccgtcctt cttcccatca tcttaggcgt
     51  ttctcacgca acggctgcat cgcccgcgcc caacagaccg acggtacacg
    101  ccgccccac gctccaaaca cccgaaaccc tcacggcggc acacatcggt
    151  atcgaccttc aaagcaggca gactttatcc gccaaaaaca ccaatacccc
    201  tgtcgaaccg gcggcactaa cccaactgat gaccgcata tgggttttca
    251  aaaacatgaa atcgggaaat atccaatctg aagaaaactt aaaaataccc
    301  gaatccgcat gggcttcaga aggaagcaga atgtttgtac gtcccgcgca
    351  tacggtcagc accgacaaac tcttaaaagg catgattgcc ctatgcgcaa
    401  acgatgccgc cctaaccctt gccgaccggc tgggcaacgg ctcgattgaa
    451  aattttgtgc aacaaatgaa caaagaagcc cgacgcttgg gcatgaagaa
    501  caccgtattc aaaaaccgca caggcttggg tagagaagga cagggtttcca
    551  ccgccaagaa cctctccctg ctgtctgaag cattgatgcg cgactttccg
    601  gaattattac cgctgttttc catcaaactg ttcaagtgtt aaaaacataga
    651  acaaaacaac cgcaatatcc ttttatatag ggacaacaat gtaaacggcc
    701  tgaaagccgg gcacacagaa agcggcggtt acaaccttgc cgtgtcatac
    751  tccggcaacg gcaggcacat ccttgtcatc acactagggt cggaatcggc
    801  ggaaaccgca gcacgcgaca acagcaagct gctgaaccgg gcattgcagg
    851  ccttcgatac gcccaaaata tatccgaaag gcaaaaccgt tgcccaaatc
    901  caaatttccg gaggcagcaa aaaaaccgtc cgcgcagggt tcctcaaaga
    951  agcctacatc actctgccac ataaagaagc gaaaatggca gaacagattt
   1001  tggaaccatc acagccgatt cccgccccgg taaaaaaagg gcagatttta
   1051  ggaaaaatca aaatcaggca aaacggacat accattgccg aaaaagaaat
   1101  cgtcgcaact gaaaacgtag aaaaaagaag ccggtggcaa aggccttggg
   1151  cgctctgac agggcagtaa
```

This corresponds to the amino acid sequence <SEQ ID 1626; ORF 554.ng>:

```
m554.pep..
      1  MTAHKILPVL LPIILGVSHA TAASPAPNRP TVHAAPTLLQ PETLTAAHIV
     51  IDLQSRQTL AKNTNTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
    101  ESAWASEGSR MFVRPGDVS TDKLLKGMIA LCANDAALTL ADRLGNGSIE
    151  NFVQQMNKEA RRLGMKNTVF KNPTGLGREG QVSTAKDLSL LSEALMRDFP
    201  EYYPLFSIKS FKFNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
    251  SGNRHLVI TLGSESAETR ASDNSKLLNR ALQAFDTPKI YPKGKTVAQI
    301  QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
    351  GKIKIRQNGH TIAEKEIVAL ENVEKRSRWQ RLWTRLTGQ*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1627>:

```
m554.seq..
      1  ATGACAGCAC ATAAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
     51  TTCTCAGCCA ACGGCTGCAT CGCCCGCGCC CAACAGACCG ACGGTACACG
    101  CCGCCCCAC GTTCCAAACA CCGGAAACCC TCACAGCGGC ACACATCGTT
    151  ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAAACA TCAATACCCC
    201  TGTGTAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTC
    251  AAAACATGAA ATCGGGCAAT ATCCAATCTG AAGAAAACCT AAAAATACCC
```

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```

301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGTAC GTCCCGGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCCCTT GCCGGCCGCG TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAACCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCTG CTGTCTGAAG CATTGATGCG CGACTTTCCG
601 GAATATTACC CGCTGTTTTC CATCAAATCT TTCAAATTCA AAAATATAGA
651 ACAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCATAC
751 TCCGGCAACG GCAGGCACAT CCTTGTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAGG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1628; ORF 554>:

m554.pep..

```

1  MTAHKILPVL LSIILGVSHA TAASPAPNRP TVHAAPTFTQ PETLTAAHIV
51  IDLSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSGN IQSEENLKIP
101 ESAWASEGSR MFVRPGDTV TDKLLKGMIA LSANDAALTL AGR LGNSIE
151 NFVQOMNKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAL LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHLIIVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKT V RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACLTGQ*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 554 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 554.ng) from *N. gonorrhoeae*:

m554/g554

	10	20	30	40	50	60
m554.pep	MTAHKILPVLLSIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLSKQILS					
	: : : : :					
g554	MTAHKILPVLLPIILGVSHATAASPAPNRP TVHAAPTFTQ PETLTAAHIV IDLSKQILS					
	10	20	30	40	50	60
m554.pep	70	80	90	100	110	120
	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTV					
	: : : : :					
g554	AKNINTPVEPAALTQLMTAYLVFKNMKSGNIQSEENLKIPESAWASEGSRMFVRPGDTV					
	70	80	90	100	110	120
m554.pep	130	140	150	160	170	180
	TDKLLKGMIALSANDAALTL AGR LGNSIENFVQOMNKEARRLGMKNTVFKNPTGLSREG					
	: : : : :					
g554	TDKLLKGMIALCANDAALTL ADR LGNSIENFVQOMNKEARRLGMKNTVFKNPTGLGREG					
	130	140	150	160	170	180
m554.pep	190	200	210	220	230	240
	QVSTAKDLALLSEALMRDFPEYYPLFSIKSFKFKNIEQNNRNILLYRDNNVNGLKAGHTE					
	: : : : :					
g554	QVSTAKDLSLLSEALMRDFPEYYPLFSIKSFKFENIEQNNRNILLYRDNNVNGLKAGHTE					
	190	200	210	220	230	240
m554.pep	250	260	270	280	290	300
	SGGYNLAVSYSGNRHLIIVITLGSESAETR ASDNSKLLNWALQAFDTPKIYPKGKTVAQI					
	: : : : :					

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```

g554      SGGYNLAVSYSGNGRHILVITLGSESAETRASDNSKLLNRLQAFDTPKIYPKGKTVAQI
           250      260      270      280      290      300
m554 . pep      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGY
           310      320      330      340      350      360
g554      QISGGSKKTVRAGFLKEAYITLPHKEAKMAEQILETIQPIAPVKKGQILGKIKIRQNGH
           310      320      330      340      350      360

m554 . pep      TIAEKEIVALENVKKRSRWQRLWACL TGQX
           370      380      390
g554      TIAEKEIVALENVEKRSRWQRLWTRLTGQX
           370      380      390

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1629>:

```

a554 . seq
1   ATGACAGCAC ATAAATCCT GCCCGTCCTG CTTTCCATCA TCTTAGGCGT
51  TTCTCACGCA ACGGCTGCAT CGCCCCGCGC CAACAGACCG ACGGCACACG
101 CCGCCCCCAC GTTCCAAACA CCCGAAACCC TCACAGCGGC ACACATCGTT
151 ATCGACCTTC AAAGCAAACA GATTTTATCC GCCAAAACA TCAATACCCC
201 TGTGGAACCG GCGGCACTAA CCCAACTGAT GACCGCATAT CTGGTTTTCa
251 AAAACATGAA ATCGGGAAAT ATCCGATCTG AAGAAAACCT AAAAATACCC
301 GAATCCGCAT GGGCTTCAGA AGGAAGCAGA ATGTTTGATG GTCCCAGCGA
351 TACGGTCAGC ACCGACAAAC TCTTAAAGG CATGATTGCA CTATCCGCAA
401 ACGATGCCGC CCTAACCTTT GCCGCGCGGC TGGGCAACGG CTCGATTGAA
451 AATTTTGTGC AACAAATGAA CAAAGAAGCC CGACGCTTGG GCATGAAGAA
501 CACTGTATTC AAAAATCCGA CAGGCTTGAG TAGAGAAGGA CAGGTTTCCA
551 CCGCCAAAGA CCTCGCCCAG CTGTCTGAAG CATTGATGCG CGACTTTCGG
601 GAATATTACC CGCTGTTTTT CATCAAATCT TTCAAATTCA AAAATATAGA
651 GCAAAACAAC CGCAATATCC TTTTATATAG GGACAACAAT GTAAACGGTC
701 TGAAAGCCGG ACACACAGAA AGCGGCGGCT ACAACCTTGC CGTGTCAATC
751 TCCGGCAACG GCAGGCACAT CCTTGTCTATC ACATTGGGTT CGGAATCGGC
801 GGAAACACGC GCATCAGACA ACAGCAAGCT GCTGAACTGG GCATTGCAAG
851 CCTTCGATAC GCCCAAATA TATCCGAAAG GCAAAACCGT TGCCCAAATC
901 CAAATTTCCG GAGGCAGCAA AAAAACCGTC CGCGCAGGCT TCCTCAAAGA
951 AGCCTACATC ACTCTGCCAC ATAAGGAAGC GAAAATGGCA GAACAAATTC
1001 TAGAAACCAT ACAGCCGATT CCCGCCCCAG TAAAAAAAGG GCAAATTTTA
1051 GGAAAAATCA AAATCAGACA AAACGGATAC ACCATTGCCG AAAAAGAAAT
1101 CGTCGCACTG GAAAATGTAA AAAAAAGAAG CCGGTGGCAA AGGCTTTGGG
1151 CGTGTCTGAC AGGGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1630; ORF 554.a>:

```

a554 . pep
1   MTAHKILPVL LSIILGVSHA TAASPAPNRP TAHAAPTFTQ PETLTAHIV
51  IDLQSKQILS AKNINTPVEP AALTQLMTAY LVFKNMKSNG IRSEENLKIP
101 ESAWASEGSR MFVRPGD TVS TDKLLKGMIA LSANDAALT AGRLNGSIE
151 NFVQQMKEA RRLGMKNTVF KNPTGLSREG QVSTAKDLAQ LSEALMRDFP
201 EYYPLFSIKS FKFKNIEQNN RNILLYRDNN VNGLKAGHTE SGGYNLAVSY
251 SGNRHILVI TLGSESAETR ASDNSKLLNW ALQAFDTPKI YPKGKTVAQI
301 QISGGSKKTV RAGFLKEAYI TLPHEAKMA EQILETIQPI PAPVKKGQIL
351 GKIKIRQNGY TIAEKEIVAL ENVKKRSRWQ RLWACL TGQ*

```

m554/a554 99.2% identity in 389 aa overlap

```

           10      20      30      40      50      60
m554 . pep      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQTPETLTAHIVIDLQSKQILS
           10      20      30      40      50      60
a554      MTAHKILPVLLSIILGVSHATAASPAPNRPVHAAPTFTQTPETLTAHIVIDLQSKQILS
           10      20      30      40      50      60

           70      80      90      100     110     120
m554 . pep      AKNINTPVEPAALTQLMTAYLVFKNMKSNGNIQSEENLKIPESAWASEGSRMFVRPGD TVS
           70      80      90      100     110     120
a554      AKNINTPVEPAALTQLMTAYLVFKNMKSNGNIRSEENLKIPESAWASEGSRMFVRPGD TVS

```

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	70	80	90	100	110	120
	130	140	150	160	170	180
m554.pep	TDKLLKGMIALSANDAALTL	LAGRLGN	SIENFVQ	QMNKEARR	LGMKNTV	FKNPTGLSREG
a554	TDKLLKGMIALSANDAALTL	LAGRLGN	SIENFVQ	QMNKEARR	LGMKNTV	FKNPTGLSREG
	190	200	210	220	230	240
m554.pep	QVSTAKDLALLSEALMRD	FPEYYPL	FSIKSFK	FKNIEQNN	RNILLYR	DNNVNLKAGHTE
a554	QVSTAKDLAQLSEALMRD	FPEYYPL	FSIKSFK	FKNIEQNN	RNILLYR	DNNVNLKAGHTE
	250	260	270	280	290	300
m554.pep	SGGYNLAVSYSGNGRHIL	VITLGSE	SAETRASN	SKLLNWAL	QAFDTPK	IYPKGKTVAQI
a554	SGGYNLAVSYSGNGRHIL	VITLGSE	SAETRASN	SKLLNWAL	QAFDTPK	IYPKGKTVAQI
	310	320	330	340	350	360
m554.pep	QISGGSKKTVRAGFLKEA	YITLPHK	EAKMAEQI	LETIQPI	PAPVKKG	QILGKIKIRQNGY
a554	QISGGSKKTVRAGFLKEA	YITLPHK	EAKMAEQI	LETIQPI	PAPVKKG	QILGKIKIRQNGY
	370	380	390			
m554.pep	TIAEKEIVALENVKKRSR	WQRLWACL	TGQX			
a554	TIAEKEIVALENVKKRSR	WQRLWACL	TGQX			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1631>:

g556.seq..

```

1  atggacaata agaccaaact gcgcttgggc ggcctgattt tactgaccac
51  cgccgtttta agcctcatta tcgtattgat tgcgattcc tggccgcttg
101 ccatcctgct tgccgccgtc atcgtcgccg ccgctgcggg cggctttggt
151 tggacatccc gccgacagca acgccagttt atcgacgctc tgaaaaaatt
201 cgacatcgat cccgaaaaag gcagaatcaa cgaggcaaac ctgcgccgta
251 tgtaccacag cggcgggaaa caccagaaag atgcgattac cctgatctgc
301 ctgtcgcaaa aatgttcggt ggacgaggcg cagctatgt tcaaaaaacg
351 cccgacacgt caggaaatca atcaaatggc ggcaaaacag tcgcgcggtc
401 agaaacgtcc gcaccgttaa

```

This corresponds to the amino acid sequence <SEQ ID 1632; ORF 556.ng>:

g556.pep.

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC
101 LSQKCSVDEA HAMFKKRPT RQEINQMAAQ SRGQKRPHR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1633>:

m556.seq..

```

1  ATGGACAATA AGACCAAAC T GCGCTTGGGC GGCCTGATTT TACTGACCAC
51  CGCCGTTTTA AGCCTCATTA TCGTATTGAT TGTCGATTCC TGGCCGCTTG
101 CCATCCTGCT TGCAGCCGTC ATTGTCTGCTG CCGCTGCGGG CGGTTTTGTT
151 TGGACATCCC GCCGACAGCA ACGCCAGTTT ATCGAACGCC TGAAAAAATT
201 CGACATCGAT CCCGAAAAAG GCAGAATCAA CGAGGCAAAC CTGCGCCGTA
251 TGTACCACAG CGGCGGACAA CACCAGAAAG ATGCGATTAC CCTGATCTGC
301 CTGTGCAAAA AATGTTTCGGT GGACGAGGCG CACGCTATGT TCAAAAAACG
351 CCCGACACGT CAGGAAATCA ATCAAATGGC GGCAAAACAG TCGCGCGGTC
401 AGAAACGTCC GCACCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1634; ORF 556>:

m556.pep..

```

1  MDNKTKLRLG GLILLTTAVL SLIIVLIVDS WPLAILLAIV IVAAAAGGFV
51  WTSRRQQRQF IERLKKFDID PEKGRINEAN LRRMYHSGGQ HQKDAITLIC

```

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101 LSQKCSVDEA HAMFKKRPTR QEINQMAAKQ SRGQKRPHR*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*ORF 556 shows 100.0% identity over a 139 aa overlap with a predicted ORF (ORF 556.ng) from *N. gonorrhoeae*:

m556/g556

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
g556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
g556	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQK	RPHRX		
g556	QEINQ	MAAKQ	SRGQK	RPHRX		
	130	140				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1635>:

a556.seq

1	ATG	GACAATA	AGACCAA	ACT	GCGCT	TGGGC	GGCCT	GATTT	TACTG	ACCAC
51	CGC	CGTTT	TA	AGCCT	CATTA	TCGTAT	TGAT	TGTCG	ATTCC	TGGCC
101	CCAT	CCTGC	T	TGCCG	CCGTC	ATCGT	CGCCG	CCGCT	GCGGG	CGGCT
151	TGG	ACATCCC	GCCGAC	AGCA	ACGCC	AGTTT	ATCGA	ACGTC	TGAAAA	AATT
201	CGA	CATCG	AT	CCCGAAA	AAG	GCAGA	AATCA	CGAGG	CAAAC	CTGCG
251	TGT	ACCAC	AG	CGGCG	GACAA	CACCAA	AAAG	ATGCG	ATTAC	CCTGA
301	CTG	TCGCAA	A	AATGT	TCGGT	GGACG	AGGCG	CACGT	ATGT	TCAAAA
351	CCC	GACAC	GT	CAGGA	AATCA	ATCAA	ATGGC	GGCAA	AACAG	TCGCG
401	AGA	AACGT	CC	GCACC	GTAA					

This corresponds to the amino acid sequence <SEQ ID 1636; ORF 556.a>:

a556.pep

1	MDNKT	KLRLG	GLILLT	TAVL	SLIIVL	IVDS	WPLAIL	LAIV	IVAAA	AGGFV
51	WTSRR	QQRQF	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ	HQKDA	ITLIC
101	LSQK	CSVDEA	HAMFK	KRPTR	QEINQ	MAAKQ	SRGQK	RPHR*		

m556/a556 100.0% identity in 139 aa overlap

	10	20	30	40	50	60
m556.pep	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
a556	MDNKT	KLRLG	LILLT	TAVLS	LIIVL	IVDSW
	10	20	30	40	50	60
	70	80	90	100	110	120
m556.pep	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
a556	IERLK	KFDID	PEKGR	INEAN	LRRMY	HSGGQ
	70	80	90	100	110	120
	130	140				
m556.pep	QEINQ	MAAKQ	SRGQK	RPHRX		
a556	QEINQ	MAAKQ	SRGQK	RPHRX		
	130	140				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1637>:

g557.seq

```

1  atgaacaaaa tattccttac tgccgcagcc ttgggtgctgg gcgcgtgcgg
51  tttccacctg aaaggtgcag acggcatttc tccgccgctg acctaccgga
101 gctggcacat cgaaggcggg caggcattgc aatttccttt ggaaaccgcg
151 ctgtatcagg cttcgggcag ggtggacgat gctgccggcg cgcagatgac
201 cctgcgtata gacagcgttt cccaaaacaa ggaaacctat accgttacct
251 gtgcggcagt catcaacgaa tatcttttga tattgacggg tgaagcgag
301 gtattgaaac gcggcgagcc ggtcggcaaa ccgatgaccg tgtccgtccg
351 ccgcattttg gattatgccg acaacgaaat tttgggcaaa caggaagaag
401 aagaaacctt gtggcggaat atgcggcagg atgttgccga acagattgtc
451 cgccgcctga cctttctgaa ggcggaatga

```

This corresponds to the amino acid sequence <SEQ ID 1638; ORF 557.ng>:

g557.pep..

```

1  MNKIFLTAAL LVLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
51  LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRIL DYADNEILGK QEEEEELWAE MRQDVAEQIV
151 RRLTFLKAE*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1639>:

m557.seq..

```

1  ATGAACAAAC TGTTCCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
51  TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC GGTTCCTTTT GGAAACCGCG
151 CTGTATCAGG CTCGGGCAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
201 CCTGCGTATA GACAGCGTTT CCCAAAACAA GGAAACCTAC ACCGTTACCC
251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
301 GTATTGAAAC GCGGCGAGCC GGTCCGTAAA CCGATGACCG TGTCCGTCCG
351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAAA CAGGAAGAGG
401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
451 CGCCGCCTGA CCTTCTGAA GCGGAATGA

```

This corresponds to the amino acid sequence <SEQ ID 1640; ORF 557>:

m557.pep..

```

1  MNKLFLTAAL LMLGACGFHL KGADGISPPL TYRSWHIEGG QALRFPLETA
51  LYQASGRVDD AAGAQMTRLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
101 VLKRGEFVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAEQIV
151 RRLTFLKAE*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 557 shows 94.3% identity over a 159 aa overlap with a predicted ORF (ORF 557.ng) from *N. gonorrhoeae*:

m557/g557

	10	20	30	40	50	60
m557.pep	MNKLFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALRFPLETALYQASGRVDD					
g557	MNKIFLTAALVLMGACGFHLKGADGISPPLTYRSWHIEGGQALQFPLETALYQASGRVDD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTRLIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRVL					
g557	AAGAQMTRLIDSVSQNKETYTVTRAAVINEYLLILTVEAQVLKRGEFVGKPMTVSVRRIL					
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEILGKQEEEAALWAEMRQDAEQIVRRLTFLKAEX					
g557	DYADNEILGKQEEETLWAEMRQDAEQIVRRLTFLKAEX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1641>:

840

a557.seq
 1 ATGAACAAAC TGTTTCTTAC TGCCGCAGTG CTGATGCTGG GCGCGTGCGG
 51 TTTCCACCTG AAAGGTGCAG ACGGCATTTC TCCGCCGCTG ACCTACCGGA
 101 GCTGGCACAT CGAAGGCGGA CAGGCATTGC AGTTTCCTTT GGAAACCGCG
 151 CTGTATCAGG CTTTCGGGTAG GGTGGACGAT GCTGCCGGCG CGCAGATGAC
 201 CCTGCGTATA GACAGCGTTT CCAAAAACAA GGAAACCTAC ACCGTTACCC
 251 GTGCGGCAGT CATCAACGAA TATCTTTTGA TATTGACGGT TGAAGCGCAG
 301 GTATTGAAAC GCGGCGAGCC GGTCCGGCAA CCGATGACCG TGTCCTCCG
 351 CCGCGTCCTT GCTTATGCCG ACAACGAGAT CTTGGGCAA CAGGAAGAGG
 401 AAGCGGCATT GTGGGCGGAA ATGCGGCAGG ATGCCGCCGA ACAGATTGTC
 451 CGCCGCCTGA CTTTCTGAA GCGGAATGA

This corresponds to the amino acid sequence <SEQ ID 1642; ORF 557.a>:

a557.pep
 1 MNKLFLTA AV LMLGACGFHL KGADGISPPL TYRSWHIEGG QALQFPLETA
 51 LYQASGRVDD AAGAQMTLRI DSVSQNKETY TVTRAAVINE YLLILTVEAQ
 101 VLKRGE PVGK PMTVSVRRVL AYADNEILGK QEEEAALWAE MRQDAEQIV
 151 RRLTFLKAE*

m557/a557 99.4% identity in 159 aa overlap

	10	20	30	40	50	60
m557.pep	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
a557	MNKLFLTA	AVLMLGAC	GFHLKGAD	GISPPLTY	RSWHIEGG	QALRFPLE
	10	20	30	40	50	60
	70	80	90	100	110	120
m557.pep	AAGAQMTL	RIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGE
a557	AAGAQMTL	RIDSVSQN	KETYTVTR	AAVINEYL	LLILTVEA	QVLKRGE
	70	80	90	100	110	120
	130	140	150	160		
m557.pep	AYADNEIL	GKQEEEA	ALWAEMR	QDAEQIV	RRLTFLK	AEX
a557	AYADNEIL	GKQEEEA	ALWAEMR	QDAEQIV	RRLTFLK	AEX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1643>:

g558.seq.
 1 ATGGATGCTT GTTTTTTCGT CATTCCCGCA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCGGGAATGA
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGCTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGGCTGCC CTCCGATTAG
 201 ATTCTATCGC TATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTT CGACACCTCT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1644; ORF 558.ng>:

g558.pep.
 1 MDACFFVIPA QAGIRRFIV FKRSGRILAG AGMMPYTFE ELYMLQQGTA
 51 HQAPHCVLPE RGCPIRFYR YKQTGFNRKG MGIKSISDTS RAMPSNQSP
 101 LSDGIV*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1645>:

m558.seq.
 1 ATGAATGCTT GTTTTTTCGT CATTCCACAA CAGGCGGGAA TTCGGAGATT
 51 CGGGATTGTT TTCAAACGTT CGGGTCGGAT TCTTGCCGGT GCAGGAATGA
 101 TGCCCTTATA TACTTTCTCC GAGCTTTATA TGTTTCAACA GGGGACGGCA
 151 CATCAAGCAC CGCACTGCGT GTTGCCCGAA CGAGACTACC CTCCGATTAG
 201 ATTCTATCGC CATAAACAGA CGGGTTTCAA CCGAAAAGGA ATGGGGATAA
 251 AGTCCATTTT CGACATCTsT CGGGCGATGC CGTCTGAAAA CCAATCTCCA
 301 CTTTCAGACG GCATTGTTTA G

This corresponds to the amino acid sequence <SEQ ID 1646; ORF 558>:

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 558 shows 92.5% identity over a 106 aa overlap with a predicted ORF (ORF 558.ng) from *N. gonorrhoeae*:

m558/q558

	10	20	30	40	50	60
m558.pep	MNACFFVIPTQAGIRRF	GIVFKRSGRILAGAGM	PLYTFSELYMFQQGT	AHQAPHCVLPE		
	: : : : : : : : :	: : : : : : : : :	: : : : : : : : :	: : : : : : : : :	: : : : : : : : :	: : : : : : : : :
g558	MDACFFVIPAQAGIRRF	GIVFKRSGRILAGAGM	PLYTFSELYMLQQGT	AHQAPHCVLPE		
	10	20	30	40	50	60
	70	80	90	100		
m558.pep	RDYPPIRFYRHKQTGF	NRKGMGIKSISDIXR	AMPSENQSP	LSDGIVX		
g558	RGCPPIRFYRYKQTGF	NRKGMGIKSISDTSR	AMPSENQSP	LSDGIVX		
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEO ID 1647>:

a558.seq

1	ATGAATGCTT	GTTTTTTCGT	CATTCCCACA	CAGGCGGGAA	TTCGGAGATT
51	CGGGATTGTT	TTCAAACGTT	CGGGTCGGAT	TCTTGCCGGT	GCGGGAATGA
101	TGCCCTTATA	TATAGTGGAT	TAAATTTAAA	TCAGGACAAG	GCGACGAAAGC
151	CGCAGACAGT	ACAAATAGTA	CGGCAAGGCG	AGGCAACGCC	GCTCTGGTTT
201	AAATTTAATC	CACTATACTT	TCTCCGAGCT	TTATATGTTT	CAACAGAGGA
251	CGGCACATCA	AGCACCGCAC	TGCGTGTTGC	CGAACGAGA	CTGCCCTCCG
301	ATTAGATTCT	ATCGCTATAA	ACAGACGGGT	TTCAACCGAA	AAGGAATGGG
351	AATGAAGTCC	GTTCCGACA	CCTCTCGGGC	GATGCCGTCT	GAAAACCAAT
401	CTCCACTTTC	AGACCGCATT	GTTTAG		

This corresponds to the amino acid sequence <SEQ ID 1648; ORF 558.a>:

```
a558.pep
      1 MNACFFVIPT QAGIRRFQIV FKRSGRILAG AGMMPLYIVD *I*IRTRRRS
     51 RRQYK*YGKA RQRRTGLNLI HYTFSELYMF QQRTAHQAPH CVLPERDCPP
    101 IRFYRYKOTG FNRKGMGMKS VSDTSRAMPS ENOSPLSDGI V*
```

m558/a558 70.2% identity in 141 aa overlap

```

              10      20      30
m558.pep    MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLY-----
             |||||
a558        MNACFFVIPTQAGIRRFGIVFKRSGRILAGAGMMPLYIVDXIXIRTRRRSRRQYKXYGKA
              10      20      30      40      50      60

              40      50      60      70      80
m558.pep    -----TFSELYMFQQGTAHQAPHCVLPERDYPPIRFYRHKQTGFNRKGGMGIKS
             |||||
a558        RQRRTGLNLIHYTFSELYMFQQRTAHQAPHCVLPERDCPPIRFYRYKQTGFNRKGGMGMKS
              70      80      90     100     110     120

              90      100
m558.pep    ISDIXRAMPSENQSPLSDGIVX
             :|| |
a558        VSDTSRAMPSENQSPLSDGIVX
              130     140

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEO ID 1649>:

q560.seq

1 atgctcatca tccgcaacct gatttactgg ctgatactct qttccaqccct

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```

51  gattttcctc  tttcccttta  tgctgctcgc  ctcgcctttc  cgggacgggg
101 cgcacaagat  ggcgcgggtc  tgggtcggca  tcctcaactg  gtcgctcaaa
151 cacatcgctc  ggctcaaata  ccgcatcatc  ggcgcggaac  acattccgga
201 ccgcccctcc  gtcattctgc  ccaaacacca  aagcggctgg  gaaacgctcg
251 cgctccaaga  gatttttccg  ccgcagggtt  acgttgccaa  gcgcgagttg
301 ttcaaaatcc  cctttttcgg  ctggggcttg  aaactgggtc  aaaccatagg
351 catagaccgc  aacaaccgcc  gcgaagccaa  cgaacagctc  ataaaacagg
401 gtttggcgcg  caaaaacgaa  ggttattgga  ttaccatttt  ccccgaaagg
451 acgcgccttg  cgcccggaaa  acgcggcaaa  tacaaactcg  gcggcgcgcg
501 catggcgaaa  atgtttgaga  tggacatcgt  ccccgctcgc  ctcaacagcg
551 gcgaattttg  gccgaaaaat  tcctttctga  aatatccggg  ggaaatcacc
601 gtcatcatct  gtccgaccat  cccgcacgca  agcggcagcg  aagccgaatt
651 gatggaaaaa  tgcgaacacc  tcattgaaac  gcaacaaccg  cttatttccg
701 gcgcaggccc  gtttgccgcc  gaaatgccgt  ctgaaaccgc  atga

```

This corresponds to the amino acid sequence <SEQ ID 1650; ORF 560.ng>:

g560.pep..

```

1  MLIIRNLIYW LILCSSLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAEHIPDRPS VICAKHQSGW ETLALQEIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VIICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA EMPSET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1651>:

m560.seq

```

1  ATGCTCATCA TCCGCAACCT GATTTACTGG CTGATACTCT GTTCCACCCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGGGACGGGG
101 CGCACAAGAT GGC GCGGGTGC TGGGTGCGCA TTCTCAACTG GTCGCTCAAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGC GCGGAAA ACATCCCGGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCGG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAAATCC CCTTTTTCGG CTGGGGCTTG AAAC TGGTCA AAACCATAGG
351 CATAGACCGC AACAAACGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTTGGTGCG CAAAAACGAA GGCTATTGGA TTACCATTTT CCCC GAAGGC
451 ACGCGCCTTG CGCCCGGAAA ACGCGGCAAA TACAAACTCG GCGGCGCGCG
501 CATGGCGAAA ATGTTT GAGA TGGACATCGT CCCC GTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAAC TCCTTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCCGCACGCA AGCGGCAGCG AAGCCGAATT
651 GATGGAAAAA TGCGAACATC TCATCGAAAC GCAACAACCG CTTATTCCG
701 GCGCAGGCCG GTTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1652; ORF 560>:

m560.pep

```

1  MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVGILNWSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLVRKNE GYWITIFPEG
151 TRLAPGKR GK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMEK CEHLIETQQP LISGAGPFAA KMPSETA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 560 shows 97.2% identity over a 246 aa overlap with a predicted ORF (ORF 560.ng) from *N. gonorrhoeae*:

m560/g560

```

          10      20      30      40      50      60
m560.pep  MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          |||||:|||||
g560       MLIIRNLIYWLILCSSLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLK HIVGLKYRII
          10      20      30      40      50      60

          70      80      90     100     110     120
m560.pep  GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g560       GAEHIPDRPSVICAKHQSGWETLALQEIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR

```

843

	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
g560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	:					
g560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAELEMEKCEHLIETQQPLISGAGPFAA					
	190	200	210	220	230	240
m560.pep	KMPSETAX					
	:					
g560	EMPSETX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1653>:

```

a560.seq
1   ATGCTCATCA TCCGCAACCT GATTACTGG CTGATACTCT GTTCCACCCT
51  GATTTTCCTC TTTCCCTTTA TGCTGCTCGC CTCGCCTTTC CGAGACGGGG
101 CGCACAAAGAT GGCGCGGGTC TGGGTCAAAA TCCTCAACCT CTCGCTCAA
151 CACATCGTCG GGCTCAAATA CCGCATCATC GGCGCGGAAA ACATCCCCGA
201 CCGCCCCGCC GTCATCTGCG CCAAACACCA AAGCGGCTGG GAAACGCTCG
251 CCCTTCAGGA CATTTTTCG CCGCAGGTTT ACGTTGCCAA ACGCGAGTTG
301 TTCAAATCC CTTTTCG CTGGGGCTTG AACTGGTCA AAACCATAGG
351 CATAGACCGC AACAACCGCC GCGAAGCCAA CGAGCAGCTC ATAAAACAGG
401 GGTGGCGCG CAAAACGAA GGCTATTGGA TTACCATTTT CCCCGAAGGC
451 ACACGCCTTG CGCCCGGAAA ACGCGGCAA TACAACTCG GCGCGCGCG
501 CATGGCGAAA ATGTTTGAGA TGGACATCGT CCGCGTCGCC CTCAACAGCG
551 GCGAATTTTG GCCGAAAAC TCCTTCTGA AATATCCGGG GGAAATCACC
601 GTCGTCATCT GTCCGACCAT CCGCAGCA AGCGGCAGCG AAGCCGAATT
651 GATGGGAAA TGCGAACACC TCATCGAAAC GCAGCAGCCG CTCATTTCG
701 GCGCAGGCC GTTGCCGCC AAAATGCCGT CTGAAACCGC ATGA

```

This corresponds to the amino acid sequence <SEQ ID 1654; ORF 560.a>:

```

a560.pep
1   MLIIRNLIYW LILCSTLIFL FPFMLLASPF RDGAHKMARV WVKILNLSLK
51  HIVGLKYRII GAENIPDRPA VICAKHQSGW ETLALQDIFP PQVYVAKREL
101 FKIPFFGWGL KLVKTIGIDR NNRREANEQL IKQGLARKNE GYWITIFPEG
151 TRLAPGKRGK YKLGGARMAK MFEMDIVPVA LNSGEFWPKN SFLKYPGEIT
201 VVICPTIPHA SGSEAELEMGK CEHLIETQQP LISGAGPFAA KMPSETA*

```

m560/a560 98.4% identity in 247 aa overlap

	10	20	30	40	50	60
m560.pep	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVGILNWSLKHIVGLKYRII					
a560	MLIIRNLIYWLILCSTLIFLFPFMLLASPF RDGAHKMARVWVKILNLSLKHIVGLKYRII					
	10	20	30	40	50	60
	70	80	90	100	110	120
m560.pep	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
a560	GAENIPDRPAVICAKHQSGWETLALQDIFPPQVYVAKRELFKIPFFGWGLKLVKTIGIDR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m560.pep	NNRREANEQLIKQGLVRKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					
	:					
a560	NNRREANEQLIKQGLARKNEGYWITIFPEGTRLAPGKRGKYKLGARMAMKFEMDIVPVA					

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	130	140	150	160	170	180
	190	200	210	220	230	240
m560.pep	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMKCEHLIETQQPLISGAGPFAA				
a560	LNSGEFWPKNSFLKYPGEITVVICPTIPHASGSEAE	LMGKCEHLIETQQPLISGAGPFAA				

m560.pep	KMPSETAX					
a560	KMPSETAX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1655>:

```

m561.seq.
1   ATGATACTGC CAGCCCGTTT TTCAGACGGC ATCAGCCTTT CCCTGCGCCT
51  GAAACTCCTG ACCGGACTGT GGGTCGGGTT GGCGGCATTG TCTGTCGTTT
101 TGACACTGCT GCTCTCTTTG CGTCTGGAAA ACGCGGCCTC CGTCATCGAA
151 GAGGCGGGCA ACTTGAGAAT GCAGGCATAC CGTCTGGCAT ACATGGCGGG
201 TGAAGGCTCG CCCCCTGCGC AAATTGACAA TCAGGTTGCC GAATTTGAAA
251 AAAGTTTAAA ACGCATTGCC CAAAGCGATG CCATCCATCC GCTGATTCTT
301 TCGGACACCC CTCTTGCTTA TGATTGATA CAATCCATGC TGATTATAGA
351 TTGGCAGGCA CACATCCTCC CCCCCTCCA GTCCTACCGG CGACCGACTC
401 AGGTCGATCT CTACCGCTTT GCCGGAACA TCGAACTGTT TTTGCAGGCA
451 TTGGAAGATG CCAACGAAAA AAACACATGG TGGCTCAGGC GTTTTCAATG
501 GGCAATTATG TTGATGACGC TGGTGTCTGC TGTACTGATG CTGTTTTGGC
551 ACCAGATTGG GGTATCCGG CCGCTGCAGG CGTTAAGGGA AGGTGCGGAA
601 CGCATCGGAC GGAGGTGTTT CGATATTCCG GTTCCCGAAG GCGGTACGCC
651 GGAATTCAAA CAGGTCGGGC GTTGTTTCAA TCAAATGGGC GGCAGGTTGA
701 AAATTTTATA TGATGATTGG GAAGGACAAG TCGCCGAGCA GACACGCAGT
751 CTCGAAAAAC AAAATCAAAA CCTGACCCTG CTGTACCAA CTACACGGGA
801 CCTGCACCAA TCCTACATAC CGCAACAGGC TGCAGAACAT TTTCTAAACC
851 GTATCCTGCC CGCCGTAGGA GCAGATTCCG GCAGAGTTTG TTTGGACGGC
901 GGATCCGATG TTTATGTTTC CATTATCAT GCGGATTGCG GCACAGCAGC
951 TTCGATTGTT GGGAAAGTACC ATGAGGAAAT CTTCCCCATT GAGTACCAGA
1001 ACGAAACATT GGGCAGGCTG TTGCTCAGCT TTCCAAACGG CATTCTCTCT
1051 GATGAAGACG ACCGCATCCT GCTTCAAACA CTAGGCAGGC AATTGGGCGT
1101 ATCGCTTGCC GCGCAAAAC AGGAGGAAGA AAAACGCCTG CTTGCAGTAT
1151 TGCAGGAACG CAACCTGATT GCGCAAGGAT TACATGACAG CATCGCACAA
1201 GCATTAACGT TCCTAAACCT ACAGGTACAG ATGCTGGAAG CCGCCTTTGC
1251 CGAAACAAA CCGGAGGAAG CCGCAGAAAA CATCAGCTTT ATCAAAACAG
1301 CCGTGCAGGA ATGTTATGAA GATGTCGCGG AACTGCTGCT CAACTCCGT
1351 ACCAAAATCA GCAATAAGA ATTTCCCGAA GCCGTTGCCG ACCTATTGCG
1401 CCGCTTTACG CAACAAACCG GGATAACGGT CGAAACCGCC TGGGAAACG
1451 GTTCGTTTCT GCCGCCTCAG GAAGCGCAGC TCCAAATGAT TTTTATCCTG
1501 CAGGAAGCC TGTCCAACAT CCGCAAACAC GCCCGCGCCA CCCATGTAAA
1551 ATTACCCCTT TCCGAACACG GCGGACGCTT TACCATGACC ATCCAAGACA
1601 ACGGACAAGG TTTCGACACG GAGAAAATAG GAGAACCAC GGGCAGCCAT
1651 GTCGGACTGC ACATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

```

This corresponds to the amino acid sequence <SEQ ID 1656; ORF 561>:

```

m561.pep
1   MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLTLLSL RLENAASVIE
51  EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIWWIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQM GRLKILYDDL EGQVAEQTRS
251 LEKQNQNLT LYTTRDLHQ SYIPQQAEE FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGR LLSFPNGISL
351 DEDDRILLQ LGRQLGVSLA GAKQEEERL LAVLQERNLI AQGLHDSIAQ
401 ALTFLNLQV MLETAFAENK REEAENISF IKTGVQECYE DVRELLLNFR
451 TKISNKEFPE AVADLFARFT QQTGITVETA WENGSLFPQ EAQLQMFIL

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501 QESLSNIRKH ARATHVKFTL SEHGRFTMT IQDNGQFDT EKIGEPTGSH
 551 VGLHIMQERA KRIHAVLEIR SQAQQTTS LTVASEESLK *

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m561/g561 89.7% identity in 223 aa overlap

	10	20	30	40	50	60
m561.pep	MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRL	ENAASVIEEAGNLRMQAY				
	:					
g561	MILPTRFSDGIPLSLRLKLLTGLWVGLAALSVVLTLLLSFR	LENAASVIEEAGNLKMQAY				
	10	20	30	40	50	60
	70	80	90	100	110	120
m561.pep	RLAYMAGEGSPRAQIDNQVAEFESLKRISQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA					
g561	RLAYMAGEGSPRAQIDNQIAEFESLKRISQSDAIHPLIPSDNPLAYDLIQSMLIIDWQA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m561.pep	HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLTLVSSVLM					
	:	:	:	:	:	:
g561	NILPPLQAYRRPTQIELYRFAGNIELFLQALENAGEKNTWWLRRFQWVIMLTLVSSVLM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m561.pep	LFWHQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRLLKILYDDL					
					:	:
g561	LFWHQIWVIRPLQALREGAERIGRHFDPVPEDVRPNRSGGVSTKWRSGX					
	190	200	210	220	230	
	250	260	270	280	290	300
m561.pep	EGQVAEQTRSLEKQNLTLTYQTTTRDLHQSYPQAAEHFLNRLPAVGADSGRVCLDG					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1657>:

a561.seq

1	ATGATACTGC	CAGCCCGTTT	TTCAGACGGC	ATCAGCCTTT	CCCTGCGCCT
51	GAAACTCCTG	ACCGGACTGT	GGGTCGGGTT	GGCGGCATTG	TCTGTCTGTTT
101	TGACACTGCT	GCTCTCTTTG	CGTCTGGAAA	ACGCGGCCTC	CGTCATCGAA
151	GAGGCGGGCA	ACTTGAGAAT	GCAGGCATAC	CGTCTGGCAT	ACATGGCGGG
201	TGAAGGCTCG	CCCCGTGCGC	AAATTGACAA	TCAGGTGCC	GAATTTGAAA
251	AAAGTTTAAA	ACGCATTGCC	CAAAGCGATG	CCATCCATCC	GCTGATTCCCT
301	TCGGACACCC	CTCTTGCTTA	TGATTTGATA	CAATCCATGC	TGATTATAGA
351	TTGGCAGGCA	CACATCCTCC	CCCCGCTCCA	GTCCTACCGG	CGACCGACTC
401	AGGTCGATCT	CTACCGCTTT	GCCGGAAACA	TCGAACGTGT	TTTGCAGGCA
451	TTGGAATATG	CCAACGAAAA	AAACACATGG	TGGCTCAGGC	GTTTTCAATG
501	GGCAATTATG	TTGATGACGC	TGGTGTCTGC	TGTACTGATG	CTGTTTTGGC
551	ACCAGATTTG	GGTTATCCGG	CCGCTGCAGG	CGTTAAGGGA	AGGTGCGGAA
601	CGCATCGGAC	GGAGGTGTTT	CGATATTCCG	GTTCCCGAAG	GCGGTACGCC
651	GGAATTCAAA	CAGGTCGGGC	GTTGTTTCAA	TCAAATGGGC	GGCAGGTTGA
701	AAATTTTATA	TGATGATTTG	GAAGGACAAG	TCGCCGAGCA	GACACGCAGT
751	CTCGAAAAAC	AAAATCAAAA	CCTGACCTTG	CTGTACCAAA	CTACACGGGA
801	TCTGCACCAA	TCCTACATAC	CGCAACAGGC	TGCAGAACAT	TTTCTAAACC
851	GTATCCTGCC	CGCCGTAGGA	GCAGATTCCG	GCAGAGTTTG	TTTGGACGGC
901	GGATCCGATG	TTTATGTTTC	CATTCATCAT	GCGGATTGCG	GCACAGCAGC
951	TTCGGATTTG	GGGAAGTACC	ATGAGGAAAT	CTTCCCCATT	GAGTACCAGA
1001	ACGAAACATT	GGGAGGCTG	TTGCTCAGCT	TTCCAAACGG	CATTTCTCTT
1051	GATGAAGACG	ACCGCATCCT	GCTTCAAACA	CTAGGCAGGC	AATTGGGCGT
1101	ATCGCTTGCC	GGCGCAAAAC	AGGAGGAAGA	AAAACGCCTG	CTTGCAGTAT
1151	TGCAGGAACG	CAACCTGATT	GCGCAAGGAT	TACATGACAG	CATCGCACAA
1201	GCATTAACGT	TCCTAAACCT	ACAGGTACAG	ATGCTGAAAA	CCGCCTTTGC
1251	CGAAAAACAA	CGGGAGGAAG	CCGCAGAAAA	CATCGGCTTC	ATCAAAACAG
1301	GCGTGCAGGA	ATGTTATGAA	GATGTCCGCG	AACTGCTGCT	CAACTTCCGT
1351	ACCAAAATCA	GTAATAAAGA	ATTTCCCGAA	GCCGTTGCCG	ACCTATTCTC

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1401 GCGCTTTACG CAACAGACCG GCACGACTGT CGAAACCGCT TGGGAAAACG
1451 GCACGCACCT GCCTACACAG GACGAGCAGC TCCAAATGAT TTTCATCCTG
1501 CAAGAAAGCT TGTCCAACAT CCGAAAACAT GCCCAGGCCA CCCATATCAA
1551 ATTCAAGACTG CTCAAACAGG ATGGAAGTTT TACAATGACC ATTCAGACA
1601 ACGGACAGGG TTTTGACACG GAAAACATTG GAGAACCATC GGCAGCCAT
1651 GTCGGACTGC ATATCATGCA GGAGCGTGCC AAACGCATCC ATGCCGTTT
1701 AGAAATCCGT TCCCAAGCTC AACAGGGAAC CACCGTCTCA TTGACGGTTG
1751 CATCTGAAGA AAGCTTGAAA TGA

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This corresponds to the amino acid sequence <SEQ ID 1658; ORF 561.a>:

```

a561.pep
  1 MILPARFSDG ISLSRLKLL TGLWVGLAAL SVVLTLLLSL RLENAASVIE
 51 EAGNLRMQAY RLAYMAGEGS PRAQIDNQVA EFEKSLKRIA QSDAIHPLIP
101 SDTPLAYDLI QSMLIIDWQA HILPPLQSYR RPTQVDLYRF AGNIELFLQA
151 LENANEKNTW WLRRFQWAIM LMTLVSSVLM LFHWQIWVIR PLQALREGAE
201 RIGRRCFDIP VPEGGTPEFK QVGRCFNQMG GRKILYDDL EGQVAEQTRS
251 LEKQNQNLTL LYQTTRDLHQ SYIPQQAEEH FLNRILPAVG ADSGRVCLDG
301 GSDVYVSIHH ADCGTAASDL GKYHEEIFPI EYQNETLGRL LLSFPNGISL
351 DEDDRILLQT LGRQLGVSLA GAKQEEKRL LAVLQERNLI AQGLHDSIAQ
401 ALTFNLQVQ MLETAFENK REEAENIGF IKTGVQECYE DVRELLNFR
451 TKISNKEFPE AVADLFSRFT QQTGTTVETA WENGTHLPTQ DEQLQMIFIL
501 QESLSNIRKH AHATHIKERL LKQDGSFTMT IQDNGQGFDI ENIGEPGSGH
551 VGLHIMQERA KRIHAVLEIR SQAQQTTSV LTVASEESLK *

m561/a561    96.9% identity in 590 aa overlap

      10      20      30      40      50      60
m561.pep    MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY
a561         MILPARFSDGISLSRLKLLTGLWVGLAALSVVLTLLLSRLLENAASVIEEAGNLRMQAY
      10      20      30      40      50      60

      70      80      90     100     110     120
m561.pep    RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
a561         RLAYMAGEGSPRAQIDNQVAEFEKSLKRIAQSDAIHPLIPSDTPLAYDLIQSMLIIDWQA
      70      80      90     100     110     120

      130     140     150     160     170     180
m561.pep    HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
a561         HILPPLQSYRRPTQVDLYRFAGNIELFLQALENANEKNTWWLRRFQWAIMLMTLVSSVLM
      130     140     150     160     170     180

      190     200     210     220     230     240
m561.pep    LFHWQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL
a561         LFHWQIWVIRPLQALREGAERIGRRCFDIPVPEGGTPEFKQVGRCFNQMGGRKILYDDL
      190     200     210     220     230     240

      250     260     270     280     290     300
m561.pep    EGQVAEQTRSLEKQNQNLTLTYQTTRDLHQSYIPQQAEEHFLNRILPAVGADSGRVCLDG
a561         EGQVAEQTRSLEKQNQNLTLTYQTTRDLHQSYIPQQAEEHFLNRILPAVGADSGRVCLDG
      250     260     270     280     290     300

      310     320     330     340     350     360
m561.pep    GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
a561         GSDVYVSIHHADCGTAASDLGKYHEEIFPIEYQNETLGRLLSFPNGISLDEDDRILLQT
      310     320     330     340     350     360

      370     380     390     400     410     420
m561.pep    LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK
a561         LGRQLGVSLAGAKQEEKRL LAVLQERNLIAQGLHDSIAQALTFLNLQVQMLETAFENK

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847

	370	380	390	400	410	420
	430	440	450	460	470	480
m561.pep	REEAAENISFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFARFTQQTGITVETA					
a561	REEAAENIGFIKTGVQECYEDVRELLLNFR TKISNKEFPEAVADLFSRFTQQTGTTVETA					
	430	440	450	460	470	480
	490	500	510	520	530	540
m561.pep	WENG SFLPPQEAQLQMIFILQESLSNIRKHARATHV KFTLSEHGGRFTMTIQDNGQGFD T					
a561	WENG THLPTQDEQLQMIFILQESLSNIRKHAHATHIKFRLLKQDGSFTMTIQDNGQGFD T					
	490	500	510	520	530	540
	550	560	570	580	590	
m561.pep	EKIGEPTGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
a561	ENIGEPSGSHVGLHIMQERAKRIHAVLEIRSQAQQGTTVSLTVASEESLKX					
	550	560	570	580	590	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1659>:

g562.seq..

1	atggcaagcc	cgtcgagtc	gcctttcaat	tcgggcaaga	ccaaaccgac
51	ggcttttgcc	gcgccggtt	tggtcggaat	catgttttcc	acgccgctgc
101	ggcgcgccg	caggtcttg	tgccgcacgt	cggtaacggt	ttggtcgttg
151	gtcagtcgt	ggatggtgt	cattgcgcct	ttgacgatgc	cgacgcttc
201	gctcaacact	ttggcaaccg	gcgagaggca	gttggtggtg	caggaagcgt
251	tggaaacgac	ggcatgtcg	gcggtcagga	cgctgtcgtt	cacgccgtac
301	acgacggtt	catcgacatc	gtcgccgccc	ggtgcgga	tgaggacttt
351	tttcgcgcc	cttcgaggt	ggattttggc	ttttctttg	ctggtgaacg
401	cgccggtgca	ttccatgacc	aaatcgacac	cgagttcttt	ccacggcagt
451	tcggcaggg	tgccggtcga	gaagaagggg	attttgcgc	cgttgacgat
501	gaggttgccg	ccgtcgtggg	atacgtcggc	ttcaaagcgt	ccgtgtacgg
551	tgtcgaattt	ggtcagatgg	gcgttggttt	caaggctgcc	gctggcggtg
601	acggcgacga	tttgagttg	gtcttga		

This corresponds to the amino acid sequence <SEQ ID 1660; ORF 562.ng>:

g562.pep

1	MASPS	SLPFN	SGKTK	PATAFA	APVLV	GIMFS	TPLRARR	RRSL	WRTSV	TVWSL
51	VSAWM	VVIAP	LTMP	TL	SLNT	LATGE	RQLVV	QEALE	TTVMS	AVRTL
101	TVAST	SSPP	GAEMR	TF	FAP	LSRW	ILAFSL	LVNAP	VHSMT	KSTPS
151	SAGLR	VEKKG	ILSPL	TM	RLP	PSWDT	SASKR	PCTVS	NLVRW	ALVSR
201	TATI	WSWS*								

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1661>:

m562.seq

1	ATGGCAAGCC	CGTCGAGCCT	GCCTTTCAAT	TCGGGCAGTA	CCAAACCGAC
51	GGCTTTTGCC	GCGCCGTTT	TGGTCGGAAT	CATGTTTTC	ACGCCGCTGC
101	GGGCGCGCG	CAGGTCTTTG	TGGCGCACGT	CGGTAACGGT	TTGGTCGTTG
151	GTCAGCGCGT	GGATGGTGGT	CATCGCGCCT	TTGACGATGC	CGACGCTTTC
201	GCTCAACACT	TTGGCAACCG	GCGAGAGGCA	GTTGGTGGTG	CAGGAAGCGT
251	TGGAAACGAC	GGTCATGTCG	GCGGTCAGGA	CGCTGTCGTT	CACGCCGTAC
301	ACGACGTTG	CATCGACATC	GTGCGCGCCC	GGTGCGGAAA	TGAGGACTTT
351	TTTCGCGCCG	CTTCGAGGT	GGATTTTGGC	TTTTCTTTG	CTGGTGAACG
401	CGCCGGTGCA	TTCCATGACC	AAATCGACAC	CGAGTTCTTT	CCACGGCAGT
451	TCGGCAGGGT	TGCGGGTCGA	GAAGAAGGGG	ATTTGTGCGC	CGTTGACGAT
501	GAGGTTGCCG	CCGTCGTGGG	ATACGTCGGC	TTCAAAGCGT	CCGTCACGGG
551	TGTCGAATTT	GGTCAGATGG	GCGTTGGTTT	CAAGGCTGCC	GCTGGCGTTG
601	ACGGCGACGA	GTTGGAGTTG	GTCTTGA		

This corresponds to the amino acid sequence <SEQ ID 1662; ORF 562>:

m562.pep

1	MASPS	SLPFN	SGSTK	PATAFA	APVLV	GIMFS	TPLRARR	RRSL	WRTSV	TVWSL
51	VSAWM	VVIAP	LTMP	TL	SLNT	LATGE	RQLVV	QEALE	TTVMS	AVRTL

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101 TTVASTSSPP GAEMRTFFAP LSRWILAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVEKKG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLAL
201 TATSWWS*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m562/g562 99.0% identity in 208 aa overlap

```

                10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWLSLVSAMMVVIAP
                |||||:|||||
g562          MASPSSLPFNSGKTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWLSLVSAMMVVIAP
                10      20      30      40      50      60

                70      80      90     100     110     120
m562.pep      LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP
                |||||:|||||
g562          LTMPTLSLNTLATGERQLVVQEALETTVMSAVRTLSFTPYTTVASTSSPPGAEMRTFFAP
                70      80      90     100     110     120

                130     140     150     160     170     180
m562.pep      LSRWILAFSLLVNAPVHSMKSTPSSFHGSSAGLRVEKKGILSPLTMLRPSPWDTASAKR
                |||||:|||||
g562          LSRWILAFSLLVNAPVHSMKSTPSSFHGSSAGLRVEKKGILSPLTMLRPSPWDTASAKR
                130     140     150     160     170     180

                190     200     209
m562.pep      PCTVSNLVRWALVSRPLALTATSWWSX
                |||||:|||||
g562          PCTVSNLVRWALVSRPLALTATIWSWSX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1663>:

```

a562.seq
1  ATGGCAAGCC CGTCGAGTTT GTCTTTCAAT TCGGGCAGTA CCAAACCGAC
51 GGCTTTTGCC GCGCCAGTTT TGGTCGGAAT CATGTTTCC ACGCCGCTGC
101 GGGCGCGCG CAGGTCTTGT TGGCGCACGT CGGTAACGGT TTGGTCGTTG
151 GTCAGCGCGT GGATGGTGGT CATCGCGCCT TTGACGATGC CGACGCTTTC
201 GCTCAACACT TTGGCAACCG GCGAGAGGCA GTTGGTGGTG CAGGAAGCGT
251 TGGAAACGAC GGTCAATGTC GCGGTCAGGA TGCTGTCGTT CACGCCGTAC
301 ACGACGGTTG CATCGACATC GTCGCCGCC GGTGCGGAAA TGAGGACTTT
351 TTTCCGCGCG CTTTCCAGAT GAACTTTGGC TTTTCTTTG CTGGTGAACG
401 CGCCGGTGCA TTCCATGACC AAATCGACAC CGAGTTCTTT CCACGGCAGT
451 TCGGCAGGGT TGCGGGTCNA GAAGAANGGG ATTTTGTCGC CGTTGACGAT
501 GAGGTTGCCG CCGTCGTGGG ATACGTCGGC TTCAAAGCGT CCGTGACGG
551 TGTCGAATTT GGTGAGGTGG GCGTTGGTTT CAAGGCTGCC GCTGGCGTTG
601 ACGGCGACGA TTTGGAGTTG GTCTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1664; ORF 562.a>:

```

a562.pep
1  MASPSSLSFN SGSTKPTAFA APVLVGIMFS TPLRARRRSL WRTSVTVWSL
51 VSAWMVVIAP LTMPTLSLNT LATGERQLVV QEALETTVMS AVRMLSFTHY
101 TTVASTSSPP GAEMRTFFAP LSR*TLAFSL LVNAPVHSM TSTPSSFHGS
151 SAGLRVXKXG ILSPLTMLRP PSWDTASAKR PCTVSNLVRW ALVSRPLAL
201 TATIWSWS*

```

m562/a562 96.6% identity in 208 aa overlap

```

                10      20      30      40      50      60
m562.pep      MASPSSLPFNSGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWLSLVSAMMVVIAP
                |||||:|||||
a562          MASPSSLSFN SGSTKPTAFAAPVLVGIMFSTPLRARRRSLWRTSVTVWLSLVSAMMVVIAP
                10      20      30      40      50      60

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	70	80	90	100	110	120
m562 . pep	LTMP T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R T L S F T P Y T T V A S T S S P P G A E M R T F F A P					
a562	L T M P T L S L N T L A T G E R Q L V V Q E A L E T T V M S A V R M L S F T P Y T T V A S T S S P P G A E M R T F F A P					
	70	80	90	100	110	120
	130	140	150	160	170	180
m562 . pep	L S R W I L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V E K K G I L S P L T M R L P P S W D T S A S K R					
a562	L S R X T L A F S L L V N A P V H S M T K S T P S S F H G S S A G L R V X K X G I L S P L T M R L P P S W D T S A S K R					
	130	140	150	160	170	180
	190	200	209			
m562 . pep	P C T V S N L V R W A L V S R L P L A L T A T S W S W S X					
a562	P C T V S N L V R W A L V S R L P L A L T A T I W S W S X					
	190	200				

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1665>:

g563 . seq

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1  ATGAACAAAA CCCTCTATCG TGTGATTTTC AACCGCAAAC GCGGTGCTGT
51  GGTAGCTGTT GCCGAAACCA CCAAGCGCGA AGGTAAAAGC TGTGCCGATA
101 GTGGTTTCGGG CAGCGTTTAT GTGAAATCCG TTTCTTTCAT TCCTACTCAT
151 TCCAAAGCCT TTTGTTTTTC TGCATTAGGC TTTTCTTTAT GTTTGGCTTT
201 GGGTACGGTC AATATTGCTT TTGCTGACGG CATTATTACT GATAAAGCTG
251 CTCCTAAAAC CCAACAAGCC ACGATTCTGC AAACAGGTAA CGGCATACCG
301 CAAGTCAATA TTCAAACCCc tACTTCGGCa ggGGTTTCTG TTAATCAATA
351 TGCCCAGTTT GATGTGGGTA ATcgCGGGC GATTTTAAAC AACAGTCGCA
401 GCAACACCCA AACACAGCTA GGCGGTGGA TTCAAGGCAA TCCTTGGTTG
451 ACAAGGGGCG AAGCACGTGT GGTGTGTAAC CAAATCAACA GCAGCCATCC
501 TTCACAACG AATGGCTATA TTGAAGTGGG TGGACGACGT GCAGAAGTCG
551 TTATTGCCAA TCCGGCAGGG ATTGCAGTCA ATGGTGGTGG TTTTATCAAT
601 GCTTCCCGTG CCACTTTGAC GACAGGCCAA CCGCAATATC AAGCAGGAGA
651 CTTTAGCGGC TTAAAGATAA GGCAAGGCAA TGCTGTAATC GCCGGACACG
701 GTTTGGATGC CCGTGATACC GATTTACACG GTATTCTTTT GTATGCCAAC
751 AAAATCACCT TGATCAGTAC GGCCGAACAA GCAGGCATTC GTAATCAAGG
801 GCAGTTGTTT GCTTCTTCCG GTAATGTGGC GATTGATGCA AATGGCCGTT
851 TGGTCAATAG TGGCAGCATG GCTGCCGCCA ATGTGCAAGA TATGAATAAT
901 ACAGCGGAAC ACAAAAGTCAA TATCCGCAGT CAAGCCTTTG AAAACAGCGG
951 TACGGCGGTA TCGCAACAAG GCACTCAAAT TCACAGTCAA TCGATTCAAA
1001 ACACTGGCAA ATTATTGTCG GCAGGAACAG AGGATTTAGC CGTTTCAGGC
1051 AGCCTGAACA ATCAAAATGG CGAAATAGCG ACCAATCAAC AACTGATTAT
1101 TCACGATGGT CAGCAATCTA CCGTTGTCAT TGATAATACG AATGGCACGA
1151 TACAATCAGG CCGTGATGTT GCCATTCAGG CAAAATCGTT ATCCAACAAC
1201 GGCACACTTG CCGCTGATAA TAAACTGGAT ATTGCGTTAC AAGATGATTT
1251 TTATGTAGAA CGCAAGATCG TGGCGGGCAA TGAATTGTCT CTCAGTACAC
1301 GAGGCAGCCT GAAAAATTCA CATACTTGC AAGCAGGAAA ACGCATTCCG
1351 ATTAAAGCAA ATAACCTTGA TAATGCAGTA CAAGGCAACA TTCAATCCGG
1401 CGGTACGACA GACATTGGCA CGCAGCACAA TTAAACCAAT AGAGGCTTGA
1451 TTGACGGACA ACAAACCAAA ATCCAAGCCG GGCAAATGAA TAATATCGGT
1501 ACAGGTCGGA TTTATGGCGA CAATATCGCT ATTGCGGCTA CCCGCTTAGA
1551 CAATCAAGAT GAAAACGGTA CAGGTGCCGC CATTGCGGCA CGCGAAAACC
1601 TGAATTTAGG CATTGAACAA TAAATAACC GTGAAAACAG TCTGATTTAC
1651 AGCGGTAACG ATATGGCGGT TGGCGGCGCA TTAGATACCA ATGACCAAGC
1701 CACAGGCAAA GCCCAAAGGA TACACAATGC CGGCGCAATC ATTGAAGCTG
1751 CAGGCAAAAT GCGTTTAGGT GTAGAAAAGC TGCACAATAC CAATGAGCAT
1801 TTGAAAACGC AGTTGGTAGA AACAGGGCGC GAGCGTATTG TTGATTACGA
1851 AGCATTGGA CGACACGAAT TATTGCGAGA AGGCACGCAA CATGAATTAG
1901 GCTGGTTTGT CTACAACAAT GAATCAGACC ACTTACGCAC CCCTGATGGA
1951 GTGGCGCATG AAAATTGGCA TAAATACGAT TATGAAAAAG TAACGCAAGA
2001 AACTCAAGTA ACCGGAAGT GGCCTGCTAA AATCATTGCA GGTAGCGATT
2051 TGATTATTGA TAGCAAAGCA GTCTTCAACA GCGACAGCCG AATCATTGCC

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2101 GGCGGCCAAT TGCTTGTGCA AACAGAAAAA GACGGTTTGC ATAACGAGCA
2151 AACCTTTGGC GAGAAGAAAG TCTTCAGCGA AAATGGTAAG TTGCACAACCT
2201 ACTGGCGTGC GCGTCGTAAA GGACATGATG AAACAGGGCA TCGTGAACAA
2251 AATTATACTT TGCCGGAGGA AATCACACGC GACATTTTAC TGGGTTCATT
2301 TGCCTATGAA TCGCATAGCA AAGCATTAAAG CCGTCATGCG CCCAGCCAAG
2351 GCACTGAGTT GCCACAAAGT AACCGGGATA ATATCCGTAC TCGGAAAAGC
2401 AACGGTATTT CGCTACCCTA TACGCCCAAT TCTTTTACCC CATTACCCGG
2451 CAGCAGCTTA TACATTATCA ATCCTGCCAA TAAAGGCTAT CTTGTTGAAA
2501 CCGATCCACG CTTTGCCAAC TACCGTCAAT GGTGCGGTAG TGAATATATG
2551 CTGGGCAGCC TCAAACCTAGA CCCAAACAAT TTACATAAAC GTTTGGGTGA
2601 TGGTTATTAC GAGCAACGTT TAATCAATGA ACAAATCGCA GAGCTGACAG
2651 GGCATCGTCG TTTAGACGGT TATCAAAACG ACGAAGAACA ATTTAAAGCC
2701 TTAATGAGATA ATGGCGCGAC TGCGGCACGT TCGATGAATC TCAGCGTTGG
2751 CATTGCATTA AGTGCCGAGC AAGCAGCGCA ACTGACCAGC GATATTGTTT
2801 GGTGTTGTTACA AAAAGAAGTT AAACCTCCTG ATGGCGGCAC ACAAACCGTA
2851 TTGATGCCAC AGGTTTATGT ACGCGTTAAA AATGGCGGCA TAGACGGTAA
2901 AGGTGCATTG TTGTCAGGCA GCAATACACA AATCAATGTT TCAGGCAGCC
2951 TGAAAACTC AGGCACGATT GCAGGGCGCA ATGCGCTTAT TATCAATACC
3001 GATACGCTAG ACAATATCGG TGGCGGTATT CATGCGCAAA AATCAGCGGT
3051 TACGGCCACA CAAGACATCA ATAATATTGG CGGCATTCTT TCTGCCGAAC
3101 AGACATTATT GCTCAATGCG GGTAACAACA TCAACAACCA AAGCACGGCC
3151 AAGAGCAGTC AAAATGCACA AGGTAGCAGC ACCTACCTAG ACCGAATGGC
3201 AGGTATTTAT ATCACAGGCA AAGAAAAAGG TGTTTTAGCA GCGCAGGCAG
3251 GCAAAGACAT CAACATCATT GCCGGTCAA TCAGCAATCA ATCAGATCAA
3301 GGGCAAACCC GGCTGCAGGC AGGACGCGAC ATTAACCTGG ATACGGTACA
3351 AACCGGCAAA TATCAAGAAA TCCATTTTGA TGCCGATAAC CATACCATCC
3401 GAGGTTCAAC GAACGAAGTC GGCAGCAGCA TTCAAACAAA AGGCGATGTT
3451 ACCCTatTGT CAGGGAATAA TCTCAATGCC AAAGCTGCCG AAGTCGGCAG
3501 CGCAAAGGC AACTTTGCCG TGTATGCTAA AAATGACATT ACTATCAGCT
3551 CAGGCATCCA TGCCGGCCAA GTTGATGATG CGTCCAAACA TACAGGCAGA
3601 AGCGCGCGCG GTAATAAATT AGTCATTACC GATAAAGCCC AAAGTCATCA
3651 CGAACTGCT CAAAGCAGCA CCTTTGAAGG CAAGCAAGTT GTATTGCAGG
3701 CAGGAAACGA TGCCAACATC CTTGGCAGTA ATGTTATTTC CGATAATGGC
3751 ACCCGGATTC AAGCAGGCAA TCATGTTCCG ATTGGTACAA CCCAACTCA
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The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1667>:

m563.seq..

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This corresponds to the amino acid sequence <SEQ ID 1668; ORF 563>:

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851 AQRIHNAGAT IEAAGKMLRG VEKLHNTNEH LKTQLVETGR EHIVDYEAFG
901 RHELLRECTQ HELGWSVYND ESDHLRTPDG AAHENWHKYD YEKVTQKTQV
951 TQTAPAKIIS GNDLTIDGKE VFNTDSQIIA GGNLIVQTEK DGLHNEQTFG
1001 EKKVFSENGK LHSYWREKHK GRDSTGHSEQ NYTLPEEITR NISLGSFAYE
1051 SHRKALSHHA PSQGTLPQS NGISLPYTSN SFTPLPSSSL YIINPVNKG Y
1101 LVETDPRFAN YRQWLGS DYM LDSLKLDPNN LHKRLGDGYY EORLINEQIA
1151 ELTGHRRLDG YONDEEQFKA LMDNGATAAR SMNLSVGIAL SAEQVAOLTS
1201 DIVWLQKEV KLPDGGTQTV LVPQVYVRVK NGDIDGKGAL LSGSNTQINV
1251 SGSLKNSGTI AGRNALIINT DTLDNIGGRI HAQKSAVTAT QDINNIGGML
1301 SAEQTLLENA GNNINSQSTT ASSQNTQGSS TYLDRMAGIY ITGKEKGVLA
1351 AQAGKDINII AGQISNQSEQ GQTRLQAGRD INLDTVQTSK HQATHFDADN
1401 HVIRGSTNEV GSSIQTGKDV TLLSGNNLNA KAAEVSSANG TLAVSAKNDI
1451 NISAGINTTH VDDASKHTGR SGGGNKLVIT DKAQSHHETA QSSTFEGKQV
1501 VLQAGNDANI LGSNVIDSNG TQIQAGNHVR IGTQTQTSQS ETYHQTQKSG

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855

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1551 LMSAGIGFTI GSKTNTQENQ SQSNEHTGST VGSCLKGDTTI VAGKHYEQIG
1601 STVSSPEGNN TIYAQSIDIQ AAHNKLNST TQTYEQKGLT VAFSSPVTDL
1651 AQQAIAVAQS SKQVGQSKND RVNAMAANA GWQAYQTGKS AQNLANGTTN
1701 AKQVVISITY GEQQNRQTQ VQANQAQASQ IQAGGKTTLI ATGAAEQSNI
1751 NIAGSDVAGK AGTILIADND ITLQSAEQSN TERGQNKASG WNAGAAVSFG
1801 QGGWSLGVTA GGNVKGKGYGN GDSITHRSH IGDKGSQTLI QSGGDTTIKG
1851 AQVRGKGVQV NAKNLSIQSV QDRETYQSKQ QNASAQVTVG YGFSAGGDYS
1901 QSKIRADHVS VTEQSGIYAG EDGYQIKVGN HTDLKGGIIT STQSAEDKKG
1951 NRFQTATLTH SDIKNHSQYK GESFGLGASA SISGKTLGQG AQNKPNKHL
2001 TSVADKNSAS SSVGYGSDSD SQSSITKSGI NTRNIQITDE AAQIRLTGKT
2051 AAQTKADIDT NVTDTAERH SGSLKNTFNK EAVQSELDLQ RTVSQDFSKN
2101 VQQANTEINQ HLDKCLKADKE AAETAAAEAL ANGDMETAKR KAHEAQDAAA
2151 KADNWQQGV ILNMLASGLA APTQSGAGIA AATASPAVS Y AIGQHFCDLA
2201 QONANGKLT SQETAHVLAH AVLGAAVAAV GDNALAGAL SAGGSEAAAP
2251 YISKWLYGKE KGSDLTAEK ETVTAITNVL GTATGAAVGN SATDAAQGS
2301 NAQSAVENND TVEQVKFALR HPRIAIAGS VHKGPGSTLE PNISTIATF
2351 QLNLPNSEF GEGGVGNF RHVLWQATIT REFGKDIQV VGNSHESGEK
2401 INYSIRNLS LDKADEMIDQ LNNEIGREIA LNTNRLNKE LVGLILETYK
2451 NNGFYQAERN SNGNYDVVRK RLSEKDYQNT SNILHLDNT GAGFKIQRR
2501 KQIRAQISAR QWRR*

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Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 563 shows 79.1% identity over a 2316 aa overlap with a predicted ORF (ORF 563.ng) from *N. gonorrhoeae*:

m563/g563

```

              10      20      30      40      50
g563 . pep    MNKTLRYVIFNRKRGAVVAVAETTKREGKSCADSGSGSVYVKSVSFIPTH-----SKAFC
              |||||
m563 . pep    MNKTLRYVIFNRKRGAVVAVAETTKREGKSCADSDSGSAHVKSVPFGTTHAPVCRSNIFS
              10      20      30      40      50      60

              60      70      80      90      100     110
g563 . pep    FSALGFSCLALGTVNIAFADGIITDKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
              |||||
m563 . pep    FSLLGFSCLAVGTANIAFADGIADKAAPKTQQATILQTGNGIPQVNIQTPTSAGVSVN
              70      80      90      100     110     120

              120     130     140     150     160     170
g563 . pep    QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLTRGEARVVVNQINSSHPSQLNGYIE
              |||||
m563 . pep    QYAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSQMNGYIE
              130     140     150     160     170     180

              180     190     200     210     220     230
g563 . pep    VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDFSGFKIRQGNVIAIGHGL
              |||||
m563 . pep    VGGRRAEVVIANPAGIAVNGGGFINASRATLTGQPQYQAGDLSGFKIRQGNVIAIGHGL
              190     200     210     220     230     240

              240
g563 . pep    DARDTDFTRIL-----
              |||||
m563 . pep    DARDTDFTRILSYHSKIDAPVWQDVRVVGQNDVVATGNAHSPILNNAANTSNNNTANN
              250     260     270     280     290     300

              250     260     270     280     290
g563 . pep    -----LYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM
              :|||
m563 . pep    GTHIPLFAIDTGKLGMYANKITLISTAEQAGIRNQGQLFASSGNVAIDANGRLVNSGTM
              310     320     330     340     350     360

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856

	300	310	320	330	340
g563 . pep	AAANVQDMNNTAEHKVNIRSQAFENSGTAVSQQGTQIHSQSIQNTGKLLSAGT-----				
	:: : :				
m563 . pep	AAANAKDTDNTAEHKVNIRSQGVENSGTAVSQQGTQIHSQSIQNTGTLSSGEILIHNSG				
	370	380	390	400	410 420
g563 . pep	-----				
m563 . pep	SLKNETSGTIEAARLAIDTDTLNNQGKLSQTSQKLHIDAQGMKMDNRGRMGLQDTAPTAS				
	430	440	450	460	470 480
g563 . pep	-----				
m563 . pep	NGSSNQTGNSYNASFHSSTTTPTTATGTGTATVSIENITAPTTFADGTIRTHGALDNSGSI				
	490	500	510	520	530 540
g563 . pep	-----				
m563 . pep	IANGQTDVSAQQGLNNAQIDIHQLNAKGSADFHNHGTIISDAVHIQAGSLNNQNGNITT				
	550	560	570	580	590 600
g563 . pep	-----EDLAVSGSLNNQNGEIATNQQLIIHDGQQSTVVIDNT				
m563 . pep	RQQLEIETDQLDNAHGKLLSAEIALAVSGSLNNQNGEIATNQQLIIHDGQQSTAVIDNT				
	610	620	630	640	650 660
g563 . pep	390	400	410	420	430 440
	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERKIVAGNELSLSTRGSLKNS				
m563 . pep	NGTIQSGRDVAIQAKSLSNNGTLAADNKLDIALQDDFYVERNIVAGNELSLSTRGSLKNS				
	670	680	690	700	710 720
g563 . pep	450	460	470	480	490 500
	HTLQAGKRIRIKANNLDNAVQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG				
m563 . pep	HTLQAGKRIRIKANNLDNAAQGNIQSGGTTDIGTQHNLNTRGLIDGQQTQKIAGQMNNIG				
	730	740	750	760	770 780
g563 . pep	510	520	530	540	550 560
	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIEQLNNRENSLIYSGNDMAVGGA				
m563 . pep	TGRIYGDNIAIAATRLDNQDENGTTGAAIAARENLNLGIGQLNNRENSLIYSGNDMAVGGA				
	790	800	810	820	830 840
g563 . pep	570	580	590	600	610 620
	LDTNDQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGRERIVDYEAFG				
m563 . pep	LDTNGQATGKAQRIHNAGATIEAAGKMRLGVEKLHNTNEHLKTQLVETGREHIVDYEAFG				
	850	860	870	880	890 900
g563 . pep	630	640	650	660	670 680
	RHELLREGTQHELGFVYNNESDHLRTPDGAHENWHKYDYEKVTQETQVTTGAPAKIIA				
m563 . pep	RHELLREGTQHELGWSVYNDES DHLRTPDGAHENWHKYDYEKVTQKTQVTTGAPAKIIS				
	910	920	930	940	950 960
	690	700	710	720	730 740

859

	1950	1960	1970	1980	1990	2000
g563.pep	TASQETAHVLAHAVLGAAVAAAXGNNAPAGALGAGGSEAAAP IIGKWLYGKGDGGSLSNAE					
	: : : : :: :					
m563.pep	TASQETAHVLAHAVLGAAVAAVGDNNALAGALSAGGSEAAAPYISKWLYGKEKGSDDLTAET					
	2210	2220	2230	2240	2250	2260

	2010	2020	2030	2040	2049	
g563.pep	EKETVSAITRMLGTAAGAAEGNSSADAVWGCFTASDFASSFSYPINMX					
	: : : : : ::					
m563.pep	EKETVTAITNVLTATGAAVGNSATDAAQGSLSNAQSAVENNDTVEQVKFALRHPRIAIAI					
	2270	2280	2290	2300	2310	2320

m563.pep	GSVHKDPGSTLEPNISTIASTFQLNLFNSEFGGEGGVGNAFRHVLWQATITREFGKDIA					
	2330	2340	2350	2360	2370	2380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1669>:

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m564.seq
1   ATGAACCGCA CCCTGTACAA AGTTGTATTT AACAAACATC GAAACTGCAT
51  GATAGCCGTT GCTGAAAATG CCAAACGCGA GGGCAAAAAC ACAGCCGACA
101 CCCAAGCTGT AGGTATTTTG CCAATGATA TTGCGGGCTT TGCGGGTTTT
151 ATCCATTCTA TCTCTGTTAT CTCATTCTCC CTTTCATTAC TGCTCGGTTT
201 TGCCCTTATC CTGACTTCTT CTTCTGCTAC TGCCCAAGGT ATCGTTGCCG
251 ACAAATCCGC ACCTGCACAG CAACAGCCTA CCATCCTGCA AACAGGTAAC
301 GGCATACCGC AAGTCAATAT TCAAACCCCT ACTTCGGCAG GGGTTTCTGT
351 TAATCAATAC GCCCAGTTTG ATGTGGGTAA TCGCGGGGCG ATTTTAAACA
401 ACAGTCGCAG CAACACCCAA ACACAGCTAG GCGGTTGGAT TCAAGGCAAT
451 CCTTG GTTGG CAAGGGGCGA AGCACGTGTG GTTGTAACC AAATCAACAG
501 CAGCCATTCT TCACAATGTA ATGGCTATAT TGAAGTGGGC GGACGACGTG
551 CAGAAGTCGT TATTGCCAAT CCGGCAGGGA TTGCAGTCAA TGGTGGTGGT
601 TTTATCAATG CTTCCCGTGC CACTTTGACG ACAGCCCAAC CGCAATATCA
651 AGCAGGAGAC CTTAGCGGCT TTAAGATAAG GCAAGGCAAT GTTGTAAATC
701 CCGGACACGG TTTGGATGCA CGTGATACCG ATTACACACG TATTCTCAGT
751 TATCATTCCA AAATTGATGC ACCCGTATGG GGACAAGATG TTCGTGTCGT
801 CGCGGGACAA AACGATGTGG CCGCAACAGG TGATGCACAT TCGCCTATTC
851 TCAATAATGC TGCTGCCAAT ACGTCAAACA ATACAGCCAA CAACGGCACA
901 CATATCCCTT TATTTGCGAT TGATACAGGC AAATTAGGAG GTATGTATGC
951 CAACAAAATC ACCTTGATCA GTACGGTCGA GCAAGCAGGC ATTCGTAATC
1001 AAGGGCAATG GTTTGCCTCA GCCGGCAATG TGGCAGTGAA TGCTGAGGGT
1051 AAAGTGGTCA ACACGGGCAT GATTGCAGCG ACGGGAGAAA ATCATGCGGT
1101 TTCATTCTAT GCCCGCAATG TTCATAATAG CGGTACGGTT GCCTCACAGG
1151 ATGATGCCAA TATTCACAGC CAGACGCTGG ACAATTCAGG TACGGTCTTA
1201 TCCTCAGGTC GATTGACTGT TCGTAATTTA GGCCGTCTGA AAAACCAAAA
1251 CAACGGTACG ATCCAGGCTG CCCGCTTAGA TATGTCAACA GGTGGTTTGG
1301 ATAACACAGG TAATATTACT CAAACAGGTT CACAAGCATT GGATTTGGTA
1351 TCTGCCGCA AATTCGATAA CAGTGGCAAG ATTGGTGTA GTGACGTTCC
1401 ACAGACCGGT TTGAATCCCA ATCCATCAGT CATACCACAG ATTCCGAGTA
1451 CTGCAACAGG TTCAGGCAGC AGCACTGTCT CGGTATCTAA GCCTGGTTCA
1501 AACAATCCCG TTTCACCTAC AGCACCTGCA AAAAATACG CCGTAGGACG
1551 CATTCAAACA ACAGGAGCAT TTGACAATGC AGGATCAATT AATGCGGGTG
1601 GGCAAAATGA CATTGCCGCC CAAAACGGTT TGGGAAATTC GGGTAGTCTG
1651 AATGCGGCTA AACTACGAGT ATCAGGCGAT TCATTTAACA ATACGGTAAA
1701 AGGCAAACTC CAGGCACACG ATCTGGCTGT TAACACTCAA ACTGCTAAAA
1751 ACAGCGGTCA CTTATTAACT CAAACCGGCA AGATTGATAA CCGTGAAGTG
1801 CATAATGCCG GAGAAATTGC CGCCAACAAT CTGACACTCA TTCATTCCGG
1851 CCGCTTGAGC AATGATAAAA AAGGCAATAT TCGAGCTGCA CATTTACAGC
1901 TTGATACCGC CGGTTTACAT AATGCAGGTA ACATTCTTGC CGATAGTGGG
1951 ACCGTTACCA CCAAGAATAA TCTTCGCAAT ACAGGAAAAG TTTCTGTTGC
2001 ACGACTGAAT ACCGAAGGTC AGACTCTAGA TAATACGCGC GGACGTATAG
2051 AGGCTGAAAC GGTAAACATC CAAAGTCAGC AACTGACTAA CCAAAGCGGC
2101 CATATTACTG CTACCGAACA ACTGACTATC AATAGTCGAA ATGTAGACAA
2151 CCAAAACGGC AAATCCTAT CTGCAAAACA AGCACAATTA GCTGTTTCAG
2201 ACGGCCTATA CAACCAACAT GGTGAAATTG CCACCAACCG GCAGTTGTCT

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2251	ATTACGATA	AAAATCAAAA	CACTTTGGCG	TTAAACAATG	CGGATGGCAC
2301	GATTCAATCT	GCCGGTAATG	TATCGCTACA	AGCCAAATCA	CTCGCCAACA
2351	ATGGCACATT	AACAGCCGGT	AACAACTGG	ATATTGCTTT	GACGGACGAT
2401	TTCTGCTAG	AGCGCGACCT	CACTGCAGGC	AAACAATTAA	ATCTAAGCAT
2451	AAAAGGCCGT	CTGAAAAATA	CCCATACCCT	ACAAGCAGGC	CATACGCTCA
2501	AACTCAATGC	CGGCAATATA	GATAACCAAG	TTACAGGCAA	AATTATTGGT
2551	GGAGAACAAA	CGGACATCAC	ATCCGAACAG	CATGTTGACA	ACAGGGGCTT
2601	GATCAACAGC	GACGGTTTGA	CCCACATCGG	TGCAGGTCAA	ACCCTGACCA
2651	ACACCGGGAC	AGGCAAAATC	TATGGCAACC	ATATTGCCCT	GGACGCGCAA
2701	ATACTGCTTA	ACCGGGAAGA	AACGACGGAA	GGCAGTACCA	AAGCGGGGGC
2751	AATAGCTGCA	AGGAAACGTT	TGGATATTGG	AGCGAAAGAG	ATTCATAACC
2801	AAGAAGGTGC	CCTACTATCC	AGCGAAGGTA	TTTTTGCCGT	AgGTAATCGA
2851	CTGGATGAAC	AACATCATGC	GGCAGGCATG	GCCGATACCT	TTGTTAATGG
2901	CAGTGCCGGT	TTGGAAGTAC	AAGGTGATGC	ATTGATGTCC	GTTCCGGAATA
2951	TGCAGAATAT	CAATAATCAC	TTTAAACAG	AGACATACTT	AGCCAAAGCG
3001	GAAAAGCAAG	TCCGCGACTA	CACCGTACTG	GGGCAAAATA	CCTACTATCA
3051	GGCGGGAAAA	GACGGTTTAT	TCGACAACTC	GCAAGGACAA	AAAGACCAAA
3101	CTACTGCTAC	GTTCCATTTA	AAAAATGGTT	CTCGTATTGA	GGCCAACCAA
3151	TGGCATGTCC	GAGACTACCA	CATCGAGACT	TATAAAGAAC	GCATCATCGA
3201	AAACCGGCCG	GCACACATTA	CTGTGGGCGG	TGATTTGACT	GCCTCAGGTC
3251	AAAATTGGCT	GAACAAAGAC	AGCCGGATTG	TAGTAGGCGG	GCGTATTATC
3301	ACTGATGATT	TAAACCAGAA	AGAAATTACC	AATCAAAGTA	CAACAGGCAA
3351	AGGTCGCACA	GATGCTGTCT	GCACACAGTG	GGATTCAAGT	ACAAAAAAG
3401	GATGGTACAG	CGGTAGAAAA	AGACAACGCC	GTAAGTAAAG	AAACCATACT
3451	CCTTACCATG	ATACCCAAT	ATTTACCCAC	GAATTCGACA	CGCCTGTATC
3501	CGTCATCCAA	CAGAATGCCG	CCTCCCCTTC	CTTTCAACCC	GCCCGTACTG
3551	CAATCAAAT	GATTGACGGA	GTATCCACGG	CAGCCGTCAA	TGGTCAGCGC
3601	ATCCATACCG	GTAATGTGGT	CTCGTTAAAT	AACGCTACTG	TTACTCTGCC
3651	TAACAGCAGC	CTCTATACCA	CCATCCTGA	CAATAAAGGC	TGGTTGGTTG
3701	AAACCGATCC	TCAATTTGCA	GAATACCGCC	GCTGGTTGGG	CAGCGACTAC
3751	ATGTTGCAAC	AACTGCAATT	GGACACCAAT	CATCTACACA	AACGGCTTGG
3801	CGACGGCTAC	TACGAACAAA	AACTTGTTAA	TGAACAAATC	CATCAGTTAA
3851	CAGGCTACCG	CCGACTCGAC	GGCTACAGGA	GTGATGAAGA	ACAATTCAAA
3901	GCTCTGATGG	ACAACGGCCT	TACTGCTGCC	AAAACATTCG	GTCTCACCCC
3951	AGGTATCGCC	TTGAGTGCAG	AGCAAGTTGC	CCGCTTAACT	TCAGATATCG
4001	TTTGGATGGA	AAATCAAACC	GTCAACCCTGT	CTGACGGTTC	GACTCAAACC
4051	GTAATGGTTC	CTAAAGTCTA	TGCCCTGGCG	CGCAAAGGTG	ATCTCAATAC
4101	CTCCGGTGGC	CTGATTAGTG	CCGAACAAGT	CTTACTTAAA	CTGCAAAACG
4151	GCAACCTGAC	TAACAGCGGT	ACCATTGCGG	GGCGACAGGC	CGTACTCATC
4201	CAGGCACGGA	ATATTAACAG	CAACGGTAAC	ATTCAAGCCG	ACCAAAATCGG
4251	CTTAAAGCT	GAAAAAAGTA	TCAATATCGA	CGGCGGGCAG	GTACAAGCAG
4301	GCAGACTGCT	GAATGCCCCA	GCGCAAAATA	TCAACCTTAA	CGGTACAACC
4351	CAAACCTCCG	GTAATGAACG	TAACGGCAAT	ACCGCCATCG	ATCGTATGGC
4401	CGGCATTAAC	GTGGTCGGAA	GCCATACTGA	ACAAGTAGAT	AACAGAAGCTT
4451	CAGACGGCAT	CCTATCCCTG	CATGCCAGCA	ACGATATCAA	CCTCAATGCG
4501	GCCACCGTCT	CTAACCAAGT	TAAAGACGGC	ACTACCCAAA	TTACCGCCGG
4551	CAATAATCTC	AACCTCGGCA	CCATCCGTAC	CGAACATCGC	GAAGCCTATG
4601	GTACATTAGA	TGACGAGAAC	CATCGCCATG	TCCGCCAAAG	TACCGAAGTC
4651	GGCAGCAGTA	TCCGCACGCA	AAACGGCGCA	CTGCTTAGAG	CCGGTAACGA
4701	CTTAAAAATC	CGCCAAGGCG	AACTGGAGGC	CGAAGAAGGC	AAAACCGTCC
4751	TTGCCGCGAG	ACGTGATGTC	ACTATCAGCG	AAGGACGCCA	AATAACCGAA
4801	CTGGATACCT	CGGTAAGCGG	AAAAAGCAAA	GGCATCCTTT	CCAGTACCAA
4851	AACACACGAC	CGCTACCGCT	TCAGTCATGA	TGAAGCAGTC	GGCAGCAACA
4901	TCCGCGGCGG	CAAAATGATT	GTTGCAGCCG	GGCAGGATAT	CAATGTACGC
4951	GGCAGCAACC	TTATTTCTGA	TAAGGGCATT	GTTTTAAAAG	CAGGACACGA
5001	CATCGATATT	TCTACTGCCC	ATAATCGCTA	TACCGGCAAT	GAATACACG
5051	AGAGCAAAAA	ATCAGGCGTC	ATGGGTACTG	GCGGATTGGG	CTTTACTATC
5101	GGTAACCGGA	AACTACCGA	TGACACTGAT	CGTACCAATA	TTGTCCATAC
5151	AGGCAGCATT	ATAGGCAGCC	TGAATGGAGA	CACCGTTACA	GTTCAGGAA
5201	ACCGCTACCG	ACAAACCGGC	AGTACCGTCT	CCAGCCCCGA	GGGGCGCAAT
5251	ACCGTCACAG	CCAAAAGCAT	AGATGTAGAG	TTCGCAAAACA	ACCGGATATGC
5301	CACTGACTAC	GCCCATACCC	AGGAACAAAA	AGGCCTTACC	GTCGCCCTCA
5351	ATGTCCCGGT	TGTCCAAGCT	GCACAAAAT	TCATACAAGC	AGCCCAAAAT
5401	GTGGGCAAAA	GTAATAATAA	ACGCGTTAAT	GCCATGGCTG	CAGCCAATGC
5451	TGCATGGCAG	AGTTATCAAG	CAACCAACA	AATGCAACAA	TTTGCTCCAA
5501	GCAGCAGTGC	GGGACAAGGT	CAAAACAACA	ATCAAAGCCC	CAGTATCAGT

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5551 GTGTCCATTA CCTACGGCGA ACAGAAAAGT CGTAACGAGC AAAAAAGACA
5601 TTACACCGAA GCGGCAGCAA GTCAAATTAT CGGCAAAGGG CAAACCACAC
5651 TTGCGGCAAC AGGAAGTGGG GAGCAGTCCA ATATCAATAT TACAGGTTCC
5701 GATGTCATCG GCCATGCAAG TACTGCCCTC ATTGCCGACA ACCATATCAG
5751 ACTCCAATCT GCCAAACAGG ACGGCAGCGA GCAAAGCAAA AACAAAAGCA
5801 GTGGTTGGAA TGCAGGCGTA GCCGTCAAAA TAGGCAACGG CATCAGGTTT
5851 GGAATTACCG CCGGAGGAAA TATCGGTAAA GGTAAGAGC AAGGGGGAAG
5901 TACTACCCAC CGCCACACCC ATGTCGGCAG CACAACCGGC AAAACTACCA
5951 TCCGAAGCGG CGGGGATACC ACCCTCAAAG GTGTGCAGCT CATCGGCAAA
6001 GGCATACAGG CAGATACGCG CAACCTGCAT ATAGAAAGTG TTCAAGATAC
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6201 CTATCAAATC AAAGTCAGAG ACAACACAGA CCTCAAGGGC GGTATCATCA
6251 CGTCTAGCCA AAGCGCAGAA GATAAGGGCA AAAACCTTTT TCAGACGGCC
6301 ACCCTTACTG CCAGCGACAT TCAAAACCAC AGCCGCTACG AAGGCAGAAAG
6351 CTTCCGCATA GCGGCGAGTT TCGACCTGAA CCGCGGCTGG GACGGCACGG
6401 TTACCGACAA ACAAGGCAGG CCTACCGACA GGATAAGCCC GGCAGCCGGC
6451 TACGGCAGCG ACGGAGACAG CAAAAACAGC ACCACCCGCA GCGGCGTCAA
6501 CACCCACAAC ATACACATCA CCGACGAAGC GGGACAACCT GCCCGAACAG
6551 GCAGGACTGC AAAAGAAACC GAAGCGCGTA TCTACACCGG CATCGACACC
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6651 CGCGGTCGCC AAAGAGATCA ACCTGCAAAG GGAAGTAACG AAGGAGTTCC
6701 GCAGAAACGC CGCCCAAGCC GTAGCGGCCG TTGCCGACAA ACTCGGCAAT
6751 ACCCAAAGTT ACGAACGGTA TCAGGAAGCC CGAACCTGCT TGGAGGCCGA
6801 ACTGCAAAAC ACGGACAGCG AAGCCGAAAA AGCCGCCTTC CGCGCATCCC
6851 TCGGCCAAGT AAACGCCTAT CTTGCCGAAA ACCAAAGCCG CTACGACACC
6901 TGGAAGAAG GCGGCATAGG CAGGAGCATA CTGCACGGGG CGGCAGGCGG
6951 ACTGACGACC GGCAGCCTCG GCGGCATACT GGCCGGCGGC GGCATTCCC
7001 TTGCCGCACC GTATTTGGAC AAAGCGGCGG AAAACCTCGG TCCGGCGGGC
7051 AAAGCGGCGG TCAACGCACT GGGCGGTGCG GCCATCGGCT ATGCAAGTGG
7101 TGGTAGTGGT GGTGCTGTGG TGGGTGCGAA TGTAAGTTGG AACAAAGGC
7151 AGCTGCATCC GAAAGAAATG GCGTTGGCCG ACAAATATGC CGAAGCCCTC
7201 AAGCGCGAAG TTGAAAAACG CGAAGGCAGA AAAATCAGCA GCCAAGAAGC
7251 GGCAATGAGA ATCCGCAGGC AGATACTGCG TTGGGTGGAC AAAGGTTCCC
7301 AAGACGGCTA TACCGACCAA AGCGTCATAT CCCTTATCGG AATGAAAGGC
7351 GAAGACAAAG CCTTGGGTTA TACTTGGGAC TACCGCGACT ACGGCGCAAG
7401 AAATCCGCAA ACCTACAACG ATCCGAAGCT GTTTGAGGAA TACCGCCGAC
7451 AGGACAAACC CGAATACCGC AACCTGACCT GGCTGCACAG CGGGACGAAA
7501 GACACCAAAA TCAGGCAGGG AGAGCGGAAA AACGAAGAGT TTGCACTGAA
7551 CGTTGCCGAA GGAAGTACGA GCCTTGTCAG CCCCAATCCG AGGATAAAAG
7601 TCCCGATTCT TGCAGGCATC CGCAACCTGA AAAACATCAA GCCGACAGTT
7651 ACCGGCAGCG ATCCCTTATT GCGGGGTGCG GGAATATCC GTATCCCTGC
7701 AAACGGCAAT GTTGCGAAGG GGGACAGGAT TCCGGATACG GCATTGGCTA
7751 GCAAGGGAAT CAAACATAAA GATCGTAAAG ATCAACTGGA GAAAAATAA

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This corresponds to the amino acid sequence <SEQ ID 1670; ORF 564>:

m564.pep

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1  MNRTLYKVVF NKHRNCMIIV AENAKREGKN TADTQAVGIL PNDIAGFAGF
51  IHSISVISFS LSLLLGSALI LTSSSATAQG IVADKSAPAQ QQPTILQTGN
101 GIPQVNIQTP TSAGVSVNQY AQFDVGNRGA ILNNSRSNTQ TQLGGWIQGN
151 PWLARGEARV VVNQINSSHS SQLNGYIEVG GRRAEVVIAN PAGIAVNGGS
201 FINASRATLT TAQPQYQAGD LSGFKIRQGN VVIAGHGLDA RDTDYTRILS
251 YHSKIDAPVW GQDVRVVAGQ NDVAATGDAH SPILNNAAN TSNNTANNGT
301 HIPLFAIDTG KLGGMYANKI TLISTVEQAG IRNQGWQFAS AGNVAVNAEG
351 KLVNTGMIAA TGENHAVSLH ARNVHNSGTV ASQDDANIHS QTLDNSGTVL
401 SSGRLTVRNL GRLKNQNNGT IQAARLDMST GGLDNTGNIT QTSQALDLV
451 SAGKFDNSGK IGVSDVPQTG LNPNPSPVQP IPSTATSGSG STVSVPKPGS
501 NNPVSPTAPA KNYAVGRIQT TGAFDNAGSI NAGGQIDIAA QNGLGNSGSL
551 NAAKLRVSGD SFNNTVKGKL QAHDLAVENTQ TAKNSGHLLT QTKIDNREL
601 HNAGEIAANN LTLIHSGRLS NDKKGNIIRAA HLQLDTAGLH NAGNILADSG
651 TVTTKNNLRN TGKVSVARLN TEGQTLDNTR GRIEAEVNI QSQQLTNQSG
701 HITATEQLTI NSRNVDNQNG KLLSANQAQL AVSDGLYNQH GEIATNRQLS
751 IHDKNQNTLA LNNADGTIQS AGNVSLQAKS LANNGTLTAG NKLDIALTDD
801 FVVERDLTAG KQLNLSIKGR LKNTHTLQAG HTLKLNAGNI DNQVTGKIIG
851 GEQTDITSEQ HVDNRGLINS DGLTHIGAGQ TLTNTGTGKI YGNHIALDAQ

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901 ILLNREETTE GSTKAGAIAA RKRLDIGAKE IHNQEGALLS SEGIFAVGNR
951 LDEQHHAGM ADTFVNGSAG LEVQGDALMS VRNMQNNNH FKTETYLAKA
1001 EKQVRDYTEVL GQNTYYQAGK DGLFDNSQGG KDQTTATFHL KNGSRIEANK
1051 WHVRDYHIET YKERIENRP AHITVGGDLT ASGQNLWLNKD SRIVVGGRII
1101 TDDLNQKEIT NQSTTGKGRD DAVGTQWDSV TKGKWSGRK RQRRTERNHT
1151 PYHDTQLFTH DEDTPVSVIQ QNAASPSFQP AASAIKLIDG VSTAAVNGQR
1201 IHTGNVSLN NATVTLPNSS LYTHPDNKG WLVEDPQFA DYRRWLGS DY
1251 MLQQLQLDTN HLHKRLGDGY YEQLVNEQI HQLTGYRRLD GYRSDEEQFK
1301 ALMDNGLTAA KTFGLTPGIA LSAEQVARLT SDIVWMENQT VTLSDGSTQT
1351 VLVPKVYALA RKGDLNTSGG LISAEQVLLK LQNGNLTNSG TIAGRQAVLI
1401 QARNINSNGN IQADQIGLKA EKSINIDGGQ VQAGRLLTAQ AQNINLNGTT
1451 QTSNGERNNGN TAIDRMAGIN VVGSHTQVD NRTSDGILSL HASNDINLNA
1501 ATVSNQVKDG TTQITAGNNL NLGTIRTEHR EAYGLDDEN HRHVRQSTEV
1551 GSSIRTQNGA LLRAGNDLKI RQGELEAEEG KTVLAAGR DV TISEGRQITE
1601 LDTSVSGKSK GILSSTKTHD RYRFSHDEAV GSNIGGGKMI VAAGQDINVR
1651 GSNLISDKGI VLKAGHDIDI STAHNRYTGN EYHESKSGV MGTGGLGFTI
1701 GNRKTTDDTD RTNIVHTGSI IGSINGDTVT VAGNRYRQTG STVSSPEGRN
1751 TVTAKSIDVE FANNRYATDY AHTQEQKGLT VALNVPVQA AQNFIAAQN
1801 VGKSKNKR VN AMAAANA AWQ SYQATQOMQ FAPSSSAGQG QNNNQSPSIS
1851 VSITYGEQKS RNEQKRHYTE AAASQIGKG QTTLAATGSG EQSNINITGS
1901 DVIGHAGTAL IADNHIRLQS AKQDGEQSK NKSSGWNAGV AVKIGNGIRF
1951 GITAGGNIGK GKEQGGSTTH RHTHVSGTTG KTTIRSGGDT TLKGVQLIGK
2001 GIQADTRNLH IESVQDTETY QSKQONGNVQ VTVGYGFSAS GSYRQSKVKA
2051 DHASVTGQSG IYAGEDGYQI KVRDNTDLKG GIITSSQSAE DKGKNLFTQA
2101 TLTASDIQNH SRYEGRSFGI GGSFDLNGGW DGTVTDKQGR PTDRISPAAG
2151 YGSDGDSKNS TTRSGVNTHN IHITDEAGQL ARTGRTAKET EARIYTIDT
2201 ETADQHSGLH KNSFDKDAVA KEINLQREVT KEFGRNAAQA VAAVADKLGN
2251 TQSYERYQEA RTLLEAELQN TDSEAEKAAF RASLGQVNAY LAENQSRDYT
2301 WKEGGIGRSI LHGAAGGLTT GSLGGILAGG GTSLAAPYLD KAAENLGPA
2351 KAAVNALGGA AIGYATGGSG GAVVGANVDW NNRQLHPKEM ALADKYAEAL
2401 KREVEKREGR KISSQEAAMR IRRQILRWVD KGSQDGYTDQ SVISLGMKG
2451 EDKALGYTWD YRDYGARNPQ TYNDPKLFEE YRRQDKPEYR NLTWLHSGTK
2501 DTKIRQGERK NEEFALNVAE GLTSLVNP NP RIKVPILAGI RNLKNIKPTV
2551 TGSDPLLAGA GNIRIPANGN VAKGDRI PDT ALASKGIKHK DRKDQLEKK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with fha

m564/fha

```

ID FHAB_BORPE STANDARD; PRT; 3591 AA.
AC P12255;
DT 01-OCT-1989 (REL. 12, CREATED)
DT 01-FEB-1996 (REL. 33, LAST SEQUENCE UPDATE)
DT 01-FEB-1996 (REL. 33, LAST ANNOTATION UPDATE)
DE FILAMENTOUS HEMAGGLUTININ. . . .

```

SCORES Init1: 190 Initn: 524 Opt: 594
 Smith-Waterman score: 866; 21.7% identity in 2427 aa overlap

```

              10      20      30      40      50      60
m564 .pep MNRTLYKVVFNKHRNCMIAVAENAKREGKNTADTQAVGILPNDIAGFAGFIHSISVISFS
           || :||:| :||: | : : | :| : | || : : | : | : | :| : :
fhab_borpe MNTNLYRLVFVSHVRGMLVPVSEHCTV-G-NTFCGRTRG---QARSGARATSLSVAPNALA
              10      20      30      40      50
              70      80      90     100     110     119
m564 .pep LSLLLG-SALILTSSSATAQGIVADKSAPAAQQOPTILQTGNGIPQVNIQTPTSAGVSVNQ
           :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
fhab_borpe WALMLACTGLPLVTH---AQGLV-----P-QGQTQVLQGGNKVPVVNIADPNSGGVSHNK
              60      70      80      90     100
              120     130     140     150     160     170     179
m564 .pep YAQFDVGNRGAILNNSRSNTQTQLGGWIQGNPWLARGEARVVVNQINSSHSSQLNGYIEV
           :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
fhab_borpe FQQFNVANPGVVFNNGLTGVSRIIGGALTKNPNLTR-QASAILAEVTDTSPSRLAGTLEV
              110     120     130     140     150     160

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	180	190	200	210	220	230	239
m564 .pep	GGRRAEVVIANPAGIAVNGGGFINASRATLTTAQPQYQAGDLGFKIRQGNVVIAGHGLD						
	: :: : : : : : : :						
fhab_borpe	YGKGADLIIANPNGISVNGSLTNASNLTLTTGRPSVNGGRI-GLDVQQTVTIERGGVN						
	170	180	190	200	210	220	
	240	250	260	270	280	290	
m564 .pep	ARDDYTRILSYHSKIDAPV---WGQ---DVRVVAGQNDVAATGDAHSPILNNAANTSN						
	: : : : : : : : : : : : : :						
fhab_borpe	ATGLGYFDVVARLVKLQGAUSSKQKPLADIAVVAGANRYDHATRRATPI----AAGARG						
	230	240	250	260	270	280	
	300	310	320	330	340	350	
m564 .pep	NTANNGTHIPLFAIDTGKLGMYANKITLISTVEQAGIRNQGWQFASAGNVAVNAEGKLV						
	: : : : : : : : : : : : :						
fhab_borpe	AAAGA-----YIDGTAAGAMYGKHITLVSSDSGLGVRQLGS-LSSPSAITVSSQGEIA						
	290	300	310	320	330		
	360	370	380	390	400	410	
m564 .pep	NTGMIAATGENHAVSLHARNVHNSGTVASQDDANIHSQTLDNSGTVLSSGRLTVRNLGRL						
	: : : : : : : : : : : : : : : : :						
fhab_borpe	---LGDATVQRGPLSLKGAGVVSAGKLASGGGAV---NVAGGGAVKIA---SASSVGNL						
	340	350	360	370	380		
	420	430	440	450	460	470	
m564 .pep	KNQNNGTIQAARLDMSTGGLDNTGNITQTGSQALDLVSAGKFDNSGKIGVSDVPQTGLNP						
	: : : : : : : : : : : : : : : : :						
fhab_borpe	AVQGGGKVQATLLNAG-----GTLVSGRQAVQLGAASSRQALSVNAGGALKADKLSA						
	390	400	410	420	430		
	480	490	500	510	520	530	
m564 .pep	NPSV-IPQIPSTATGSGSSTVSVPKPGSNNPVSPTAPAKNYAVGRIQTTGAFFD-NAGSIN						
	: : : : : : : : : : : : : : : :						
fhab_borpe	TRRVVDVGKQAVALGSASSNALSVRAGGA-----LKAGKLSATGRLDVDGKQAVTLGSA						
	440	450	460	470	480	490	
	540	550	560	570	580	590	
m564 .pep	AGGQIDIAAQNGLGNSGSLNAAKLRSVSG-----DSFNNT-----VKGKLQAHDLAVNT						
	: : : : : : : : : : : : : : : : :						
fhab_borpe	SDGALSVSAGGNLRANELVSSAQLEVRGQREVALDDASSARGMTVVAAGALAARNLQSKG						
	500	510	520	530	540	550	
	580	590	600	610	620	630	
m564 .pep	QTAKNSGHLTQTGKIDNRELH--NAGEIAANNLTLIHSGRLSNDKKGNIRAAHLQDLTA						
	: : : : : : : : : : : : : : : : : : : : :						
fhab_borpe	AIGVQGGGEAVSVANANSDAELRVGRGQVDLHDLAARGADISGEGRVNIAGRSDSDVK						
	560	570	580	590	600	610	
	640	650	660	670	680	690	
m564 .pep	GLHNAGNILADSGTVTTKNNLRNTGKVSVARLNTGQTLDNTRGRIEAEVNIQSQQLTN						
	: : : : : : : : : : : : : : : :						
fhab_borpe	-VSAHGALSIDSMTALGAIGVQAGGSVSAKDMRSRGAVTVSGGG-----AVNLGDVQ---						
	620	630	640	650	660		
	700	710	720	730	740	750	
m564 .pep	QSGHITATEQLTINSRNVNQNKKLLSANQAQLAVSDGLYNQHGEIATNRQLSIHDKNQ						
	: : : : : : : : : : : : : : : : : : : : : : : :						
fhab_borpe	SDGQVRATSAGAMTVRDV-----AAAADLALQAGDALQAGFLKSAGAMTVNGRDAV						
	670	680	690	700	710		

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	760	770	780	790	800	810
m564 .pep	TLALNNADGTIQSAGNVSLQAKSLANNGTLTAGNKLDIALTDDEFVVERDLTAGKQL-NLS					
		: :: :: ::::	: : :: :::	:	:	: :
fhab_borpe	RL-----DGA-HAGGQLRVSSDGOAALGSLAAKGELTVSAARAATVA-EL---KSLDNIS					
		720	730	740	750	760
	820	830	840	850	860	870
m564 .pep	IKGRLK-NHTLQAGHTLKLNA-GNIDNQVTGKIIGGEQTDITSEQHVDNRGLINS DGLT					
	:	: :::: :::	: :: :	: : : ::		: ::::
fhab_borpe	VTGGERVSVQSVNSASRVSAISAHGALD---VGKV--SAKSGIGLE---GWGAVGADSL-					
	770	780	790	800	810	
	880	890	900	910	920	930
m564 .pep	HIGAGQTLTNTGTGKIYGNHIALDAQILLNREETTEGSTKAGATAARKRLDI-GAKEIHN					
	: ::::	: ::	: :	: :: :	: : :::	: ::::
fhab_borpe	--GSDGAISVSGRDAVRVDQARSLADISLG----AEGGATLGAVEAAGSIDVRGGSTV--					
	820	830	840	850	860	
	940	950	960	970	980	990
m564 .pep	QEGALLSSEGIFAVGNRLDEQHHAAGMADTFVNGSAGLEVQGDALMSVRNMQINNHFKT					
	:: ::::	:	: :::: :::	: : :::	: : :::	: ::::
fhab_borpe	AANSLHANRDVRVSGK--DAVRVTAATSGGGLHVSSGRQLDLGAVQA-RGALALDGGAGV					
	870	880	890	900	910	920
	1000	1010	1020	1030	1040	1050
m564 .pep	ETYLAKAEK--QVRDYYTVLGQNTYYQAGKDGLFDNSQGGKQDTTATFHLKNGSRIEANQ-					
		: :	:	:	:	: : : :
fhab_borpe	ALQSAKASGTLHVQGGELDLGLTAAVGAVDV----NGTGDVRVAKLVSDAGADLQAGRS					
	930	940	950	960	970	
	1060	1070	1080	1090	1100	
m564 .pep	--WHVRDYHIETYKERIENRPAHITVGGDLTASGQNWLNKDSRIVVGGRIITDDLNOKE					
	:	: :	: :::	::	: : :::	:
fhab_borpe	MTLGIVDTTGDQLARAQQKLELGSVKSDGGLQAAAGGALSAAAEEVAGALELS---GQGV					
	980	990	1000	1010	1020	1030
	1110	1120	1130	1140	1150	1160
m564 .pep	ITNQSTTGKGRDQAVGTQWDSVTKGWY--SGRKRQRRTERNHTPYHDTQLFTHDFDTPV					
	: :::: :::	: :	: ::	: :: :	:	:
fhab_borpe	TVDRASARARIDSTGSVGIGALKAGAVEAASPRRRARRL-----QDFFTPG					
	1040	1050	1060	1070		1080
	1170	1180	1190	1200	1210	1220
m564 .pep	SVI---QQNAASPSFQPAASAIKLIDGVSTAANGQRIHTGNVVSINNATVTLNSSLYT					
	:	: :	:	: ::	:	: : : :
fhab_borpe	SVVVRAQGNVTVGRGDPHQGVLAQGDIIIMDA--KGGTLLLRNDALTENGTVTISADSAVL					
	1090	1100	1110	1120	1130	1140
	1230	1240	1250	1260	1270	1280
m564 .pep	THPDNKGWLVETD-PQFADYRRWLGS DYMLQQLQLDTNHLHKLRLGDGYEYEQKLVNEQIHQ					
		: ::::	:	:	: ::	:
fhab_borpe	EHSTIESKISQSVLAAGDKGKPAVSVKVAKKLFL--NGTLRAVNDN--NETMSGRQIDV					
	1150	1160	1170	1180	1190	
	1290	1300	1310	1320	1330	1340
m564 .pep	LTGYRRLDGYRSDEEQFKALMDNGLTAAKTFLGTPG-IALSAEQVARLTSDIVWMENQTV					
	:	: ::	:	: ::::	: ::	: : :::
fhab_borpe	VDGRPQI-----TDAVTGEARKDESVS DAALVADGGPIVVEAGELVSHAGGIGNGRNK--					
	1200	1210	1220	1230	1240	1250

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		1350	1360	1370	1380	1390	1400
m564	.pep	TLDGSTQTVLVPKVYALARKGDLNTSGGLISAEQVLLKLQNGNLNTSGTIAGRQAVLIQ					
		: :: :	:	: : :	: :: :	: :: :	: :
fhab_borpe		--ENGASVTVRTT-----GNLVNKGYSAGKQGVLEV-GGALTNEFLVGSDDGTQRIE					
		1260		1270	1280	1290	1300
		1410	1420	1430	1440	1450	
m564	.pep	ARNINSNGNIQ-----ADQIGLKAESINIDGGQVQAGRLLTAQ----AQNINLNGTT					
		: :: :	:	: :: :	: :	: :	: :
fhab_borpe		AQRIENRGTFQSQAPAGTAGALVVKAAEAIVHDGVMATKGEMQIAGKGGGSPTVTAGAKA					
		1310	1320	1330	1340	1350	1360
		1460	1470	1480	1490	1500	
m564	.pep	QTSGNERNGNTAI-DRMAGINVV-GSHTEQVDNRTSD-GILSLHASNDINLNAATVSNQV					
		: : :	: :	: :: :	: :	: :	: :
fhab_borpe		TTSANKLSVDVASWDNAGSLDIKKGGAQVTVAGRYAEHGEVSIQGDYTVSADAIALAAQV					
		1370	1380	1390	1400	1410	1420
		1510	1520	1530	1540	1550	
m564	.pep	--KDGTQTITAGNNLNLGT-IRTE---HREAYGTLDDENHRHVRQST-----EVGS					
		: :: :	: :	: :	: :	: :	: :
fhab_borpe		TQRGGAANLTSRHDTRFSNKIRLMGPLQVNAGGPVSNTGNLKVREGVTVTAASFDNETGA					
		1430	1440	1450	1460	1470	1480
		1560	1570	1580	1590	1600	
m564	.pep	SIRTQNGALLRAGNDLKIRQGELEAEEGKTVLAAGRDV--TISEGRQITELDTS---VSG					
		: :: :	: :	: :: :	: :	: :	: :
fhab_borpe		EVMAKSATLTTSGAARN--AGKMQVKEAATIVAASVSNPGTFTAGKDITVTSRGGFDNEG					
		1490	1500	1510	1520	1530	
		1610	1620	1630	1640	1650	1660
m564	.pep	K---SKGILSSTKTHDRYF---SHDEAV-GSNIGGGKMIVAAGQDINVGRSNLISDKGI					
		:	: :	: :	: :	: :	: :
fhab_borpe		KMESNKDIVIKTEQFSNGRVLDAKHDLTVTASGQADNRGSLKAGHDFTVQAQRI--DNSG					
		1540	1550	1560	1570	1580	1590
		1670	1680	1690	1700	1710	
m564	.pep	VLKAGHDIDISTAHNRYTG-----NEYHESKSGVMGTGGLGFTIGNRKTTDDTDRTNIV					
		: :: :	: :	: :	: :	: :	: :
fhab_borpe		TMAAGHDATLKAPHLRNTGQVVAGHDIHIINSAKLENTGRV--DARNDIALDVADFTN--					
		1600	1610	1620	1630	1640	1650
		1720	1730	1740	1750	1760	1770
m564	.pep	HTGSIIGSLNGDVTVAGNRRYQT---GSTVSSPEGRNTVTAKSIDVEFANNRYATDYA					
		: :	: :	: :	: :	: :	: :
fhab_borpe		-TGSLYAEHDA-TLTLAQGTQRDLVVDQDHILPVAEGTLRVKAKSLTTEIETGNPGLIA					
		1660	1670	1680	1690	1700	1710
		1780	1790	1800	1810	1820	1830
m564	.pep	HTQEOKGLTVALNVPVQAAQNFIAQAQNVGKSKNKRNVNMAAANAA-WQSYQATQMQQ					
		: :	: :	: :	: :	: :	: :
fhab_borpe		EVQE-----NIDNKQA----IVVGKDLTSL-SAHGNVANEANALLWAAGELTVKAQN					
		1720	1730	1740	1750		
		1840	1850	1860	1870	1880	1890
m564	.pep	FAPSSSAGQGQNNNQSPSISVSITYGEQKSRNEQKRHYTEAAASQIIGKQTTLAATGSG					
		: :	: :	: :	: :	: :	: :
fhab_borpe		ITNKRAALIEAGGNARLTAVALLNKLGRIRAGEDMHLD---APRI----ENTAKLSGEV					
		1760	1770	1780	1790	1800	1810
		1900	1910	1920	1930	1940	1950
m564	.pep	EQSNINITGSDVIGHAGTALIADNHIRLQSAKQDGEQSKNKSSGWNAGVAVKIGNGIRF					
		: :	: :	: :	: :	: :	: :
fhab_borpe		QRKGVQDVGGGEHGRWSGIGYVNYWLRAGNGKKAGT-----IAAPWYGGDLTAEQSLIEV					
		1820	1830	1840	1850	1860	

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		1960	1970	1980	1990	2000	2010
m564	.pep	GITAGGNIGKGKEQGGSTTHRHTHVGSTTGKTTIRSGGDTTLKGVQLIGKGIQADTRNLH					
				::		::	::::
fhab_borpe		GKDLVYNAGARKDE-----HRHL-----LNEGVIQAGGHGHIGG-----DVDNRSV-					
		1870	1880	1890	1900		

		2020	2030	2040	2050	2060
m564	.pep	IESVQDTETYQSKQQNGNVQVTVGYGFSASGSYRQSKVKA-----DHASVTGQSGIYAGE				
		::::	:::	:::	:::	:::
fhab_borpe		VRTVSAMEYFKTLPVSLTALDNRAGLSPATWNFQSTYELLDYLLDQNRYEYIWGLYPTY				
		1910	1920	1930	1940	1950

		2070	2080	2090	2100	2110	2120
m564	.pep	DGYQIKVRDNTDLKGGIITSSQSAEDKGKGNLFQTATLTASDIQNHS--RYEGRSFGIGGS					
		:::::					
fhab_borpe		TEWSVNTLKNLDL-GYQAKPAPTAPPMPKA-----PELDLRGHTLESAEGRKI-FGEY					
		1970	1980	1990	2000	2010	

		2130	2140	2150	2160	2170
m564	.pep	FDLNGGWDGT-----VTDKQGRPTDRISPAAGYGSDDSKNSTTRSGVNTNHIHITDEAG				
		:::	:::	:::	:::	:::
fhab_borpe		KKLQGEYEKAKMAVQAVEAYGEATRVRVDQLG-----QRYGKALGGMDAETKEVDGIIQ				
		2020	2030	2040	2050	2060

		2180	2190	2200	2210	2220	2230
m564	.pep	QLARTGRTAKETEARIYTGIDTETADQHSGHLKNSFDKDAVAKEINLQREVTKEFGRNAA					
		:::	:::	:::	:::	:::	:::
fhab_borpe		EFAADLRTVYAKQADQAT-IDAET-DKVAQRYKSQID--AVRLQAIQPGVRT--LAKALS					
		2080	2090	2100	2110	2120	

		2240	2250	2260	2270	2280	2290
m564	.pep	QAVAAVADKLGNTQSYERYQEARTLLE-AELQNTDSEAEKAAFRASLGQVNAYL-----					
		:::	:::	:::	:::	:::	:::
fhab_borpe		AALGADWRALGHSQLMQRWKDFKAGKRGAEIAFYPKQTVLAAGAGLTLSNGAIHNGENA					
		2130	2140	2150	2160	2170	2180

		2300	2310	2320	2330	2340	2350
m564	.pep	AENQSRDYDTWKEGGIGRSILHGAAGGLTTGSLGGILAGGGTSLAAPYLDKAAENLGPAGK					
		:::	:::	:::	:::	:::	:::
fhab_borpe		AQNRGRPEGLKIGAHSAVSFSGSFDALRDVGLEKRLDIDDALA AVLNPHIFTRIGAAQT					
		2190	2200	2210	2220	2230	2240

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1671>:

```

g565.seq
1  atggacagca cattgtctaa aacgtgttgc gtttcgtgca tattgttgag
51  cgtaaccacc accatthttcg ccggtcccag accggcggct tccaatactt
101 ccctgcgttt cgcacgcgcg aacgacaccg gctcgctgca acttctggct
151 acctgcacgc gtgcgatgac caagtcgagc gcgaaatacg gaataccttc
201 tttgggcgaa gacgcgtccg accgtctgcc cgcccctgcc gaagccgaca
251 atcagcacat gatcagactt gctcatcgct tccaccaaca tgctgtgcag
301 atcgagcgac ttcattgtccc agcttgga

```

This corresponds to the amino acid sequence <SEQ ID 1672; ORF 565.ng>:

```

g565.pep
1  MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
51  TCTRAMSKSS AKYGISSLGE DASDRLPAPA EADNQHMIRL AHRFHQHAVQ
101 IERLHVPA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1673>:

```

m565.seq
1  ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
51  CGTAACCACC ACCATTTTCG CCCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA

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251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGCGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTGGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT CAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1674; ORF 565>:

```

m565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSGETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m565/g565 100.0% identity in 67 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||
g565           MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                10      20      30      40      50      60

                70      80      90      100     110     120
m565.pep      AKYGISSWARTRPTVCPPLPKPTISTWSDLLMVSTSILCRSSDFMSQLDLTKRPTSASLP
                |||||
g565           AKYGISSLGEDASDRLPAPAEADNQHMIRLAHRFHQHAVQIERLHVPAX

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1675>:

```

a565.seq
  1 ATGGACAGCA CATTGTCTAA AACGTGTTGC GTTTCGTGCA TATTGTTGAG
 51 CGTAACCACC ACCATTTTCG CCGTCCCAG ACCGGCGGCT TCCAATACTT
101 CCCTGCGTTT CGCATCGCCG AACGACACCG GTTCGCCCCG ACTTCTGGCA
151 ACCTGCACCC GCGCAATGTC CAAGTCGAGC GCGAAATACG GAATATCCTC
201 TTGGGCAAGG ACGCGTCCGA CCGTCTGCCC GCCCCTGCCG AAGCCGACAA
251 TCAGCACATG GTCGGACTTG CTCATGGTTT CTACCAGCAT ACTGTGCAGA
301 TCGAGCGACT TCATGTCCCA GCTTGACTTG ACCAAACGCC CGACCAGTGC
351 ATCGCTGCCG CCCAAGAGGA AGGGCGCGAT AATCATCGAC AGCAGAACCG
401 CCGCCGTCGC CGCCTGTTCC CATTCTAGCG AAACCATATC AAGCTGCCCC
451 GCAATGGCCA GCATCACGAA GCCGAACGCG CCGCCCTGCG CGAGATACAA
501 AGCCGTTTGG AGGCTGTCGC CGACCGAATG TTTCATTTTG AAGGCAATGG
551 CAAACACAAC CAGTGCCTTC AACACCAGCA GCATTGCCAA CAGCATCAAT
601 ACCTGCCGCC AGCCGCCGAT TAATGCCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1676; ORF 565.a>:

```

a565.pep
  1 MDSTLSKTCC VSCILLSVTT TIFARPRPAA SNTSLRFASP NDTGSPALLA
 51 TCTRAMSKSS AKYGISSWAR TRPTVCPPLP KPTISTWSDL LMVSTSILCR
101 SSDFMSQLDL TKRPTSASLP PKRKGAIID SRTAAVAACS HSSETISSCP
151 AMASITKPNS PPCARYKAVL RLSPTTECFIL KAMANTTSF NTSSSIANSIN
201 TCRQPPINA*

```

m565/a565 99.5% identity in 209 aa overlap

```

                10      20      30      40      50      60
m565.pep      MDSTLSKTCCVSCILLSVTTTIFARPRPAA SNTSLRFASPNDTGSPALLATCTRAMSKSS
                |||||

```

868

```

a565      MDSTLSKTCCVSCILLSVTTTIFARPRPAASNTSLRFASPNDTGSFALLATCTRAMSKSS
           10      20      30      40      50      60
           70      80      90      100     110     120
m565.pep  AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           |||||
a565      AKYGISSWARTRPTVCPLPKPTISTWSDLLMVSTSIILCRSSDFMSQLDLTKRPTSASLP
           70      80      90      100     110     120
           130     140     150     160     170     180
m565.pep  PKRKGAIIDSRTAAVAACSHSGETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           |||||
a565      PKRKGAIIDSRTAAVAACSHSSETISSCPAMASITKPNSPPCARYKAVLRLSPTECFIL
           130     140     150     160     170     180
           190     200     210
m565.pep  KAMANTTSAFNTSSIANSLNCRQPPINAX
           |||||
a565      KAMANTTSAFNTSSIANSLNCRQPPINAX
           190     200     210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1677>:

```

g566.seq..
1  atgccgtctg aacaatatct tttcagacgg cattttgtat ggggggttaac
51  ggttggtcag cccgagtagc tcctgcatat cgtacaaacc cgttttgccg
101 tttacccaaa ctgcggcgcg gacggcaccg gcggcaaagg tcatgcggtc
151 gccggctttg tgggtgattt ccacgcgttc gccgtcgggt gcgaagaggg
201 cgggtgtggtc gccgactatg tcgcctgcgc ggacggtggc aaagccgatg
251 gtggaaggat cgcgcggacc agtgtggcct tcgcggccgt aaacggcgca
301 ttgtttgagg tcgcggccga gcgcgccggc gatgacttcg cccattcgta
351 a

```

This corresponds to the amino acid sequence <SEQ ID 1678; ORF 566.ng>:

```

g566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVYPNCGA DGTGGKGHAA
51  AGFVGDFHAF AVGGEEGGVV ADYVACADGG KADGGRIART SVAFAAVNGA
101 LFEVAAERAG DDFAH*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1679>:

```

m566.seq..
1  ATGCCGTCTG AACAAATATCT TTTCAGACGG CATTTTGTAT GGGGGTTAAC
51  GGTGTGTTAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTGTCCG
101 TTGACCCAAA CTGCGGCGCG GACGGCACC GCGGCAAAGG TCATGCGGCT
151 GCTGGCCTTG TGGGTGATTT CCACGCGCTC GCCGTCGGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCTGCGC GGACGGTGGC AAAGCCGATG
251 GTCGACGGAT CGCGCGGACC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1680; ORF 566>:

```

m566.pep..
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFAVDPNCGA DGTGGKGHAA
51  AGLVGDFHAL AVGGEEGGVV ADDVACADGG KADGRRRIART GVAFAAVNGA
101 LFEVSAERAG DDFAH*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m566/g566 93.1% identity in 116 aa overlap

```

           10      20      30      40      50      60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||

```

869

```

g566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVYPNCGADGTGGKGHAAAGFVGDFHAF
           10          20          30          40          50          60
           70          80          90          100         110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||
g566      AVGGEEGGVVADYVACADGGKADGGRIARTSVAFAAVNGALFEVAAERAGDDFAHSX
           70          80          90          100         110

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1681>:

```

a566.seq
1  ATGCCGCTCTG AACAAATATCT TTTCAGACGG CATTGTGTAT GGGGGTTAAC
51 GGTGTTCAG CCCGAGTACG TCCTGCATAT CGTACAAACC CGTTTACC
101 TTTACCCAAA CTGCGGCGCG GACGGCGCCG GCGGCAAAGG TCATGCGGCT
151 GCTTGCCTTG TGGGTGATTT CCACGCGCTC GCCGTGCGTG GCGAAGAGGG
201 CGGTGTGGTC GCCGACGATG TCGCCCGCGC GGACGGTGGC AAAGCCGATG
251 GTGGACGGAT CGCGCGGGCC GGTGTGGCCT TCGCGGCCGT AAACGGCGCA
301 TTGTTTGAGG TCTCTGCCGA GCGCGCCGGC GATGACTTCG CCCATGCGTA
351 A

```

This corresponds to the amino acid sequence <SEQ ID 1682; ORF 566.a>:

```

a566.pep
1  MPSEQYLFRR HFVWGLTVVQ PEYVLHIVQT RFTVYPNCGA DGAGGKGHAA
51 ACLVGDFHAL AVGGEEGGVV ADDVARADGG KADGGRIARA GVAFAAVNGA
101 LFEVSAERAG DDFAHAX*

```

m566/a566 94.0% identity in 116 aa overlap

```

           10          20          30          40          50          60
m566.pep  MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFAVDPNCGADGTGGKGHAAAGLVGDFHAL
           |||||
a566      MPSEQYLFRRHFVWGLTVVQPEYVLHIVQTRFTVYPNCGADGAGGKGHAAACLVGDFHAL
           10          20          30          40          50          60
           70          80          90          100         110
m566.pep  AVGGEEGGVVADDVACADGGKADGRRRIARTGVAFAAVNGALFEVSAERAGDDFAHAX
           |||||
a566      AVGGEEGGVVADDVARADGGKADGGRIARAGVAFAAVNGALFEVSAERAGDDFAHAX
           70          80          90          100         110

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1683>:

```

g567.seq.
1  atgcgacgac gggcagcggc atcgacaagg cgggtttgca gtccggcggtt
51 tatcaggtct tattgggcga tgcggacgtg cagtcggcgg cggtagcgag
101 caaagagggc ggatacggcg tgttgggtgc gaacgcgcgc gcttgccggc
151 gcggaaatcg agctggtgca ggaaatcgcc cgggaagtgc gtttgaaaaa
201 cgcgctcaag gcagtgccgg aagattacga ctttatcctg atcgactgtc
251 cgccttcgct gacgtgttg acgcttaacg gcttgggtgc ggcgggcggc
301 gtgattgtgc cgatgtttgt cgaatattac gcgctggaag ggatttccga
351 tttgattgcg accgtgcgca aaatccgtca ggcggtcaat cccgatttgg
401 acatcacggg catcgtgcgt acgatgtacg acagccgcag caggctgggt
451 gccgaagtca gcgaacagtt gcgcagccat ttcggggatt tgctttttga
501 aaccgccatc ccgcgcaata tccgccttgc ggaagcgccg agccacggta
551 tgccggtgat ggcttacgac gcgcaggcaa agggtgccaa ggcgtatcct
601 gccttggcgg acgaactggc ggcgaggggtg tcggggaaat ag

```

This corresponds to the amino acid sequence <SEQ ID 1684; ORF 567.ng>:

```

g567.pep
1  MRRRAAATR RVCSPAFIRS YWAMRTCSRR RYAAKRADTA CWVRTRALAG
51 AEIELVQEIA REVRLKNALK AVAEDYDFIL IDCPPSLTLL TLNGLVAAGG
101 VIVPMLCEYY ALEGISDLIA TVRKIRQAVN PDLDITGIVR TMYDSRSLV
151 AEVSEQLRSH FGDLLFETAI PRNIRLAEAP SHGMPVMAYD AQAKGAKAYL
201 ALADELAARV SGK*

```

870

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1685>:

```
m567.seq..
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTCGATTTC GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGGGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGCAGTCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
251 CTGTGTTGGG TGCGAACCGC GCGCTGGCCG GCGCGGAAAT CGAACTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGA
351 AGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CGGGCTGGTG GCGGCGGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCG GATTTGATTG CGACCGTGCG
501 CAAATCCGT CAGGCGGTCA ATCCCGATTG GGACATCACG GGCATCGTGC
551 GCACGATGTA CGACAGCCGC AGCAGGCTGG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTACG
701 ACGCGCAGGC AAAGGTACC AAGGCGTATC TTGCCTTGCG GGACGAGCTG
751 GCGGCGAGGG TGTCGGGGAA ATAG
```

This corresponds to the amino acid sequence <SEQ ID 1686; ORF 567>:

```
m567.pep..
1  MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51  GIDKAGLQSG VYQVLLGDAD VQSAAVRSKE GGYAVLGANR ALAGAEIELV
101 QEIAREVRLK NALKA VEEDY DFILIDCPPS LTLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGT KAYLALADEL
251 AARVSGK*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m567/g567 98.2% identity in 168 aa overlap

m567.pep 60 70 80 90 100 110 119
          GVIQVLLGDADVQSAAVRSKEGGYAVLGANRALAGAEIELVQEIAREVRLKNALKAVEED
          |||||
g567      AFIRSYWAMRTCSRRRYAAKRADTACWVRTRALAGAEIELVQEIAREVRLKNALKAVEED
          20 30 40 50 60 70

m567.pep 120 130 140 150 160 170 179
          YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
          |||||
g567      YDFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLDI
          80 90 100 110 120 130

m567.pep 180 190 200 210 220 230 239
          TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKG
          |||||
g567      TGIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETAIPRNIRLAEAPSHGMPVMAYDAQAKG
          140 150 160 170 180 190

m567.pep 240 250
          TKAYLALADELAARVSGKX
          :|||
g567      AKAYLALADELAARVSGKX
          200 210
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1687>:

```
a567.seq
1  ATGAGTGC GA ACATCCTTGC CATCGCCAAT CAGAAGGGCG GTGTGGGCAA
51  AACGACGACG ACGGTAAATT TGGCGGCTTC GCTGGCATCG CGCGGCAAAC
101 GCGTGCTGGT GGTCGATTTC GATCCGCAGG GCAATGCGAC GACGGGCAGC
151 GGCATCGACA AGGCGAGTTT GCAGTCCGGC GTTTATCAGG TCTTATTGGG
201 CGATGCGGAC GTGAAATCGG CGGCGGTACG CAGCAAAGAG GGCGGATACG
```


871

```

251 GCGTGTGGG TCGAACC GCCTGGCCG GCGCGGAAAT CGAGCTGGTG
301 CAGGAAATCG CCCGGGAAGT GCGTTTGAAA AACGCGCTCA AGGCAGTGGC
351 GGAAGATTAC GACTTTATCC TGATCGACTG CCCGCCTTCG CTGACGCTGT
401 TGACGCTTAA CCGCTTGGTG GCGGCAGGCG GCGTGATTGT GCCGATGTTG
451 TGCGAATATT ACGCGCTGGA AGGGATTTCC GATTTGATTG CGACCGTGCG
501 CAAAATCCGT CAGGCGGTCA ATCCCGATTG GGATATCACG GGCATCGTGC
551 GTACGATGTA CGACAGCCGC AGCAGGCTAG TTGCCGAAGT CAGCGAACAG
601 TTGCGCAGCC ATTTCCGGGA TTTGCTGTTT GAAACCGTCA TCCCGCGCAA
651 TATCCGCCTT GCGGAAGCGC CGAGCCACGG TATGCCGGTG ATGGCTTATG
701 ATGCGCAGGC AAAGGGTGCC AAGGCGTATC TTGCCTTGGC GGACGAGCTG
751 ATGGCGAGGG TGTCGGGGAA ATAG

```

This corresponds to the amino acid sequence <SEQ ID 1688; ORF 567.a>:

```

a567.pep
1 MSANILAIAN QKGGVGKTTT TVNLAASLAS RGKRVLVVDL DPQGNATTGS
51 GIDKASLQSG VYQVLLGDAD VKSAAVRSKE GYGVLGANR ALAGAEIELV
101 QEIAREVRLK NALKAVAEDY DFILIDCPPS LTLLTLNGLV AAGGVIVPML
151 CEYYALEGIS DLIATVRKIR QAVNPDLIT GIVRTMYDSR SRLVAEVSEQ
201 LRSHFGDLLF ETVIPRNIRL AEAPSHGMPV MAYDAQAKGA KAYLALADEL
251 MARVSGK*

m567/a567 97.7% identity in 257 aa overlap

10 20 30 40 50 60
m567.pep MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
|||||
a567 MSANILAIANQKGGVGKTTT TVNLAASLASRGKRVLVVDLDPQGNATTGSGIDKASLQSG
10 20 30 40 50 60

70 80 90 100 110 120
m567.pep VYQVLLGDADVQSAAVRSKEGGYAVLGNRALAGAEIELVQEIAREVRLKNALKAVEEDY
|||||
a567 VYQVLLGDADVQSAAVRSKEGGYAVLGNRALAGAEIELVQEIAREVRLKNALKAVEEDY
70 80 90 100 110 120

130 140 150 160 170 180
m567.pep DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
|||||
a567 DFILIDCPPSLTLLTLNGLVAAGGVIVPMLCEYYALEGISDLIATVRKIRQAVNPDLIT
130 140 150 160 170 180

190 200 210 220 230 240
m567.pep GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGT
|||||
a567 GIVRTMYDSRSRLVAEVSEQLRSHFGDLLFETVIPRNIRLAEAPSHGMPVMAYDAQAKGA
190 200 210 220 230 240

250
m567.pep KAYLALADELAARVSGKX
|||||
a567 KAYLALADELMARVSGKX
250

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1689>:

```

g568.seq
1 atgtctcaggg tcagaccggt attatttgcc gtcaaggctt ccgcctcttc
51 gataccttgc agaattctgcc gattaaagcg ttcgcggctg cccaatattt
101 tcaggcgcac attgttttcg tgcaggcggc gtacctgttt ttgcaaagcc
151 tgtaaaaaca gcccacacag gaacgaaact tcgtcttcg ggcgacgcca
201 gttttcgggt gaaaaggcaa acacggtcag atattgcacg cccagtttgg
251 cgcaatgctt caccatattt tccaacgcgt ccaagccgcg tttgtgtccc
301 attatacgcg ggagaaaacg ttttttcgcc caacggcgtg tgccgtccat
351 aattacggcg atgtgcctcg ggatggcggg gtgttccaaa atgggtctgcg

```

q568.pep

```

1 MLRVRPVLFA VKASASSIPC RICRLKRSRL PNIFRRILFS CRRRTCFCKA
51 CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IIRGRKRFFA QRPLPSIITA MCLGMAVCSK MVCVLLFISA FRGSAFKCRL
151 NAAP*

```

m568.seq

1	ATGCTCAGGG	TCAGGCCGGT	ATTGTTTGCC	GTCAACGCTT	CCGCCTCTTC
51	GATGCCTTGC	AGAACTCGCC	GGTTGAAGCG	TTCGCGGCTG	CCCAATATCT
101	TCAGGCGCAT	ATTGTTTTTC	TGCAGGCGGC	GTACCTGTTT	TTGCAAAGCC
151	TGTAAAAACA	GCCCCATCAG	GAACGAAACT	TCGTCTTCGG	GGCGGCGCCA
201	GTTTTTCGGT	GAAGAAGCAA	ACACGGTCAG	ATATTGCACA	CCAGTTTGGG
251	CGCAATGCTT	CACCATATTT	TCCAATGCGT	CCAAACCGCG	TTTGTGTCCC
301	ATTATGCGCG	GGAGGAAACG	TTTTTTCGCC	CAACGGCCGT	TGCCGTCCAT
351	AATCACGGCG	ATATGCTTGG	GAATGGCGGT	GTGTTCCAAA	ACGGCCTGCG
401	TGCTGCTTAT	CATGCTCTGC	TTTCGCGGTT	CGGCATTCAA	ATGCCGTCGT
451	AACGCCGAAC	CGTGCAGGTT	AAATTGCCAT	CAATCTTCT	TCTTTGGCAG
501	TCAGAGTTT	GTCGCGTTCG	GTAAATGTATT	TGTCGGTCAG	TTTTTGAACC
551	GCTTCTTCGC	CGCGACGTGC	CTCGTCTTCG	GAAATTTCTT	TGTCTTTGAG
601	GAGTTTTTTG	ATGTGGTCGT	TGGCATCGCG	GCGCACGTTG	CGGATAGAGA
651	CGCGGCGCTT	TTCCGCTTCG	CCGCGTACGA	CTTTAATCAG	GTCTTTGCGG
701	CGTTCCTTCG	TCAGCATGGG	CATCGGCACG	CGGATCAGGT	CGCCGACAGC
751	TGCGCGGGTT	AGTCCCAAGT	TTGA		

m568.pap.

1	MLRVRPVLFA	VNASASSMPC	RICRLKRSRL	PNIFRRILFS	CRRRTCCKA
51	CKNSPIRNET	SSSGRRQFSV	EKANTVRYCT	PSLAQCFTIF	SNASKPRLCP
101	IMRGKRFFFA	QRPLPSIITA	ICLGMVCSK	TACVLLFMSA	FRGSAFKCRL
151	NAEPCRLNCH	QIFFFGSQEF	VGFGNVFVGQ	FLNRFFAATC	LVFGNFFVFE
201	EFFDVVVGIA	AHVADRDAAF	FRFAAYDFNQ	VFAAFLGQHG	HRHADQVADS
251	CRVOSOV*				

Homology with a predicted ORF from *N. gonorrhoeae*

m568/q568 94.8% identity in 154 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMP	CRICRLKRSRLPNIFRRILF	SCRRRTCFCKACKNSPIRNET			
		:	:	:	:	:
g568	MLRVRPVLFAVKASASSIP	CRICRLKRSRLPNIFRRILF	SCRRRTCFCKACKNSPIRNET			
	10	20	30	40	50	60
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCT	PSLAQCFTIFSNASKPRLCP	IMRGRKRFFAQRP	LPSIIITA		
					:	:
g568	SSSGRRQFSVEKANTVRYCT	PSLAQCFTIFSNASKPRLCP	IIRGRKRFFAQRP	LPSIIITA		
	70	80	90	100	110	120
	130	140	150	160	170	180
m568.pep	ICLGMVCSKTACVLLFMSA	FRGSAFKCRLNAEPCRLN	CHQIFFFGSQEFVGF	GNVFGV	QG	
	:	:	:	:	:	:
g568	MCLGMVCSKMCVCLLFISA	FRGSAFKCRLNAAPX				
	130	140	150			
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVGFNFVF	EEFFDVVVGIAAHVADRD	AAFFRF	AAFDENOVFAAFL	GOH	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1693>:

```
a568.seq
1   ATGCTCAGGG TCAGGCCGGT ATTGTTTGCC GTCAAGGCTT CCGCCTCTTC
51  GATGCCCTTC AGGATTTGAC GGTGAAGCG TTCGCGGCTG CCCAGTATTT
101 TCAGGCGCAT ATTGTTTTTC TGCAGGCGGC GTACCTGTTT TTGCAAAGCC
151 TGTA AAAACA GCCCATCAG GAACGAACT TCGTCTTCGG GCGGCGCCA
201 GTTTTTCGGT GAAAAGGCAA ACACGGTCAG ATATTGCACA CCCAGTTTGG
251 CGCAATGCTT CACCATATTT TCCAATGCGT CCAAACCGCG TTTGTGTCCC
301 ATTATGCGCG GGAGGAAACG TTTTTCGCC CAACGGCCGT TGCCGTCCAT
351 AATCAGGCG ATATGCTTGG GAATGGCGGT GTGTCCAAA ACGGCCTGCG
401 TGCTGCTTTT CATGTCTGCC TTTTCGGGT CCGCATTCAG ATGCCGCTG
451 AACGCCGAAC CGTGCAGGTT AAATTGCCAT CAAATCTTCT TCTTTGGCAG
501 TCAGGAGTTT GTCGGCTTCG GTAATGTATT TGTCGGTCAG TTTTGAACC
551 GCTTCTTCGC CGCGACGTGC CTCGTCTTCG GAAATTTCTT TGTCTTTGAG
601 GAGTTTTTTG ATGTGGTCGT TGGCATCGCG GCGCACGTTG CGGATGGAGA
651 CGCGGCCTTC TTCCGCTTCG CCGCGTACGA CTTTAATCAG GTCTTTGCGG
701 CGTTCCTCGG TCAGCATGGG CATCGGCACG CCGATCAGGT CGCCGACAGC
751 TGCCGGGTTC AGTCCCAAGT TTGA
```

This corresponds to the amino acid sequence <SEQ ID 1694; ORF 568.a>:

```
a568.pep
1   MLRVRPVLFA VKASASSMPF RI*RLKRSRL PSIFRRILFS CRRRTCFCCKA
51  CKNSPIRNET SSSGRRQFSV EKANTVRYCT PSLAQCFITF SNASKPRLCP
101 IMRGRKRFFA QRPLPSIITA ICLGMAVCSK TACVLLFMSA FRGSAFKCRL
151 NAEPCLNCH QIFFFGSQEF VGFGNVFVGQ FLNRFFAATC LVFGNFFVFE
201 EFFDVVVGIA AHVADGDAF FRFAAYDFNQ VFAAFLGQHG HRHADQVADS
251 CRVQSQV*
```

m568/a568 98.1% identity in 257 aa overlap

	10	20	30	40	50	60
m568.pep	MLRVRPVLFAVNASASSMPCRICRLKRSRLPNIFRRILFSRRRTCFCCKACKNSPIRNET					
a568	MLRVRPVLFAVKASASSMPFRIXRLKRSRLPSIFRRILFSRRRTCFCCKACKNSPIRNET					
	10	20	30	40	50	60
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
	70	80	90	100	110	120
m568.pep	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
a568	SSSGRRQFSVEKANTVRYCTPSLAQCFTIFSNAKPRLCPIMRGRKRFFAQRPLPSIITA					
	130	140	150	160	170	180
m568.pep	ICLMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLNCHQIFFFGSQEFVGFGNVFVGQ					
a568	ICLMAVCSKTACVLLFMSAFRGSFAFKCRLNAEPCLNCHQIFFFGSQEFVGFGNVFVGQ					
	130	140	150	160	170	180
m568.pep	FLNRFFAATCLVFGNFFVFEFFDVVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEFFDVVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	FLNRFFAATCLVFGNFFVFEFFDVVVGIAAHVADRDAFFRFAAYDFNQVFAAFLGQHG					
a568	FLNRFFAATCLVFGNFFVFEFFDVVVGIAAHVADGDAFFRFAAYDFNQVFAAFLGQHG					
	190	200	210	220	230	240
m568.pep	HRHADQVADSCRVSQVX					
a568	HRHADQVADSCRVSQVX					
	250					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1695>:

```
g569.seq..
1   atgctgaaac aacgggtaat aaccgctatg tggctgctgc cgctgatgct
51  gggcatgctg ttttacgcgc cgcaatggct gtgggctgca ttttgcgggc
101 tgattgccct gaccgccttg tgggagtatg cccgatggc cggtttgtgc
```

874

```

151 aaaaccgaaa ccaaccatta cctcgccgca accttggttt tcggcgtagt
201 tgcctatgcg ggcggctgga tgctgcctaa tttggtttgg tatgttggtt
251 tggcattttg gctcgccggt atgcctttgt gggtgagatt caaatggagg
301 ctcaacggcg gttggcaggt ttatgccgct ggctggcttt tgctcatgcc
351 gttttgggtc gcgctcgat ccctggcgcc cgcacccga tga

```

This corresponds to the amino acid sequence <SEQ ID 1696; ORF 569.ng>:

g569.pep

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALTAL WEYARMAGLC
51 KTETNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLAPASR *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1697>:

m569.seq..

```

1 ATGCTGAAAC AACGGGTAAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGC GGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC
151 AAAATTAAAA CCAACCATT A CCTCGCCGCA ACCTTG GTTT TCGGCGTGGT
201 TGCCTATGCG GCGGCTGGA TGCTGCCTAA TTTGGTTTG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTCAACGGCG GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCGCCGG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCAGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTGTGCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAAGCTGCT GCCCGACAC GCGGCGTGT TCGACCGTAC CGACAGCCTG
751 ATTGCCGTGA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1698; ORF 569>:

m569.pep..

```

1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LNGGWQVYAV GWLLMPFWF ALVSLRPHPD DALPLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAI SPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFTDGTW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSKLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

```

m569/g569 95.3% identity in 127 aa overlap

	10	20	30	40	50	60
m569.pep	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCIKTNHYLAA					
g569	MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALTALWEYARMAGLCKTETNHYLAA					
	10	20	30	40	50	60
	70	80	90	100	110	120
m569.pep	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLMPFWF					
g569	TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNNGGWQVYAVGWLLMPFWF					
	70	80	90	100	110	120
	130	140	150	160	170	180
m569.pep	ALVSLRPHPD DALPLAVMGLVWVADICAYFSGKAFGKHKIAPAI SPGKS WEGAIGGAVC					
g569	ALVSLAPASRX					
	130					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1699>:

a569.seq

```

1 ATGCTGAAAC AACGGGTGAT AACCGCCATG TGGCTGCTGC CGCTGATGCT
51 GGGCATGCTG TTTTACGCGC CGCAATGGTT GTGGGCTGCA TTTTGC GGAC
101 TGATTGCCCT GATTGCCTTG TGGGAATATG CCCGTATGGG CGGTTTGTGC

```

875

```

151 AAAATTAAAA CCAACCATTA CCTCGCCGCA ACCTTGTTT TCGGCGTGGT
201 TGCCTATGCG GCGCGCTGGA TGCTGCCTAA TTTGGTTTGG TATGTTGTTT
251 TGGCATTTTG GCTCGCCGTT ATGCCTTTAT GGTTGAGATT CAAATGGAGG
301 CTAACGCGC GTTGGCAGGT TTATGCCGTC GGCTGGCTTC TGGTCATGCC
351 GTTTTGGTTC GCGCTCGTAT CCCTGCGCCC GCATCCCGAT GATGCCCTGC
401 CGCTGCTCGC CGTGATGGGT TTGGTGTGGG TTGCCGATAT TTGCGCGTAT
451 TTCAGCGGCA AGGCGTTCGG CAAACACAAA ATCGCACCCG CAATCAGCCC
501 CGGCAAAAGC TGGGAAGGTG CAATCGGCGG CGCGGTTTGC GTGGCCGTGT
551 ACATGACCGC CGTACGAAGT GCCGGCTGGC TGGCATTCTGA TACAGGCTGG
601 TTCGATACCG TGTTAATCGG TTTGGTGTG ACCGTTGTCA GCGTATGCGG
651 CGACCTTTTG GAAAGCTGGC TCAAGCGCGC GGCAGGCATC AAAGACAGCA
701 GCAACCTGCT GCCCGGACAC GCGGCGTGT TCGACCGCAC CGACAGCCTG
751 ATTGCCGTGA TCAGCGTCTA TGCAGCGATG ATGTCGGTTT TAAATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1700; ORF 569.a>:

```

a569.pep
1 MLKQRVITAM WLLPLMLGML FYAPQWLWAA FCGLIALIAL WEYARMGGLC
51 KIKTNHYLAA TLVFGVVAYA GGWMLPNLVW YVVLAFWLAV MPLWLRFKWR
101 LGGGWQVYAV GWLLVMPFWF ALVSLRPHPD DALPLLAVMG LVWVADICAY
151 FSGKAFGKHK IAPAIKPGKS WEGAIGGAVC VAVYMTAVRS AGWLAFDTGW
201 FDTVLIGLVL TVVSVCGDLL ESWLKRAAGI KDSSNLLPGH GGVFDRTDSL
251 IAVISVYAAM MSVLN*

m569/a569 99.6% identity in 265 aa overlap

          10          20          30          40          50          60
m569.pep MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
|||||
a569 MLKQRVITAMWLLPLMLGMLFYAPQWLWAAFCGLIALIALWEYARMGGLCKIKTNHYLAA
          10          20          30          40          50          60

          70          80          90          100          110          120
m569.pep TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
|||||
a569 TLVFGVVAYAGGWMLPNLVWYVVLAFWLAVMPLWLRFKWRLNGGWQVYAVGWLLVMPFWF
          70          80          90          100          110          120

          130          140          150          160          170          180
m569.pep ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEGAIGGAVC
|||||
a569 ALVSLRPHPDALPLLAVMGLVWVADICAYFSGKAFGKHKIAPAIKPGKSWEGAIGGAVC
          130          140          150          160          170          180

          190          200          210          220          230          240
m569.pep VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSKLLPGH
|||||
a569 VAVYMTAVRSAGWLAFDTGWFDTVLIGLVLTVVSVCGDLLESWLKRAAGIKDSSNLLPGH
          190          200          210          220          230          240

          250          260
m569.pep GGVFDRTDSLIAVISVYAAMMSVLNX
|||||
a569 GGVFDRTDSLIAVISVYAAMMSVLNX
          250          260

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1701>:

```

g570.seq..
1 atgatccgtt tgaccgcgc gtttgccgcc gccctgatcg gtttatgctg
51 caccacagcg gcgcagccg acacctcca aaaaatcggc tttatcaaca
101 ccgagcgcat ctacctgaa tccaagcagg cgcgcaacat ccaaaaaacg
151 ctggacggcg aattttccgc ccgtcaggac gaattgcaaa aactgcaacg
201 cgaagccttg gatttgaaa gccagctcgc cggcgcaaaa ctaaggacg
251 caaaaaagcg gcaagccgaa gaaaaatggc gcgggctggg cgaagcgttc
301 cgcaaaaaac aggcgcagtt tgaagaagac tacaacctcc gccgcaacga
351 agagtgttgc tccctccagc aaaacgcaa ccgcgtcatc gtcaaaatcg

```

876

```

401 ccaaacagga aggttacgat gtcattttgc aggacgtgat ttacgtcaac
451 acccaatacg acgttaccga cagcgtcatt aaagaaatga acgcccgtg
501 a

```

This corresponds to the amino acid sequence <SEQ ID 1702; ORF 570.ng>:

g570.pep..

```

1 MIRLTRAFAA ALIGLCCTTG AHADTFQKIG FINTERIYLE SKQARNIQKT
51 LDGEFSARQD ELQKLQREGL DLERQLAGGK LKDAKKAQAE EKWRGLVEAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151 TQYDVTDSVI KEMNAR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1703>:

m570.seq..

```

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
51 CACCGCAGGC GCGCACGCGG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC TCGTCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAGAAACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGC GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGAACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG
501 A

```

This corresponds to the amino acid sequence <SEQ ID 1704; ORF 570>:

m570.pep

```

1 MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
51 LDSEFSARQD ELQKLQREGL DLERQLAEGK LRNAKKAQAE EKWRGLVAAF
101 RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQNVIIYN
151 TQYDVTDSVI KEMNAR*

```

m570/g570 94.6% identity in 166 aa overlap

	10	20	30	40	50	60
m570.pep	MTRLTRAFAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLDSEFSARQD					
g570	MIRLTRAFAAALIGLCCTTGAAHADTFQKIGFINTERIYLESKQARNIQKTLDGEFSARQD					
	10	20	30	40	50	60
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
m570.pep	ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA					
g570	ELQKLQREGLDLERQLAGGKLKDAKKAQAEKWRGLVEAFRKKQAQFEEDYNLRNNEEFA					
	70	80	90	100	110	120
m570.pep	SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX					
g570	SLQQNANRVIVKIAKQEGYDVILQDVIYVNTQYDVTDSVIKEMNARX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1705>:

a570.seq

```

1 ATGACCCGTT TGACCCGCGC GTTTGCCGCG GCTCTGATCG GTTTGTGCTG
51 CACCGCAGGC GCGCACGCGG ACACCTTCCA AAAAATCGGC TTTATCAACA
101 CCGAGCGCAT CTACCTCGAA TCCAAGCAGG CGCGCAAGAT TCAAAAAACG
151 CTGGACAGCG AATTTTCCGC CCGCCAGGAC GAATTGCAAA AACTGCAACG
201 CGAAGGTCTG GATTTGGAAA GGCAGCTTGC CGAAGGCAAA CTCAAAGACG
251 CAAAAAAGGC GCAAGCCGAA GAAAAATGGT GCGGGCTGGT CGCAGCGTTC
301 CGCAAAAAAC AGGCGCAGTT TGAAGAAGAC TACAACCTCC GCCGCAACGA
351 AGAGTTTGCC TCCCTCCAGC AAAACGCCAA CCGCGTCATC GTCAAAATCG
401 CCAAACAGGA AGGTTACGAT GTCATTTTGC AGGACGTGAT TTACGTCAAC
451 ACCCAATACG ACGTTACCGA CAGCGTCATT AAAGAAATGA ACGCCCGCTG

```

877

501 A

This corresponds to the amino acid sequence <SEQ ID 1706; ORF 570.a>:

```

a570.pep
  1  MTRLTRAFAA ALIGLCCTAG AHADTFQKIG FINTERIYLE SKQARKIQKT
 51  LDSEFSARQD ELQKLQREGL DLERQLAEGK LKDAKKAQAE EKWCGLVAAF
101  RKKQAQFEED YNLRNNEEFA SLQQNANRVI VKIAKQEGYD VILQDVIYVN
151  TQYDVTDSVI KEMNAR*

m570/a570  97.6% identity in 166 aa overlap

              10      20      30      40      50      60
m570.pep    MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD
              |||||
a570         MTRLTRAFAAAALIGLCCTAGAHADTFQKIGFINTERIYLESKQARKIQKTLTLDSEFSARQD
              10      20      30      40      50      60

              70      80      90      100     110     120
m570.pep    ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              |||||:|||||
a570         ELQKLQREGLDLERQLAEGKLRNAKKAQAEKWRGLVAAFRKKQAQFEEDYNLRNNEEFA
              70      80      90      100     110     120

              130     140     150     160
m570.pep    SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
              |||||:|||||
a570         SLQQNANRVIVKIAKQEGYDVILQNVIIYVNTQYDVTDSVIKEMNARX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1707>:

```

g571.seq (partial)
  1  atgcgcgttt tccgagtaaa ccgatttggt gttaccgttt tcggcggcgg
 51  tataggttct ccggtcccac acgctgcctg cgtcggcaaa caggctcagg
101  cggacggtgc gtgcgtcttt cgcaccgggc atcgggaaga gcagctcggc
151  ggagacgttg gcttttttgt tgcgcgctga gctgattttt tcgccgtatt
201  cgtcatacac ttccgggccc agcgtgccgc tttcgtagcc gcgcaccgaa
251  cccaggccgc cgcgtagaaa gttttcaaa aaggggattt ctttggttct
301  gccgtagccg cccgcaatgc cgacttcgcc gccgagcatc agcgtgaagg
351  ttttgc...

```

This corresponds to the amino acid sequence <SEQ ID 1708; ORF 571.ng>:

```

g571.pep (partial)
  1  MRVFRVNRFV VTVFGGGIGS AVPHAACVGK QAQADGACVF RTGHREEQLG
 51  GDVGFFVAAV ADFFAVFVIH FRAERAAFVA AHRTQAAAVE VFKEGDFFGS
101  AVAARNADFA AEHQREGFA...

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1709>:

```

m571.seq
  1  ATGGGTATTG CCGGCGCCGT AAATGTTTTG AACCTGCCG CCGGTGCGCG
 51  AACTGCTGTT GTCGTCGTAG GTTTTGCCGT CCCACACGCT GCCTGCGTCG
101  GCAAACAGGC TCAGGCGGAC GGTGCGCGCG TCTTTCGCGC CGGGCATCGG
151  GAAGAGCAGC TCGGCGGAGA CGTTGGCTTT TTTGTTGCCG CCGTAGCTGA
201  TTTTTCGCCG GTATTCGTCA TAGACTTTCG GACCAGCGT GCCGCTTTCG
251  TATCCGCGCA CCGAACCAGG GCCGCCCGCG TAGAAGTTTT CAAAGAAGGG
301  GATTTCCTTG GTTCTGCCGT AGCCGCCCGC AATGCCGACT TCGCCGCCGA
351  GCATCAGCGT GAAGGTTTTG CTCAGGGGGA AGAACCAGGT TTGGTTGTGG
401  GTGGCGGAGT AGTATTGCAG TTTGCTGCCA GGCAGGGCGA TTTGCGCGTT
451  CACGCCCGTC AGGTAGCCGC GCGTCGGCCA TAA

```

This corresponds to the amino acid sequence <SEQ ID 1710; ORF 571>:

```

m571.pep
  1  MGIAGAVNVL NPAAGRGTAV VVVGFAVPHA ACVGKQAQAD GARVFRAGHR
 51  EEQLGGDVGF FVAAVADFFA VFVIDFRTER AAFVSAHRTQ AAAVEVFKEG
101  DFFGSAVAAR NADFAAEHQR EGFAQGEEPG LVVGGGVVLQ FAARQGDFGV
151  HARQVAARRP *

```

878

m571/g571 93.1% identity in 102 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNV	LNPAAGRG	TAVVVVG	FAVPHAA	CVGKQAQ	ADGARVF
			:			
g571	MRVFRVNR	FVVTVFG	GGIGSAV	PHAACVG	KQAQADG	ACVFRTG
	10	20	30	40	50	
	70	80	90	100	110	120
m571.pep	FVAAVADFF	FAVFVIDF	RTERAAFV	SAHRTQA	AAVEVFKE	GDFFGSA
g571	FVAAVADFF	FAVFVIHF	RAERAAFV	AAHRTQA	AAVEVFKE	GDFFGSA
	60	70	80	90	100	110
	130	140	150	160		
m571.pep	EGFAQGEE	PGLVVGG	VVLQFAA	RQGDFGV	HARQVA	AARRPX
g571	EGFA					
	119					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1711>:

```

a571.seq
1  ATGGGTATTG  CCGGCGCCGT  AAATGTTTGT  AACCTGCCG  CCGGTCCGG
51  AACTGCTGTT  GTCGTCGTAG  GTTTTGCCGT  CCCACACGT  GCCTGCGTCG
101  GCAAACAGGC  TCAGGCGGAC  GGTGCGCGCG  TCTTTCGCG  CGGGCATCGG
151  GAAGAGCAGC  TCGGCGGAGA  CGTTGGCTTT  TTTGTGCCG  CCGTAGCTGA
201  TTTTTCGCC  GTATTCGTCA  TACACTTTCG  GACCGAGCGT  GCCGCTTTCG
251  TATCCGCGCA  CCGAACCCAG  GCCGCCGCCG  TAGAAGTTT  CAAAGAAGGG
301  GATTTCTTTG  GTTCTGCCGT  AGCCGCCCGC  AATGCCGACT  TCGCCGCCGA
351  GCATCAGCGT  GAAGGTTTGT  CTTAAGGGGA  AGAACAGGT  TTGGTTGTGG
401  GTGGCGGAGT  AGTATTGCAG  TTTGCTGCCG  GGCAGGGCGA  TTTCGGCGTT
451  CACGCCCGTC  AGGTAGCCGC  GCGTCGGCCA  TAA

```

This corresponds to the amino acid sequence <SEQ ID 1712; ORF 571.a>:

```

a571.pep
1  MGIAGAVNV  LNPAAAGRG  TAVVVVGFA  VPHAA  CVGKQAQAD  GARVFRA  GHR
51  EEQLGGDV  GF  FVAAVADFF  A  VFVIHF  RTER  AAFVSAH  RTQ  AAAVEVF  KEG
101  DFFGSAVA  AR  NADFAAEH  QR  EGFA*GEE  PG  LVVGGGV  VLQ  FAAGQGDF  GV
151  HARQVAARR  P  *

```

m571/a571 98.1% identity in 160 aa overlap

	10	20	30	40	50	60
m571.pep	MGIAGAVNV	LNPAAGRG	TAVVVVG	FAVPHAA	CVGKQAQ	ADGARVF
a571	MGIAGAVNV	LNPAAGRG	TAVVVVG	FAVPHAA	CVGKQAQ	ADGARVF
	10	20	30	40	50	60
	70	80	90	100	110	120
m571.pep	FVAAVADFF	FAVFVIDF	RTERAAFV	SAHRTQA	AAVEVFKE	GDFFGSA
a571	FVAAVADFF	FAVFVIHF	RTERAAFV	SAHRTQA	AAVEVFKE	GDFFGSA
	70	80	90	100	110	120
	130	140	150	160		
m571.pep	EGFAQGEE	PGLVVGG	VVLQFAA	RQGDFGV	HARQVA	AARRPX
a571	EGFAQGEE	PGLVVGG	VVLQFAA	RQGDFGV	HARQVA	AARRPX
	130	140	150	160		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1713>:

g572.seq..


```

1  atgtgcgcca tcgtcggggc ggcggggctg ccttccgcgc tcgcagcggc
51  gcaaaaaggc aaaaccattt atctggcaaa caaagaaacg ctggtgggtt
101 cccgcgcggt gtttatggaa accgcccgcg caaacggcgc ggcagtgttg
151 cccgtcgaca gcgaacacaa cgccattttc caagttttgc cgcgcgatta
201 cacagaccgt ctgaacgaac acggcatcga ttcgattatc ctgaccgctt
251 cccggcgccc gtttttaaca accgatttaa gcacgttcga cagcattacg
301 cccgagcagg cgggtcaaac cccaattgg cgatgggggc gcaaaatctc
351 cgtcgattca gccactatgg caaacaaggg cttggaactg attgaagcgc
401 attggctgtt caactgtccg cccgacaaac tcgaagtcgt catccatccc
451 caatccgtga tacacagtat ggtgcgctac cgcgacggct ccgtgctggc
501 gcaactgggc aatcccgcata tgcgaacgcc catcgccctat tgtttgggct
551 tgcccgcgag catcgattcg ggtgtcggca aactcgattt cggcgcatcg
601 tccgcgctga ccttccaaaa gcccgacttc ggccgcttcc cctgcctgaa
651 gttcgccctat gaaaccataa acgcaggcgg agccgcgccc tgcgtattga
701 acgcccgcga cgaaccgcc gtcgcgcgct ttttggacgg acagattaag
751 tttaccgaca ttgcaaaaac cgtcgcccac tgtcttgac aagacttttc
801 aaacggcatg ggcgatatag aaggactgtt ggcgcaagat gcccggaac
851 gcgcacaagc gcgggcattt atcggcacac tgcgctga

```

This corresponds to the amino acid sequence <SEQ ID 1714; ORF 572.ng>:

g572.pep..

```

1  MCAIVGAAGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYTDR LNEHGIDSII LTASGGPFLT TDLSTFDSIT
101 PEQAVKHPNW RMGRKISVDS ATMANKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGKLDLFGAL
201 SALTFQKPDF GRFPCLKFAY ETINAGGAAP CVLNAANETA VAAFLDGQIK

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1715>:

m572.seq..

```

1  ATGTGCGCCA TCGTCGGGGC GGTGGGGCTG CCTTCCGCGC TCGCAGCGGC
51  GCAAAAAGGC AAAACCATTT ATCTGGCAAA CAAAGAAACG CTGGTGGTTT
101 CCGGCGCGTT GTTTATGGAA ACCGCCGTG CAAACGGCGC GGCAGTGCTG
151 CCCGTCGACA GCGAACACAA CGCCGTTTTT CAAGTTTTGC CGCGCGATTA
201 CGCCGCGCGT CTGAACGAAC ACGGCATCGC TTCGATTATC CTGACCGCTT
251 CCGCGCGCCC GTTCTTGACC GCCGATTTAA ACACGTTTCA CCGCATTACG
301 CCGGCCCAAG CCGTCAAAACA CCCCATTGG CGTATGGGAC GCAAAATCTC
351 CGTCGATTCC GCCACCATGA TGAACAAAGG TTTGGAGCTG ATTGAAGCGC
401 ATTGGCTGTT CAATGTGCCG CCCGACAAAC TCGAAGTCGT CATCCATCCG
451 CAATCCGTGA TACACAGCAT GGTGCGCTAC CGCGACGGCT CCGTGCTGGC
501 GCAACTGGGC AATCCCGATA TGCGAACGCC CATCGCTTAT TGTTTGGGTT
551 TGCCCGAGCG CATCGATTCT GGTGTCGGCG ACCTGGATTT CGACGCATTG
601 TCCGCGCTGA CCTTCCAAAA GCCCGACTTT GACCGCTTCC CCTGCCTGAG
651 GCTCGCCTAT GAAGCCATGA ACGCAGGCGG AGCCGCGCCC TCGGTATTGA
701 ACGCCGCCAA CGAAGCCGCC GTCGCGCCTT TTTTGGACGG ACAGATTAAG
751 TTTACCGACA TTGCCAAAAC CGTCGCCCAC TGTCTTGCAC AAGACTTTTC
801 AGACGCATA GCGCATATAG GGGGGCTCTT GGCGCAAGAT GCCCGGACAC
851 GCGCACAAAG CCGAGCATTT ATCGGCACAC TCGCTGTA

```

This corresponds to the amino acid sequence <SEQ ID 1716; ORF 572>:

m572.pep..

```

1  MCAIVGAVGL PSALAAQKG KTIYLANKET LVVSGALFME TARANGAAVL
51  PVDSEHNAIF QVLPRDYAGR LNEHGIASII LTASGGPFLT ADLNTFDRIT
101 PAQAVKHPNW RMGRKISVDS ATMMNKGLEL IEAHWLFNCP PDKLEVVIHP
151 QSVIHSVMRY RDGSVLAQLG NPD MRTPIAY CLGLPERIDS GVGDLDFDAL
201 SALTFQKPDF DRFPCLRLAY EAMNAGGAAP CVLNAANEAA VAAFLDGQIK
251 FTDIKTVAH CLAQDFSDGI GDIGLLAQD ARTRAQARAF IGTLR*

```

m572/g572 92.9% identity in 295 aa overlap

```

          10      20      30      40      50      60
m572.pep  MCAIVGAVGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAIF
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572      MCAIVGAAGLPSALAAQKGKTIYLANKETLVVSGALFMETARANGAAVLPVDSEHNAIF
          10      20      30      40      50      60

          70      80      90     100     110     120
m572.pep  QVLPRDYAGRLNEHGIASII LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
g572      QVLPRDYTDRLNEHGIDSII LTASGGPFLTDLSTFDSITPEQAVKHPNWRMGRKISVDS

```

880

	70	80	90	100	110	120
m572 . pep	130	140	150	160	170	180
	ATMMNKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
g572	ATMANKGLELIEAHWLFNCPPDKLEVVIHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
m572 . pep	190	200	210	220	230	240
	CLGLPERIDSGVGDLDFDALSALTFOKPDFRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
g572	CLGLPERIDSGVGKLDGALSALTFOKPDFRFPCLKFAYETINAGGAAPCVLNAANETA					
	190	200	210	220	230	240
m572 . pep	250	260	270	280	290	
	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
g572	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGMDIEGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1717>:

a572 . seq	1	ATGTGCGCCA	TCGTGCGGGC	GGTGGGGCTG	CCTTCCGCGC	TCGCAGCGGC
	51	GCAAAAAGGC	AAAACCATTT	ATCTGGCGAA	CAAAGAGACG	CTGGTGGTTT
	101	CCGGCGCGTT	GTTTATGGAA	ACCGCCCGTG	CAAACGGCGC	GGCAGTGCTG
	151	CCCGTCGACA	GCGAACACAA	CGCCGTTTTT	CAAGTTTTGC	CGCGCGATTA
	201	CACAGGTCGC	CTGAACGAAC	ACGGCATCGC	TTGATTATC	CTGACCGCTT
	251	CCGGCGGCCC	GTTTCTGACC	GCCGATTAA	ACACGTTTGA	CAGCATTACG
	301	CCCGACCAAG	CGGTCAAACA	CCCCAATTGG	CGTATGGGAC	GCAAAATCTC
	351	CGTCGATTCC	GCCACCATGA	TGAACAAAGG	TTTGGAGCTG	ATTGAAGCGC
	401	ATTGGCTGTT	CAACTGTCCG	CCCACAAAC	TCGAAGTCGT	CATCCATCCG
	451	CAATCTGTGA	TACACAGCAT	GGTGCCTAC	CGCGACGGCT	CCGTGTTGGC
	501	GCAACTGGGC	AATCCCGATA	TGCGAACGCC	TATCGCTTAT	TGTTTGGGTT
	551	TGCCCGAGCG	CATCGATTTC	GGTGTGCGCG	ACCTGGATT	CGACGCATTG
	601	TCCGCGCTGA	CCTTCCAAAA	GCCCGACTTT	GACCGCTTCC	CCTGCCTGAA
	651	GCTCGCTTAT	GAAGCCATGA	ACGCAGGCGG	AGCCGCGCCC	TGCGTATTGA
	701	ACGCCGCCAA	CGAAGCCGCC	GTCGCCGCTT	TTTGGACGG	ACAGATTAAG
	751	TTTACCGACA	TTGCCAAAAC	CGTCGCCCAT	TGCTTTTAC	AAGACTTTTC
	801	AGACGGCATA	GGCGACATAG	GGGGGCTCTT	GGCGCAAGAT	GCCCGGACAC
	851	GCGACAAGC	GCGGGCATTT	ATCGGCACAC	TGCGCTGA	

This corresponds to the amino acid sequence <SEQ ID 1718; ORF 572.a>:

a572 . pep	1	MCAIVGAVGL	PSALAAQKG	KTIYLANKET	LTVSGALFME	TARANGAAVL
	51	PVDSEHNAVF	QVLPRDYTR	LNEHGIASII	LTASGGPFLT	ADLNTFDSIT
	101	PDQAVKHPNW	RMGRKISVDS	ATMMNKGLEL	IEAHWLFNCP	PDKLEVVIHP
	151	QSVIHSMVRY	RDGSVLAQLG	NPDMRTPIAY	CLGLPERIDS	GVGDLDFDAL
	201	SALTFOKPDF	DRFPCLKLAY	EAMNAGGAAP	CVLNAANEAA	VAAFLDGQIK
	251	FTDIAKTVAH	CLSQDFSDGI	GDIGLLAQD	ARTRAQARAF	IGTLR*

m572/a572 98.3% identity in 295 aa overlap

	10	20	30	40	50	60
m572 . pep	MCAIVGAVGLPSALAAQKGKTIYLANKETLTVSGALFMETARANGAAVL					
a572	MCAIVGAVGLPSALAAQKGKTIYLANKETLTVSGALFMETARANGAAVL					
	10	20	30	40	50	60
m572 . pep	QVLPRDYAGRLNEHGIASII					
a572	QVLPRDYTGRLNEHGIASII					
	70	80	90	100	110	120
m572 . pep	LTASGGPFLTADLNTFDRITPAQAVKHPNWRMGRKISVDS					
a572	LTASGGPFLTADLNTFDSITPDQAVKHPNWRMGRKISVDS					
	70	80	90	100	110	120

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	130	140	150	160	170	180
m572.pep	ATMMNKGLELIEAHWLFNCPDKEVVVHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
a572	ATMMNKGLELIEAHWLFNCPDKEVVVHPQSVIHSMVRYRDGSVLAQLGNPDMRTPIAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m572.pep	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
a572	CLGLPERIDSGVGDLDFDALSALTFQKPDFDRFPCLRLAYEAMNAGGAAPCVLNAANEAA					
	190	200	210	220	230	240
	250	260	270	280	290	
m572.pep	VAAFLDGQIKFTDIAKTVAHCLAQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
a572	VAAFLDGQIKFTDIAKTVAHCLSQDFSDGIGDIGLLAQDARTRAQARAFIGTLRX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1719>:

g573.seq..

```

1  atgcctgtt  tgtgccgct  taatcgcaat  atcggcagtt  tccaaatcac
51  gaatctcacc  gaccataatg  atgtccgggt  cctgacgcag  gaaagacttc
101 aaagcagcgg  caaaagtcag  accctgctta  tcattgacgt  taacctgatt
151 gatgcccgcc  aggttaatat  cggcagggtc  ttccgccggt  gcaatattta
201 ccgactccgt  attcaaaata  ttcaaacagg  tatagagcga  caccgtctta
251 ccgaaacccg  tcggaccggt  taccagcacc  atcccgtaat  gacggatgaat
301 cgcttccaac  aacaattttt  tctggaacgg  ctcaaaaccc  agctggtcga
351 tgttcaaaag  cgccgcatcg  gaattcaaaa  tccgcatcac  gaccttttcg
401 ccaaacagcg  tcggcaatgt  gctgacacgg  aaatcgacag  gcttgccgcc
451 cttttgaaag  gtcagctgca  tctaccgtc  ctgcggtatc  cgtttttcgg
501 aatgtccaa  acgcgacatt  accttaatcc  gggaagcaag  ctgccccctt
551 accgcaatgg  cgccgtgaac  cacctcgccg  agctgcccgt  ccacacggaa
601 acggatacgc  gcatttgtgt  cgtaaaactc  gaaatggatg  tcggatgccc
651 cgctacgcaa  ggcacccgac  aaagtattat  ggataaacct  cggaacaggg
701 ccgtctctcg  cctcctcgtc  gtcgatatac  aggggtgtgg  tttcctcttc
751 ctcttgcccc  tccccaaagt  cctgaagcag  cgatgtcgaa  cgcaacccca
801 ccccaatcag  caaacccgcc  aactggtcat  cctcgacaat  gaccaactca
851 accgcaatcc  ctgcccgcga  aaccgttttc  tgaatttgcg  gcatctgggt
901 cggatcggaa  accgcaaaaa  atactttgtc  gccccacgg  aaaaccggca
951 cacagtggaa  ctccaccatc  tgctcctcgg  tcaacacccc  catcagcacc
1001 ctgtggcgcg  gataatgacg  caaatcaaga  atcgataaac  tgaacaccct
1051 cgcaatcaat  gccgcaagcg  acttggcgga  aatgacacgg  tctga

```

This corresponds to the amino acid sequence <SEQ ID 1720; ORF 573.ng>:

g573.pep..

```

1  MPCLCRINRN  IGSFQITNLT  DHNDVRVLTQ  ERLQSSGKSO  TLLIIDVNLI
51  DARQVNLGRV  FRCNIYRLR  IQNIQTGIER  HRLTRTRRTG  YQHPVVRTVN
101 RFQQQFFLER  LKTELVDVQR  RGIGIQNPBH  DLFAKQRRQC  ADTEIDRLAA
151 LLKQQLHPTV  LRPFFGNVQ  TRHYLNPGSK  LPPYRNGRLN  HLAELPVHTE
201 TDTRIVFVKL  EMDVGCPATQ  GIRQSFMDKP  RNRAVFCLLV  VDIQGVAFLE
251 LLPLPKLLKQ  RCRTTRTHPI  QTRQLVILDN  DQLNRNPCGR  NRFLNLRHLG
301 RIGNRKKYFV  APTENRHTVE  LHHLLLRQHP  HQHPVARIMT  QIKNRITEHP
351 RNQCRKRLGR  NDTV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1721>:

m573.seq..

```

1  ATGCCCTGTT  TGTGCCGCTT  TAATCGCAAT  ATCGGCAGTT  TCCAAATCAC
51  GAATCTCACC  GACCATAATG  ATGTCCGGGT  CCTGACGCAG  GAAAGACTTC
101 AAAGCAGCGG  CAAAAGTCAG  GCCCTGCTTA  TCATTGACGT  TAACCTGATT
151 GATGCCCGGC  AGGTTAATCT  CGGCAGGCTC  TTCCGCCGTT  GCAATATTTA
201 CCGACTCCGT  ATTCAAAATA  TTCAAACAGG  TATAGAGCGA  CACCGTCTTA
251 CCCGAACCCG  TCGGACCGGT  TACCAGCACC  ATCCCGTAGG  GACGGTGAAT
301 CGTTACCAAC  aCaw.TTTT  TCTGAAACGG  CTCAAAACCG  AGCTGGTCTG
351 TGTTCAAAGA  CGCGGCATCG  GAATTCAAAA  TCCGCATCAC  GACCTTTTCG
401 CCAAACAGCG  TCGGCAATGT  GCTGACACGG  AAATCGACAG  GCTTGCCGCC
451 CTTTGTAAAG  GTCAGCTGCA  TCCTGCCGTC  CTGCGGTATC  CGTTTTTCGG
501 AAATGTCCAA  ACGCGACATT  ACCTTAATCC  GTGAAGCAAG  CTGCCCCCTT

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```

551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTCGAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTC TGAATTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCG TCAACACCCC CATCAGCACC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1722; ORF 573>:

m573.pep..

```

1 MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ ALLIIDVNLI
51 DARQVNLGRV FRRNCIYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RYQHXXFLLK RKTDLVDVQR RGIGIQNPBH DLFQKRRQC ADTEIDRLAA
151 LLKQLHPAV LRYPPFGNVQ TRHYLNP*SK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/g573 95.9% identity in 364 aa overlap

m573.pep	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
g573	10	20	30	40	50	60
	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQTLIIIDVNLI DARQVNLGRV					
m573.pep	70	80	90	100	110	120
	FRRNCIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTVNRYQHXXFLLKRLKTELVDVQR					
g573	70	80	90	100	110	120
	FRRNCIYRLRIQNIQTGIERHRLTRTRRTGYQHHPVRTVNRFQQQFFLERLKTELVDVQR					
m573.pep	130	140	150	160	170	180
	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPXSK					
g573	130	140	150	160	170	180
	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPTVLRYPPFGNVQTRHYLNPGSK					
m573.pep	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
g573	190	200	210	220	230	240
	LPPYRNGRLNHLAELPVHTETDTRIVFVKLEMDVGCPTAQGIRQSFMDKPRNRAVFCLLV					
m573.pep	250	260	270	280	290	300
	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
g573	250	260	270	280	290	300
	VDIQGVAFLLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNRNPGCRNRFNLRHLG					
m573.pep	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
g573	310	320	330	340	350	360
	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
m573.pep	NDTVX					
g573	NDTVX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1723>:

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a573.seq

```

1  ATGCCCTGTT TGTGCCGCCT TAATCGCAAT ATCGGCAGTT TCCAAATCAC
51  GAATCTCACC GACCATAATG ATGTCCGGGT CCTGACGCAG GAAAGACTTC
101 AAAGCAGCGG CAAAAGTCAG ACCCTGCTTA TCATTGACGT TAACCTGATT
151 GATGCCCGGC AGGTTAATCT CGGCAGGGTC TTCCGCCGTT GCAATATTTA
201 CCGACTCCGT ATTCAAAATA TTCAAACAGG TATAGAGCGA CACCGTCTTA
251 CCCGAACCCG TCGGACCGGT TACCAGCACC ATCCCGTAGG GACGGTGAAT
301 CGCTTCCAAC AACAATTTTT TCTGAAACGG CTCAAACCG AGCTGGTCTGA
351 TGTTCAAAGA CGCGGCATCG GAATTCAAAA TCCGCATCAC GACCTTTTCG
401 CCAAACAGCG TCGGCAATGT GCTGACACGG AAATCGACAG GCTTGCCGCC
451 CTTTTGAAAG GTCAGCTGCA TCCTGCCGTC CTGCGGTATC CGTTTTTCGG
501 AAATGTCCAA ACGCGACATT ACCTTAATCC GGAAGCAAG CTGCCCCCTT
551 ACCGCAATGG GCGGCTGAAC CACCTCGCGG AGCTGCCCCG CCACACGGAA
601 ACGGATACGG GCATTGTGTT CGTAAACTC GAAATGGATG TCCGATGCCC
651 CGCTGCGCAA GGCATCCGAC AAAGTCTTAT GGATAAACCT CGGAACAGGG
701 CCGTCTTCTG CCTCCTCGTT GTCGATATAC AGGGTGTGGC TTTCCTCTTC
751 CTCCTGCCCC TCCCCAAGCT CCTGAAGCAG CGATGTGCAA CGCGAACCCA
801 CCCAATCGAG CAAACCCGCC AACTGGTCAT CCTCGACAAT GACCAACTCA
851 ACCTCAATCC CTGCGGCAGA AACGGTTTTT TGAATTTGCG GCATCTGTGT
901 CGGATCGGAA ACCGCAAAAA ATACTTTGTC GCCCGACGG AAAACCGGCA
951 CACAGTGGAA CTCCACCATC TGCTCCTCCG TCAACACCCC CATCAGACCC
1001 CTGTGGCGCG GATAATGACG CAAATCAAGA ATCGAATAAC TGAACACCCCT
1051 CGCAATCAAT GCCGCAAGCG ACTTGGGCGA AATGACACCG TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1724; ORF 573.a>:

a573.pep

```

1  MPCLCRLNRN IGSFQITNLT DHNDVRVLTQ ERLQSSGKSQ TLLIIDVNLI
51  DARQVNLGRV FRRCNLYRLR IQNIQTGIER HRLTRTRRTG YQHHPVGTVN
101 RFQQQFFLKR LKTELVDVQR RGIGIQNPBH DLFQKRRQRC ADTEIDRLAA
151 LLKGQLHPAV LRYPPFGNVQ TRHYLNPGSK LPPYRNGRLN HLAELPVHTE
201 TDTGIVFVKL EMDVRCPAAG GIRQSLMDKP RNRAVFCLLV VDIQGVAFLE
251 LLPLPKLLKQ RCRTRTHPIE QTRQLVILDN DQLNLNPGCR NGFLNLRHLC
301 RIGNRKKYFV APTENRHTVE LHHLLLRQHP HQHPVARIMT QIKNRITEHP
351 RNQCRKRLGR NDTV*

```

m573/a573 98.6% identity in 364 aa overlap

	10	20	30	40	50	60
m573.pep	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQALLIIDVNLI DARQVNLGRV					
a573	MPCLCRLNRNIGSFQITNLT DHNDVRVLTQERLQSSGKSQ TLLIIDVNLI DARQVNLGRV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m573.pep	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRYQHFFLKR LKTELVDVQR					
a573	FRRCNLYRLRIQNIQTGIERHRLTRTRRTGYQHHPVGTNVNRFQQQFFLKR LKTELVDVQR					
	70	80	90	100	110	120
	130	140	150	160	170	180
m573.pep	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
a573	RGIGIQNPBHDLFAKQRRQCADTEIDRLAALLKGQLHPAVLRYPPFGNVQTRHYLNPGSK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m573.pep	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
a573	LPPYRNGRLNHLAELPVHTE TDTGIVFVKLEMDVRCPAAGGIRQSLMDKPRNRAVFCLLV					
	190	200	210	220	230	240
	250	260	270	280	290	300
m573.pep	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
a573	VDIQGVAFLELLPLPKLLKQRCRTRTHPIEQTRQLVILDNDQLNLNPGCRNGFLNLRHLC					
	250	260	270	280	290	300

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	310	320	330	340	350	360
m573.pep	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
a573	RIGNRKKYFVAPTENRHTVELHLLLRQHPHQHPVARIMTQIKNRITEHPRNQCRKRLGR					
	310	320	330	340	350	360
m573.pep	NDTVX					
a573	NDTVX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1725>:

g574.seq

```

1   atgctgccga atctgccaaa cagccttaag aaagccgata tggacaacga
51  attgtggatt atcctgctgc cgattatcct ttgtcccgtc ttcttcacga
101 tgggctgggt tgccgcccgc gtggatatga aaaccgtatt gaagcaggca
151 aaaagcatcc ctccgggatt ttataaaagc ctggacgctt tggctgaccg
201 caacagcggg cgcgcggaac gggagttggc ggaagtcgtc gacggccggc
251 cgcaatcgta tgatttgaac cttaccctcg gcaaaactta ccgtcagcgc
301 ggcgaaaacg acaaagccat caacatacac cggacaatgc tcgattctcc
351 cgatacggtc ggcgaaaagc gcgcgcgcgt cctgtttgaa ttggcgcaaa
401 actaccaaag cgcggtgttg gtcgatcgtg ccgaacagat tttttggggg
451 ctgcaagacg gtgaaatggc gcgtagaagg agacagcacc tgctcaatat
501 ctaccagcag gacagggatt gggaaaaagc ggttgaaacc gcccaacttc
551 ttagtcacga cgaacagaca tatcagtttg agattgcaca gttttattgc
601 gaacttgccc aagccgcgct gttcaagtcc aatttcgatg ccgcgcgttt
651 caatgtcggc aaggcactcg aagccaacaa aaaatgcacc cgcgccaaca
701 tgattttggg cgacattgaa caccgacaag gcaatttccc tgccgccgctc
751 gaagcctatg ccgccatcga gcagcaaac catgcatact tgagcatggt
801 cggcgagaag ctttacgaag cctatgccgc gcagggaaaa cctgaagaag
851 gcttgaaccg tctgacagga tatatgcaga cgtttcccga acttgacctg
901 atcaatgtcg tgtacgagaa atccctgctg cttaaggcg agaaagaagc
951 cgcgcaaac gcgctcgagc ttgtccgcgc caagcccgac ctaacggcg
1001 tgtaccgcct gctcggtttg aaactcagcg atttggatcc ggcttggaag
1051 gccgatgcgg acatgatgcg ttcggttatc ggacggcagc tccagcgag
1101 cgtgatgtac cgttgcccga actgccactt caaatcccaa gtctttttct
1151 ggcactgtcc cgctgcaac aaatggcaga cgtttacgcc gaataaaatc
1201 gaagtttaa

```

This corresponds to the amino acid sequence <SEQ ID 1726; ORF 574.ng>:

g574.pep..

```

1   MLPNLPNSLK KADMDNELWI ILLPIILLPV FFTMGWFAAR VDMKTVLKQA
51  KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTIGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGEAREEA RQHLLNIYQQ DRDWEKAVET AQLLSHDEPT YQFEIAQFYC
201 ELAQAAFLFKS NFDAARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQK PEEGLNRLTG YMQTFPELDL
301 INVVYEKSLI LKGEKEAAQT AVELVRRKPD LNGVYRLGL KLSLDLPAWK
351 ADADMMRSVI GRQLQRSVMY RCRNCHFSQ VFFWHCPACN KWQTFTPNKI
401 EV*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1727>:

m574.seq..

```

1   ATGCGCCCGA ATCTACCAA CAGCCTTAAG AAAGCCGATA TGGACAACGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTC TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AAACCGTATT GAAGCAGGCA
151 AAAAGCATCC CTTCGGGATT TTATAAAAGC TTGGACGCTT TGGTCGACCG
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GCGGAAAACG ACAAAGCCAT CAACATACAC CCGACAATGC TCATTCTCC
351 CGATACGGTC GCGGAAAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 CATACCAAAG TGCGGGGTTG GTCGATCGTG CCGAACAGAT TTTTGTGGG
451 CTGCAAGACG GTAAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAGC GGTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG TCGCGCGTTT

```

885

```
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGCATGGT
801 CGGCGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACGAGAA ATCCCTGCTG CTTAAGTGC GAGAAAGAAGC
951 CGCGCAAACC GCCGTCGAGC TTGTCCGCCG CAAGCCCCGAC CTTAACGGCG
1001 TGTACCGCCT GCTCGGTTTG AACTCAGCG ATATGAATCC GGCTTGGAAG
1051 GCCGATGCCG ACATGATGCG TTCGGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGTTGCCGCA ACTGCCACTT CAAATCCCAA GTCTTTTCTT
1151 GGCCTGCCC CGCCTGCAAC AAATGGCAGA CGTTTACCCC GAATAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1728; ORF 574>:

m574.pep..

```
1 MRPNLPNSLK KADMDNELWI ILLPIILLPV FFAMGWFAAR VDMKTVLKQA
51 KSIPSGFYKS LDALVDRNSG RAARELAEVV DGRPQSYDLN LTLGKLYRQR
101 GENDKAINIH RTMLDSPDTV GEKRARVLFE LAQNYQSAGL VDRAEQIFLG
151 LQDGKMAREA RQHLLNIYQQ DRDWEKAVET ARLLSHDDQT YQFEIAQFYC
201 ELAQALFKS NFDVARFNVG KALEANKKCT RANMILGDIE HRQGNFPAAV
251 EAYAAIEQQN HAYLSMVGEK LYEAYAAQ GK PEEGLNRLTG YMQTFPELDL
301 INVVEKSL LKCEKEAAQT AVELVRRKPD LNGVYRLGL KLSDMNPAWK
351 ADADMRSVI GRQLQRSVMY RCRNCHFKSQ VFWHCPACN KWQTFTPNKI
401 EV*
```

m573/g573 97.8% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFAMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
g574	MLPNLPNSLK	KADMDNELWI	ILLPIILLPV	FFTMGWFAAR	VDMKTVLKQA	KSIPSGFYKS
	10	20	30	40	50	60
	70	80	90	100	110	120
m574.pep	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
g574	LDALVDRNSG	RAARELAEVV	DGRPQSYDLN	LTLGKLYRQR	GENDKAINIH	RTMLDSPDTV
	70	80	90	100	110	120
	130	140	150	160	170	180
m574.pep	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGKMAREA	RQHLLNIYQQ	DRDWEKAVET
g574	GEKRARVLFE	LAQNYQSAGL	VDRAEQIFLG	LQDGEMAREA	RQHLLNIYQQ	DRDWEKAVET
	130	140	150	160	170	180
	190	200	210	220	230	240
m574.pep	ARLLSHDDQT	YQFEIAQFYC	ELAQALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
g574	AQLLSDHDEQ	TYQFEIAQFYC	ELAQALFKS	NFDVARFNVG	KALEANKKCT	RANMILGDIE
	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
g574	HRQGNFPAAV	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQ GK	PEEGLNRLTG	YMQTFPELDL
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVEKSL LK	CEKEAAQT AVEL	VRRKPD LNGVYRL	GLKLSDMNPAWK	ADADMRSVI	
g574	INVVEKSL LK	GEKEAAQT AVEL	VRRKPD LNGVYRL	GLKLSLDP	PAWKADADMRSVI	
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMY	RCRNCHFKSQ	VFWHCPACN	KWQTFTPNKI	EVX	
g574	GRQLQRSVMY	RCRNCHFKSQ	VFWHCPACN	KWQTFTPNKI	EVX	
	370	380	390	400		

```
a574.seq
1  ATGCGCCCGA ATCTGCCAAA CAGCCTTGAG AAAGCCGATA TGGACAATGA
51  ATTGTGGATT ATCCTGCTGC CGATTATCCT TTTGCCCGTT TTCTTCGCGA
101 TGGGCTGGTT TGCCGCCCGC GTGGATATGA AGACTGTATT AAAGCAGGCA
151 AAAAGCATAC TCCTCGGGATT TTATAAAAGT CTGGATGCCT TGGTGACCGC
201 CAACAGCGGG CGCGCGGCAA GGGAGTTGGC GGAAGTCGTC GACGGCCGGC
251 CGCAATCGTA TGATTTGAAC CTCACCCTCG GCAAACTTTA CCGCCAGCGT
301 GGCGAAAACG ACAAAGCCAT CAATATGCAC CAAACATTGC TTGACTCTCC
351 CGATACAACC GGAGCCAAGC GCGCGCGCGT CCTGTTTGAA TTGGCGCAAA
401 ACTACCAAAG TCGCGGGTTG GTCGATCGTG CGCAACAGAT TTTTTCGGGG
451 CTGCAAGACG GTGAAATGGC GCGTGAAGCC AGACAGCACC TGCTCAATAT
501 CTACCAACAG GACAGGGATT GGGAAAAAGC GGTTGAAACC GCCCGGCTGC
551 TCAGCCATGA CGATCAGACC TATCAGTTTG AAATCGCCCA GTTTTATTGC
601 GAACTTGCCC AAGCCGCGCT GTTCAAGTCC AATTTCGATG CCGCGCGCTT
651 CAATGTCGGC AAGGCACTCG AAGCCAACAA AAAATGCACC CGCGCCAACA
701 TGATTTTGGG CGACATCGAA CACCGACAAG GCAATTTCCC TGCCGCCGTC
751 GAAGCCTATG CCGCCATCGA GCAGCAAAAC CATGCATACT TGAGTATGGT
801 CGCGGAGAAG CTTTACGAAG CCTATGCCGC GCAGGGAAAA CCTGAAGAAG
851 GCTTGAACCG TCTGACAGGA TATATGCAGA CGTTTCCCGA ACTTGACCTG
901 ATCAATGTCG TGTACAGAA ATCCCTCGTG CTTAAGTCGC AGAAAGAAGC
951 CGCGCAAAAC CCGCTCGAGC TTGTCGCGCG CAAGCCCGAC CTC AACGCGC
1001 TGTACCGCCT GCTTGGTTTG AAACCTAGCG ATTTGGATCC GGCTTGAAA
1051 GCCGATGCCG ATATGATGCG TTCGTTATC GGACGGCAGC TACAGCGCAG
1101 CGTGATGTAC CGGTGCCGAA ACTGCCACTT CAAATCACAA GTCTTTTTCT
1151 GGCATTGTCC TGCCTGCAAC AAATGGCAGA CGTTTACGCC AAACAAAATC
1201 GAAGTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1730; ORF 574.a>:

a574.pep

1	<u>MRPNLPNSLE</u>	<u>KADMDNELWI</u>	<u>ILLPIILLPV</u>	<u>FFAMGWFAAR</u>	<u>VDMKTVLKQA</u>
51	KSIPSGFYKS	LDALVDNRNSG	RAARELAEV	DGRPQSYDLN	LTLGKLYRQR
101	GENDKAINMH	QTLLEDSPDT	GAKRARVLFE	LAQNYQSAGL	VDRAEQIFLG
151	LQDGMAREAH	RQHLLNLYQQ	GRDWEKAVET	ARLLSHDDQT	YQFEIAQFYC
201	ELAQAALFKS	NFDAARFNVG	KALEANKKCT	RANMILGDIE	YRQGNFPAAV
251	EAYAAIEQQN	HAYLSMVGEK	LYEAYAAQGK	PEEGLNRLTG	YMQTFPELDL
301	INVVEKSL	LKCEKEAAQT	AVELVRRKPD	LNGVYRLLGL	KLSDLDPAWK
351	ADADMMSVI	GRQLQRSVMY	RCRNCHFKSQ	VFFWHCPACN	KWQTFTPNKI
401	EV*				

m574/a574 97.5% identity in 402 aa overlap

	10	20	30	40	50	60
m574.pep	MRPNLPNSLKKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
a574	MRPNLPNSLEKADMDNELWIILLPIILLPVFFAMGWFAARVDMKTVLKQAKSIPSGFYKS					
	10	20	30	40	50	60
m574.pep	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINIHRTMLDSPDTV					
a574	LDALVDRNSGRAARELAEVVDGRPQSYDLNLTGKLYRQRGENDKAINMHQTLLDSPDTT					
	70	80	90	100	110	120
m574.pep	GEKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGKMAREARQHLLNIYQQDRDWEKAVET					
a574	GAKRARVLFELAQNYQSAGLVDRAEQIFLGLQDGEMAREARQHLLNIYQQDRDWEKAVET					
	130	140	150	160	170	180
m574.pep	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDFVARFNVGKALEANKKCTRANMILGDIE					
a574	ARLLSHDDQTYQFEIAQFYCELAQAALFKSNFDAARFNVGKALEANKKCTRANMILGDI					
	190	200	210	220	230	240

887

	190	200	210	220	230	240
	250	260	270	280	290	300
m574.pep	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
a574	HRQGNFPAAVEAYAAIEQQNHAYLSMVGEKLYEAYAAQ GKPEEGLNRLTG YMQTFPELDL					
	250	260	270	280	290	300
	310	320	330	340	350	360
m574.pep	INVVYEKSLLLKCEKEAAQTAVELVRRKPD LNVYRLLGLKLSDMNPAWKADADMMRSVI					
a574	INVVYEKSLLLKCEKEAAQTAVELVRRKPD LNVYRLLGLKLSDLPAWKADADMMRSVI					
	310	320	330	340	350	360
	370	380	390	400		
m574.pep	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTF TPNKIEVX					
a574	GRQLQRSVMYRCRNCHFKSQVFFWHCPACNKWQTF TPNKIEVX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1731>:

g575.seq (partial)

```

1  ..atgccgtgcc tccgccggca agcagcaagg tgtacgaacc gccgaacaga
51  ccgtaaaaca gtccgctttc ggtttcttct tccgcagaaa cctgttcgac
101 aggttcggca acgggttcgg cggcaacttc actggctgtt tccgcaacag
151 gttcggaaac ggtgttaccg gtttcgctcg tccgcgtgtc gatggcagaa
201 gcggcggctt cttggggggg cggattcggc agcggtttcc gatgcggcag
251 tatttgcagc ggggtacagg cgggttggtc gttctgtcgc cgaagccgga
301 gtttcggaca ctgcgggttt ggggttcggg cgaacggccg gtttttccgc
351 ttttgcctcg ggcgcggcaa cttttgcttc aggtttttca accggttttt
401 cgacagggtt ctctatcggg ttctccacag ttgcctgttt ggacgggtta
451 gacggcatgg atgcagtttc ggttttgggt ttccgcgttt gcggtttggg
501 ttgttcgcgt ttgatttttt tgggtgtcgc cgctttgate ctgttcagat
551 tcggaatgtg a*
```

This corresponds to the amino acid sequence <SEQ ID 1732; ORF 575.ng>:

g575.pep (partial)

```

1  ..MPCLRRQAAR CTNRRTRDQT VRFRLLRQK PVRQVRQVR RQLHWLFPQQ
51  VRKRCYRFRR SACRWQKRRL LGGADSAVS DAAVFAAGT PGWRSVAEAG
101 VSDTAGLGSG RTAGFSAFAS GAATFASGFS TGFSTGFSIG FSTVACLDGS
151 DGMDAVSALG FAVCGLGCSA LIFLGAAALI LFRFGM*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1733>:

m575.seq..

```

1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTTGTC GGAGAAATCG GTATCGACGG TTTCCGGTTT GTTTTCGGCA
151 GTTTGGGGCA CAGATTCCGG TTCGGGCGTG TCGATGACGA TTTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTGA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAATGCC GTTTTGCGCG GCTGCCAGGC TGTCGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGATAA CTCTTCTTCA GATTCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGGAGTTT CCACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGGG TTGGGCAAGG
601 CGCAAAGACA GCAGCAGGGC GATTAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGACCGTC AAACAGTCCG CTTTCGGTTT
701 CTTCTTCGGC AGAAACCTGT TCGACAGGTT CGGAAACGGC GTTACCGGTT
751 TCGTCGGTCG GCGTGTGAT GGCAGAAGCG GCGGCTTCTT GGGGGCGCGA
801 TTCGGCAGCG GTTTCCGATG CGGCAGTATT TGCAGCGGGT ACAGGTTCCG
851 GTCGAAACGG CGGTTTTTCC GCTTTTGCTT CGGGCGCGGC AACTTTGCT
901 TCAGGTTTTT CAACCGGTTT CTCTACCGTT GCCTGTTTGG ACGGTTCCGA
951 CGGCATGGAT GCGGTTTCGG CTTTGGGTTT CGCCGTTTGC GGTTCGGTT
1001 GTTCCGCTTT GATCCTGTTC AGATTCCGAA TGTGA
```

888

This corresponds to the amino acid sequence <SEQ ID 1734; ORF 575>:

m575.pep

```

1  MVSGEAEFRK PASPEGEAGF AEAUSSVPIW LFEGRLSEKS VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSL DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNRPSNSP LSVSSSAETC STGSETALPV
251 SSVGVSMAEA AASWGADSAA VSDAAVFAAG TGSGRTAGFS AFASGAATFA
301 SGFSTGFSTV ACLDGSQDMD AVSALGFAVC GLGCSALILF RFGM*

```

m575/g575 70.2% identity in 114 aa overlap

```

                240      250      260      270      280
m575.pep      SSAETCSTGSETALPVSSVGVSMAEAAASWGADSAVSDAAVFAAGTG-----
                |||||
g575           LHWLFPPQVRKRCYRFRRSACRWQKRLLGGADSAVSDAAVFAAGTGPWRSVAEAGVS
                50      60      70      80      90      100

                290      300      309      310      320
m575.pep      -----SGRTAGFSAFASGAATFASGFSTGFST-----VACLDGSQDMDAVSALGFA
                |||||
g575           DTAGLGSRTAGFSAFASGAATFASGFSTGFSTGFSIGFSTVACLDGSQDMDAVSALGFA
                110     120     130     140     150     160

                330      340
m575.pep      VCGLGCSALI-----LFRFGMX
                |||||
g575           VCGLGCSALIFLGAAALILFRFGMX
                170     180

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1735>:

a575.seq

```

1  ATGGTTTCGG GCGAGGAAGC CTTCAGGAAG CCTGCCAGTC CGGAGGGTGA
51  GGCAGGTTTT GCGGAAGCTG TTTCTTCTGT GCCGATATGG TTGTTTGAGG
101 GCAGGTGTGC GGAGAAATCG GTATCGACGG TTTCGGGTTT GTTTTCGCGA
151 GTTTGGGCGA CAGATTCGGG TTCGGGCGTG TCGATGACGA TTTCGACAGG
201 GTTGTACGGG TTGAAGGTCT CGGGCTCGTA CACGCTGTCT GTGGATTCTA
251 TGGCGTTCCA ATCGGCATCC GCGCGTTTTT GGGTTTCTTC ATCCTGCGTA
301 AGTGCGCCGG ATAAAATGCC GTTTTGCGCG GCTGCCAGGC TGTGAAATC
351 CAAGTCGATG CGGTTGGAAG GCGTATCGGT TTCGACATCG AACGTTTGTT
401 TTGCCGACAA CTCTTCTTCA GATCCCCAT CTAAGGCAAG TGTGTCGTTT
451 ACATCGTTTT TCGGAGCGGG TTCGGGCGTT GCCGAGTTT CGACTTCGGC
501 AAAGGTGATT TCTATGCCGT CGTCTGCCGC GTCGTCAGG TCAGGCTCTT
551 CCTCAGGGAC GGATTCTTCG GTACGGCGCG CGCGTTTGA TTGGGCAAGG
601 CGCAAAAGCA GCAGCAGGGC GATCAATGCC GCGCTCCGC CGGCAAGCAG
651 CAAGGTGTAC GAACCGCCGA ACAGTCCGCT TTCGGTTTCT TCTTCGGCAG
701 AAACCTGTTT GACAGGTTTC GAAACGGCGT TACCGGTTT TCCTGTCGGC
751 GTGTCGATGG CAGAAGCGGC GGCTTCTTGG GGGGCGGATT CGGCAGCGGT
801 TTCCGATGCG GCAGTATTTG CAGCGGTAC AGGTCGGGT CGAACGGCCG
851 GTTTTTCGCG TTTTGCTTCG GCGCGGCAA CTTTGCTTC AGGTTTTTCA
901 ACCGTTTCT CTACCGTTGC CTGTTTGGAC GGTCGGACG GCATGGATGC
951 GGTTCGGCT TTGGGTTTCG CCGTTTGGG TTTGGGTTGT TCCGCTTGA
1001 TCCTGTTTCA ATTCCGAATG TGA

```

This corresponds to the amino acid sequence <SEQ ID 1736; ORF 575.a>:

a575.pep

```

1  MVSGEAEFRK PASPEGEAGF AEAUSSVPIW LFEGRLSEKS VSTVSGLFSA
51  VWATDSGSGV SMTISTGLYG LKVSQSYTSL VDSMAFQSAS ARFWVSSSCV
101 SAPDKMPFCA AARLSKSKSM RLEGVSVSTS NVCFADNSSL DSPSKASVSF
151 TSFFGAGSGV AGVSTSAKVI SMPSSAASSR SGSSSGTDSS VRRARLDWAR
201 RKSSSRAINA APPPASSKVY EPPNSPLSVS SSAETCSTGS ETALPVSSVG
251 VSMAEAAASW GADSAAVSDA AVFAAGTGS RTAGFSAFAS GAATFASGFS
301 TGFSTVACLD GSDGMDAVSA LGFAVCGLGC SALILFRFGM *

```

889

m575/a575 98.8% identity in 344 aa overlap

	10	20	30	40	50	60
m575.pep	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVSTV	SGLFSAVWATD	SGSGV
a575	MVSGEEAFRK	PASPEGEAGFAE	AVSSVPIWLF	EGRLSEKSVSTV	SGLFSAVWATD	SGSGV
	70	80	90	100	110	120
m575.pep	SMTISTGLYGL	KVSGSYTSLV	SDSMAFQSA	SARFWVSSSCV	SAPDKMPFCA	AAARLSKSKSM
a575	SMTISTGLYGL	KVSGSYTSLV	SDSMAFQSA	SARFWVSSSCV	SAPDKMPFCA	AAARLSKSKSM
	130	140	150	160	170	180
m575.pep	RLEGVSVSTSN	VCFADNSSSD	SPSKASVSFT	SFFGAGSGV	AGVSTSAKVI	SIMPSSAASSR
a575	RLEGVSVSTSN	VCFADNSSSD	SPSKASVSFT	SFFGAGSGV	AGVSTSAKVI	SIMPSSAASSR
	190	200	210	220	230	240
m575.pep	SGSSSGTDSSV	RRARLDWARR	KSSSRAINA	APPPASSKV	YEPNRPNS	SPLSVSSSAETC
a575	SGSSSGTDSSV	RRARLDWARR	KSSSRAINA	APPPASSKV	YEPN-----	SPLSVSSSAETC
	250	260	270	280	290	300
m575.pep	STGSETALPV	SSVGVSM	AEAAASWG	ADSAAVSDA	AVFAAGTGS	GRTAGFSAFASGAATFA
a575	STGSETALPV	SSVGVSM	AEAAASWG	ADSAAVSDA	AVFAAGTGS	GRTAGFSAFASGAATFA
	310	320	330	340		
m575.pep	SGFSTGFSTV	ACLDGSDG	MDAVSALG	FAVCGLGCS	ALILFRFGMX	
a575	SGFSTGFSTV	ACLDGSDG	MDAVSALG	FAVCGLGCS	ALILFRFGMX	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1737>:

g576.seq.. (partial)

```

1  ..atgggcgtgg acatcggacg ctccctgaaa caaatgaagg aacagggcgc
51  ggaaatcgat ttgaaagtct ttaccgatgc catgcaggca gtgtatgacg
101 gcaaagaaat caaaatgacc gaagagcagg cccaggaagt gatgatgaaa
151 ttcctgcagg agcagcaggg taaagccgta gaaaaacaca aggcggatgc
201 gaaggccaac aaagaaaaag gcgaagcctt cctgaaggaa aatgccgccg
251 aagacggcgt gaagaccact gcttccggtc tgcagtacaa aatcaccaaa
301 caggggtgaag gcaaacagcc gacaaaagac gacatcgtaa ccgtggaata
351 cgaaggccgc ctgattgacg gtaccgtatt cgacagcagc aaagccaacg
401 gcggcccggc caccttcctt ttgagccaag tgattccggg ttggaccgaa
451 ggcgtacggc ttctgaaaga aggcggcgaa gccacgttct acatcccgtc
501 caaccttgcc taccgcgaac aggtgcgagg cgaaaaaatc ggtccgaacg
551 ccactttggt atttgacgtg aaactgggtc aaatcggcgc acccgaaaac
601 gcgcccgcga agcagccgga tcaagtcgac atcaaaaaag taaattaa

```

This corresponds to the amino acid sequence <SEQ ID 1738; ORF 576.ng>:

g576.pep.. (partial)

```

1  ..MGVDIGRSLK QMKEQGAIEID LKVFTDAMQA VYDGKEIKMT EEQAQEVMMK
51  FLQEQQAKAV EKHKADAKAN KEKGEAFLKE NAAEDGVKTT ASGLQYKITK
101 QGEGKQPTKD DIVTVEYEGR LIDGTVFDSS KANGGPATFP LSQVIPGWTE
151 GVRLLKEGGE ATFYIPSNLA YREQGAGEKI GPNATLVFDV KLVKIGAPEN
201 APAKQPDQVD IKKVN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1739>:

m576.seq.. (partial)

```

1  ..ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA

```

890

```

51   GCAAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
101  CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
151  GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGGCCGT
201  AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
251  TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
301  CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
351  CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
401  TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
451  GTGATTCCGG GTTGGACCGA AGCGGTACAG CTTCTGAAAG AAGGCGGCGA
501  AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
551  GCGACAAAAT CGGTCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
601  AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
651  CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1740; ORF 576>:

m576.pep.. (partial)

```

1   .MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
51  AQEVMVKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
101 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
151 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVDVKLV
201 KIGAPENAPA KQPAQVDIKK VN*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m576/g576 97.2% identity in 215 aa overlap

```

              10      20      30      40      50      60
m576.pep      MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ AQEVMVKFLQ
              |||:|||||
g576           MGVDIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ AQEVMVKFLQ
              10      20      30      40      50

              70      80      90      100     110     120
m576.pep      EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASGLQYKITKQ GEGKQPTKDDIV
              |||:|||||
g576           EQQAKAVEKH KADAKANKEK GEAFLENAA EDGVKTTASGLQYKITKQ GEGKQPTKDDIV
              60      70      80      90      100     110

              130     140     150     160     170     180
m576.pep      TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ VIPGWTEGV QLLKEGGEATFY IPSNLAYRE
              |||:|||||
g576           TVEYEGRLID GTVFDSSKAN GPATFPLSQ VIPGWTEGV RLLKEGGEATFY IPSNLAYRE
              120     130     140     150     160     170

              190     200     210     220
m576.pep      QGAGDKIGPN ATLVDVKLV KIGAPENAPA KQPAQVDIKK VN
              |||:|||||
g576           QGAGEKIGPN ATLVDVKLV KIGAPENAPA KQPDQVDIKK VN
              180     190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1741>:

a576.seq

```

1   ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGCGGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA

```

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```

601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCGAAC GCCACTTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1742; ORF 576.a>:

```

a576.pep
  1 MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
 51 MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

m576/a576 99.5% identity in 222 aa overlap

m576.pep
                                     10      20      30
                                     MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
a576      CGKKEAAPAS ASEPAASSA QGDTSSIGSTM MQQASYAMGV DIGRSLKQMK EQGAEIDLKV
                                     30      40      50      60      70      80

m576.pep
                                     40      50      60      70      80      90
                                     FTEAMQAVYD GKEIKMTEEQAQEVMMKFLQEQQAKAVEKH KADAKANKEK GEAFLENAA
a576      FTEAMQAVYD GKEIKMTEEQAQEVMMKFLQEQQAKAVEKH KADAKANKEK GEAFLENAA
                                     90     100     110     120     130     140

m576.pep
                                     100     110     120     130     140     150
                                     KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
a576      KDGVKTTASGLQYKITQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
                                     150     160     170     180     190     200

m576.pep
                                     160     170     180     190     200     210
                                     VIPGWTEGVQ LLKEGGEATFYIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
a576      VILGWTEGVQ LLKEGGEATFYIPSNLAYRE QGAGDKIGPN ATLVFDVKLV KIGAPENAPA
                                     210     220     230     240     250     260

m576.pep
                                     220
                                     KQPAQVDIKK VN
a576      KQPAQVDIKK VN
                                     270

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1743>:

```

g576-1.seq
  1 ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
 51 ACTTTCCGCC TCGGCGAAAA AAGAAGCCGC CCCCAGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTGCCGCG CAGGGCGACA CCTCTTCAAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC AATGGGCGTG GACATCGGAC GCTCCCTGAA
201 ACAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGATG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCCCAGGAAG TGATGATGAA ATTCTTGCA GAGCAGCAGG CTAAAGCCGT
351 AGAAAAACAC AAGCGGATG CGAAGGCCAA CAAAGAAAAA GGCGAAGCCT
401 TCCTGAAGGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGT
451 CTGCAGTACA AAATCACCAA ACAGGGTGAA GGCAAACAGC CGACAAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACCGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG CCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACGG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGAAAAAAT CGGTCCGAAC GCCACTTTGG TATTTGACGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG ATCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1744; ORF 576-1.ng>:

g576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASAA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTDAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPATFPLSQ
201 VIPGWTEGVR LLKEGGEATF YIPSNLAYRE QGAGEKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPDQVDIKK VN*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1745>:

m576-1.seq

```

1  ATGAACACCA TTTTCAAAT CAGCGCACTG ACCCTTTCGG CCGCTTTGGC
51  ACTTTCCGCC TCGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTTTCGAT CGGCAGCAGC
151 ATGCAGCAGG CAAGCTATGC GATGGGCGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATCACCAA ACAGGGCGAA GGCAAACAGC CGACCAAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCAAC GGCGGCCCGG TCACCTTCCC TTTGAGCCAA
601 GTGATTCCGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTC TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAT CGGTCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1746; ORF 576-1>:

m576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLKV FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLENAA KDGVKTTASG
151 LQYKITKQGE GKOPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VIPGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

g576-1/m576-1 97.8% identity in 272 aa overlap

	10	20	30	40	50	60
g576-1.pep	MNTIFKISAL	TLSAALALS	ACGKKEAPAS	ASEPAASAA	QGDTSSIGST	MQQASYAMGV
m576-1	MNTIFKISAL	TLSAALALS	ACGKKEAPAS	ASEPAASSA	QGDTSSIGST	MQQASYAMGV
	10	20	30	40	50	60
g576-1.pep	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEE	QAQEVMMKFLQ	EQQAKAVEKH
m576-1	DIGRSLKQMK	EQGAEIDLKV	FTDAMQAVYD	GKEIKMTEE	QAQEVMMKFLQ	EQQAKAVEKH
	70	80	90	100	110	120
g576-1.pep	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKOPTKDDIV	TVEYEGRLID
m576-1	KADAKANKEK	GEAFLENAA	KDGVKTTASG	LQYKITKQGE	GKOPTKDDIV	TVEYEGRLID
	130	140	150	160	170	180
g576-1.pep	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	RLLEKGEATF	YIPSNLAYRE	QGAGEKIGPN
m576-1	GTVFDSSKAN	GGPATFPLSQ	VIPGWTEGV	RLLEKGEATF	YIPSNLAYRE	QGAGEKIGPN
	190	200	210	220	230	240
g576-1.pep	ATLVFDVKLV	KIGAPENAPA	KQPDQVDIKK	VN		
m576-1	ATLVFDVKLV	KIGAPENAPA	KQPAQVDIKK	VN		
	250	260	270			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1747>:

a576-1.seq

893

```

1  ATGAACACCA TTTTCAAAAT CAGCGCACTG ACCCTTTCCG CCGCTTTGGC
51  ACTTTCCGCC TGGCGCAAAA AAGAAGCCGC CCCCGCATCT GCATCCGAAC
101 CTGCCGCCGC TTCTTCCGCG CAGGGCGACA CCTCTTCGAT CGGCAGCACG
151 ATGCAGCAGG CAAGCTATGC GATGGCGGTG GACATCGGAC GCTCCCTGAA
201 GCAAATGAAG GAACAGGGCG CGGAAATCGA TTGAAAGTC TTTACCGAAG
251 CCATGCAGGC AGTGTATGAC GGCAAAGAAA TCAAAATGAC CGAAGAGCAG
301 GCTCAGGAAG TCATGATGAA ATTCCTTCAG GAACAACAGG CTAAGCCGT
351 AGAAAAACAC AAGGCGGACG CGAAGGCCAA TAAAGAAAAA GGCGAAGCCT
401 TTCTGAAAGA AAATGCCGCC AAAGACGGCG TGAAGACCAC TGCTTCCGGC
451 CTGCAATACA AAATACCCAA ACAGGGCGAA GGCAAACAGC CGACCAAGA
501 CGACATCGTT ACCGTGGAAT ACGAAGGCCG CCTGATTGAC GGTACGGTAT
551 TCGACAGCAG CAAAGCCCAAC GCGGCGCCGG TCACCTTCCC TTTAGCCAA
601 GTGATTCTGG GTTGGACCGA AGGCGTACAG CTTCTGAAAG AAGGCGGCGA
651 AGCCACGTTT TACATCCCGT CCAACCTTGC CTACCGCGAA CAGGGTGCGG
701 GCGACAAAAT CGGCCCGAAC GCCACTTGG TATTTGATGT GAAACTGGTC
751 AAAATCGGCG CACCCGAAAA CGCGCCCGCC AAGCAGCCGG CTCAAGTCGA
801 CATCAAAAAA GTAAATTAA

```

This corresponds to the amino acid sequence <SEQ ID 1748; ORF 576-1.a>:

a576-1.pep

```

1  MNTIFKISAL TLSAALALSA CGKKEAAPAS ASEPAASSA QGDTSSIGST
51  MQQASYAMGV DIGRSLKQMK EQGAEIDLK FTEAMQAVYD GKEIKMTEEQ
101 AQEVMKFLQ EQQAKAVEKH KADAKANKEK GEAFLEKNA KDGVKTTASG
151 LQYKITKQGE GKQPTKDDIV TVEYEGRLID GTVFDSSKAN GGPVTFPLSQ
201 VILGWTEGVQ LLKEGGEATF YIPSNLAYRE QGAGDKIGPN ATLVFDVKLV
251 KIGAPENAPA KQPAQVDIKK VN*

```

a576-1/m576-1 99.6% identity in 272 aa overlap

	10	20	30	40	50	60
a576-1.pep	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
m576-1	MNTIFKISALTLSAALALSACGKKEAAPASASEPAASSAQGDTSSIGSTMQQASYAMGV					
	10	20	30	40	50	60
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
m576-1	DIGRSLKQMKEQGAEIDLKVFTEAMQAVYDGKEIKMTEEQAQEVMKFLQEQQAKAVEKH					
	70	80	90	100	110	120
a576-1.pep	KADAKANKEKGEAFLEKNAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLEKNAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	KADAKANKEKGEAFLEKNAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
m576-1	KADAKANKEKGEAFLEKNAAKDGVKTTASGLQYKITKQGEKGKQPTKDDIVTVEYEGRLID					
	130	140	150	160	170	180
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
m576-1	GTVFDSSKANGGPVTFPLSQVILGWTEGVQLLKEGGEATFYIPSNLAYREQGAGDKIGPN					
	190	200	210	220	230	240
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			
a576-1.pep	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
m576-1	ATLVFDVKLVKIGAPENAPAKQPAQVDIKKVN					
	250	260	270			

Expression of ORF 576

The primer described in Table 1 for ORF 576 was used to locate and clone ORF 576. ORF 576 was cloned in pET and pGex vectors and expressed in E.coli as above described. The products of protein expression and purification were analyzed by SDS-PAGE. Figure 3A shows the results of affinity purification and Figure 3B shows the expression in E.coli. Purified His-fusion protein was used to immunize mice, whose sera were used for ELISA (positive result), FACS analysis (Figure 3C), western blot (Figure 3D). These experiments confirm that ORF 576 is a surface-exposed protein and that it is a useful immunogen. The

hydrophilicity plots, antigenic index, and amphipathic regions of ORF 576 are provided in Figure 7. The AMPHI program is used to predict putative T-cell epitopes (Gao et al 1989, *J. Immunol* 143:3007; Roberts et al. 1996, *AIDS Res Human Retroviruses* 12:593; Quakyi et al. 1992, *Scand J Immunol Suppl* 11:9). The nucleic acid sequence of ORF 576 and the amino acid sequence encoded thereby is provided in Example 1.

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1749>:

```
g577.seq..
1  atggaaagga gcggtgtatt tggtaaaatt gtcggcaatc gcatactccg
51  tatgccgtcc gaacacgctg ccgcattcta tccgaaaccg tgcaaatcgt
101 ttaactaac gcaatcttgg ttcagagtgc gaagctgtcc gtgcggcggt
151 tttatttacg gagcaaacat gaaacttatc tataccgtca tcaaaatcat
201 taccctgctg ctcttctctg tgcttgccgt cattaatatg gatgccgtta
251 ccttttccta tcttcgggg cagagtgtca atctgccgct gattgtcgta
301 ttgttcggcg cgtttctcgt cggcatcgtg ttcggaatgt ttgccctggt
351 cgggcggctg ctgtccttgc gcggcgaaaa cagccgcctg cgtgcggaag
401 tgaagaaaag tgcgcgcttg agcggacaga aattgactgc accgccgata
451 caaatgctg ccgaatctgc caaacgcct taa
```

This corresponds to the amino acid sequence <SEQ ID 1750; ORF 577.ng>:

```
g577.pep
1  MERSGVFGKI VGNRILRMPS EHAAAFYPKP CKSFKLTQSW FRVRS PCGW
51  FIYGANMKLI YTVIKIILL LFLLLAVINM DAVTF SYLPG QSVNLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENSRL RAEVKKSARL SGQKLTAPPI
151 QNAESAQKP *
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1751>:

```
m577.seq..
1  ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAAATCGT
101 TTAAGTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCT GGGCGGCGTT
151 TTTATTACG GAGCAACAT GAAACTTATC TATACCGTCA TCAAAATCAT
201 TATCCTGCTG CTCTTCTTGC TGCTTGCCGT CATTAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAATTTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CATTGTAGT CCGTATTATT TTTGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTTG CGTGCCGAAG
401 TAAAGAAAAA TGCGCGTTTG ACGGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTAC CAAACAGCCT TAA
```

This corresponds to the amino acid sequence <SEQ ID 1752; ORF 577>:

```
m577.pep..
1  MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSCLGGV
51  FIYGANMKLI YTVIKIILL LFLLLAVINT DAVTF SYLPG QKFDLPLIVV
101 LFGAFVVGII FGMFALFGRL LSLRGENGRL RAEVKKNARL TGKELTAPPA
151 QNAPESTKQP *
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```
m577/g577 88.1% identity in 160 aa overlap

          10      20      30      40      50      60
m577.pep  MERNGVFGKIVGNRILRMSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
          |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g577       MERSGVFGKIVGNRILRMPSEHAAAFYPKPCKSFKLTQSWFRVRS PCGWFIYGANMKLI
          10      20      30      40      50      60

          70      80      90     100     110     120
m577.pep  YTVIKIILLFLLLAVINTDAVTF SYLPGQKFDLPLIVVLFGAFVVGII FGMFALFGRL
```


895

```

|||||
g577  YTVIKIIILLFLLLAVINMDAVTFSYLPQSVNLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130      140      150      160
m577.ppep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      |||||:|||||:||||:|:|||| ||| ||:||||
g577      LSLRGENSRLRAEVKKKSARLSGQKLTAPPIQNAAESAKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1753>:

```

a577.seq
1   ATGGAAAGGA ACGGTGTATT TGGTAAAATT GTCGGCAATC GCATACTCCG
51  TATGTCGTCC GAACACGCTG CCGCATCCTA TCCGAAACCG TGCAAATCGT
101 TTAAGCTAGC GCAATCTTGG TTCAGAGTGC GAAGCTGTCC GGGCGGCGTT
151 TTTATTTACG GAGCAAACAT GAAACTTATC TATACCGTCA TCAAATCAT
201 TATCCTGCTG CTCTTCCTGC TGCTTGCTGT CATTAAATACG GATGCCGTTA
251 CCTTTTCCTA CCTGCCGGGG CAAAAATTCG ATTTGCCGCT GATTGTCGTA
301 TTGTTCCGCG CGTTTGTCTG CGGCATCGTG TTCGGAATGT TTGCCTTGTT
351 CGGACGGTTG TTGTCGTTAC GTGGCGAGAA CGGCAGGTG CGTGCCGAAG
401 TAAAGAAAAA TGC GCGTTT AC GGGGAAGG AGCTGACCGC ACCACCGGCG
451 CAAATGCGC CCGAATCTGC CAAACAGCCT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1754; ORF 577.a>:

```

a577.ppep
1   MERNGVFGKI VGNRILRMSS EHAAASYPKP CKSFKLAQSW FRVRSPPGGV
51  FIYGANMKLI YTVIKIIILL LFLLLAVINT DAVTFSYLPQ QKFDLPLIVV
101 LFGAFVVGIV FGMFALFGRL LSLRGENGRRL RAEVKKNARL TGKELTAPPA
151 QNAPESAKQP *

```

m577/a577 98.1% identity in 160 aa overlap

```

      10      20      30      40      50      60
m577.ppep MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSFKLAQSWFRVRSCLGGVFIYGANMKLI
      |||||
a577      MERNGVFGKIVGNRILRMSSSEHAAASYPKPCKSFKLAQSWFRVRSPPGGVFIYGANMKLI
      10      20      30      40      50      60

      70      80      90      100     110     120
m577.ppep YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIIFGMFALFGRL
      |||||
a577      YTVIKIIILLFLLLAVINTDAVTFSYLPQKFDLPLIVVLFGAFVVGIVFGMFALFGRL
      70      80      90      100     110     120

      130      140      150      160
m577.ppep LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      |||||
a577      LSLRGENGRRLRAEVKKNARLTGKELTAPPAQNAPESTKQPX
      130      140      150      160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1755>:

```

g578.seq..
1   atgggaaagc tcgacatcgg gatattgttt gccgatttct tcaaagattt
51  cgcgccacag ttcggtggtt tccaaaacgt tggctttgcc tacggagcag
101 acttttttgc tgcgtttttg ggcggattgg aaggccacgt gggcgatgcg
151 gcggatttgc ctttcgctgt atttcatggt gttgtagcct tcgtgttcgc
201 cgttttccaa aacacggatg ccgcgcggtt cgccgaaata aatatcgccg
251 gtaagtgcgc gcacaatcaa aatatccaaa ccggcaacga tttcaggctt
301 gagcgtggag gcgttggtta a

```

This corresponds to the amino acid sequence <SEQ ID 1756; ORF 578.ng>:

```

g578.ppep
1   MGKLDIGILF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGHVGD
51  ADFAFVAVFHG VVAFVFAVFQ NTDAARFAEI NIAGKFAHNQ NIQTGNDFRL

```

101 ERGGVG*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1757>:

m578.seq..

```

1  ATGGGAAAGC TCGACATCAG GGTACTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAACAG
101 ACTTTTTCG TCGTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
151 GCGGATTTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACGCGGATG CCGCGCGGTT CGCCGAAATA GATGTCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCGCAACGA TTCAGGCTT

```

This corresponds to the amino acid sequence <SEQ ID 1758; ORF 578>:

m578.pep..

```

1  MGKLDIRVLF ADFFKDFAPQ FGGFQNVGFA YGTDFFAAFL GGLEGNMNGT
51  ADFAFAVFHG VVAFAFAVFQ NADAARFAEI DVAGEFAHNQ NIQTGNDFRL
101 QRGGVG*

```

m578/g578 87.7% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMNGNTADFAFAVFHG					
	: : :					
g578	MGKLDIGILFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGHVGDADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : : : :					
g578	VVAFVFAVFQNTDAARFAEINIAGKFAHNQNIQTGNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1759>:

a578.seq

```

1  ATGGGAAAGC TCGACATCAG GGTATTCTTT GCCGATTCTT TCAAAGATTT
51  CGCGCCACAA TTCGGTGGTT TCCAAAACGT TGGCTTTGCC TACGGAGCAG
101 ACTTTTTCG TCGTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
151 GCGGATTTTCG CTTTCGCTGT ATTTTCATGGT GTTGTAGCCT TCGCGTTCGC
201 CGTTTTCAG AACACGGATG CCGCGCGGTT CGCCGAAATA AATATCGCCG
251 GTGAGTTCGC GCACAATCAA AATATCCAAA CCCGCAACGA TTCAGACTT
301 GAGCGTGGAG GCGTTGGCTA G

```

This corresponds to the amino acid sequence <SEQ ID 1760; ORF 578.a>:

a578.pep

```

1  MGKLDIRVFF ADFFKDFAPQ FGGFQNVGFA YGADFFAAFL GGLEGDVGNT
51  ADFAFAVFHG VVAFAFAVFQ NTDAARFAEI NIAGEFAHNQ NIQTRNDFRL
101 ERGGVG*

```

m578/a578 91.5% identity in 106 aa overlap

	10	20	30	40	50	60
m578.pep	MGKLDIRVLFADFFKDFAPQFGGFQNVGFAYGTDFFAAFLGGLEGNMNGNTADFAFAVFHG					
	: : :					
a578	MGKLDIRVFFADFFKDFAPQFGGFQNVGFAYGADFFAAFLGGLEGDVGNTADFAFAVFHG					
	10	20	30	40	50	60
	70	80	90	100		
m578.pep	VVAFAFAVFQ NADAARFAEIDVAGEFAHNQNIQTGNDFRLQRGGVGX					
	: : : : : :					
a578	VVAFAFAVFQNTDAARFAEINIAGEFAHNQNIQTRNDFRLERGGVGX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1761>:

g579.seq..

```

1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT

```

897

```

51  TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGACG GTTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTA AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCGCTGATTA TCCTGTTCCTG CCCGTTCAAA GTCGGCGACT
251 TTATCCGTGT CGGCGGTTTT GAAGGATATG TCCGGGAAAT CAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCAGCCTG CCGCTTTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGCCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGCCCGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1762; ORF 579.ng>:

```

g579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAAE HPLSVQNEER QPAAYITALG DNAIEITLWA WANEADRRTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1763>:

```

m579.seq..
1  ATGAGGGCGG CGATGACGCG CGCGCAGGTC GATGCCACGC TGATTAGTTT
51 TTTGTGTAAT GTTGCCAATA TCGGCTTATT GATTTTGGTG ATTATTGCCG
101 CATTGGGCAG ATTGGGCGTT TCCACAACAT CCGTAACCGC CTTAATCGGC
151 GCGCGGGGTT TGGCGGTGGC GTTGTCCCTG AAAGACCAGC TGTCCAATTT
201 TGCCGCCGGC GCACTGATTA TCCTGTTCCTG CCCGTTCAAA GTCGGCGATT
251 TTATCCGCGT CGGCGGTTTT GAAGGATATG TCCGAGAGAT TAAAATGGTG
301 CAGACTTCTT TGCGGACGAC CGACAACGAA GAAGTCGTGC TGCCCAACAG
351 CGTGGTGATG GGCAACAGCA TCGTCAACCG TTCCACACTG CCGCTGTGCC
401 GCGCCCAAGT GATAGTCGGC GTCGATTACA ACTGCGATTT GAAAGTGGCG
451 AAAGAGGCGG TGTTGAAAGC CGCCGTCGAA CACCCCTTGA GCGTTCAAAA
501 CGAAGAGCGG CAGGCTGCCG CCTACATCAC CGCCTTGGGC GACAATGCCA
551 TCGAAATCAC ATTATGGGCT TGGGCAAACG AAGCAGACCG CTGGACGCTG
601 CAATGCGACT TGAACGAACA AGTGGTCGAA AACCTCCGCA AAGTCAATAT
651 CAACATCCCG TTCCCGCAAC GCGACATACA CATCATCAAT TCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1764; ORF 579>:

```

m579.pep..
1  MRAAMTRAQV DATLISFLCN VANIGLLILV IIAALGRLGV STTSVTALIG
51 GAGLAVALSL KDQLSNFAAG ALIILFRPFK VGDFIRVGGF EGYVREIKMV
101 QTSRLTTDNE EVVLPNSVVM GNSIVNRSSL PLCRAQVIVG VDYNCDLKVA
151 KEAVLKAAVE HPLSVQNEER QAAAYITALG DNAIEITLWA WANEADRRTL
201 QCDLNEQVVE NLRKVNINIP FPQORDIHIIN S*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m579/g579 98.7% identity in 231 aa overlap

```

          10      20      30      40      50      60
m579.pep  MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL
          |||||
g579       MRAAMTRAQVDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSL
          10      20      30      40      50      60

          70      80      90     100     110     120
m579.pep  KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
          |||||
g579       KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLTTDNEEVVLPNSVVM
          70      80      90     100     110     120

```

898

	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : : :					
g579	GNSIVNRSSLPLCRAQVIVGVDYNCDLKVAKEAVLKAEEHPLSVQNEERQPAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : : :					
g579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1765>:

```
a579.seq
1  ATGAGGGCGG  CGATGACGCG  CGCGCAGGTC  GATGCCACGC  TGATTAGTTT
51  TTTGTGTAAT  GTTGCCAATA  TCGGCTTATT  GATTTTGGTG  ATTATTGCCG
101 CATTGGGCAG  ATTGGGCGTT  TCCACAACAT  CCGTAACCGC  CTTAATCGGC
151 GGCGCGGGTT  TGGCGGTGGC  GTTGTCTTGG  AAAGACCAGC  TGTCCAATTT
201 TGCCGCCGGC  GCGCTGATTA  TCCTGTTCCG  CCCGTTCAAA  GTCGGCGATT
251 TTATCCGCGT  CGGCGGTTTT  GAAGGATATG  TCCGAGAGAT  TAAATGGTG
301 CAGACTTCTT  TCGCGACGAC  CGACAACGAA  GAAGTCGTGC  TGCCCAACAG
351 CGTGGTGATG  GGCAACAGCA  TCGTCAACCG  TTCCCACTG  CCGCTGTGCC
401 GCGCCCAAGT  GATAGTCGGC  GTCGATTACA  ACTGCGATTT  GAAAGTGGCG
451 AAAGAGGCGG  TGTTGAAAGC  CGCCGTCGAA  CACCCCTTGA  GCGTTCAAAA
501 CGAAGAGCGG  CAGGCCGCCG  CCTACATCAC  CGCCTTGGGC  GACAATGCCA
551 TCGAAATCAC  ATTATGGGCT  TGGGCAAACG  AAGCAGACCG  CTGGACGCTG
601 CAATGCGACT  TGAACGAACA  AGTGGTCGAA  AACCTCCGCA  AAGTCAATAT
651 CAACATCCCG  TTCCCGCAAC  GCGACATACA  CATCATCAAT  TCTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1766; ORF 579.a>:

```
a579.pep
1  MRAAMTRAQV  DATLISFLCN  VANIGLLILV  IIAALGRLGV  STTSVTALIG
51  GAGLAVALSL  KDQLSNFAAG  ALIILFRPFK  VGDFIRVGGF  EGYVREIKMV
101 QTSRLRTDNE  EVVLPNSVVM  GNSIVNRSTL  PLCRAQVIVG  VDYNCDLKVA
151 KEAVLKAAVE  HPLSVQNEER  QAAAYITALG  DNAIEITLWA  WANEADRWTL
201 QCDLNEQVVE  NLRKVNINIP  FPQORDIHIIN  S*
```

m579/a579 100.0% identity in 231 aa overlap

	10	20	30	40	50	60
m579.pep	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	: : : : : :					
a579	MRAAMTRAQVDATLISFLCNVANIGLLILVIAALGRLGVSTTSVTALIGGAGLAVALSL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m579.pep	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	: : : : : :					
a579	KDQLSNFAAGALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVVLPNSVVM					
	70	80	90	100	110	120
	130	140	150	160	170	180
m579.pep	GNSIVNRSTLPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	: : : : : :					
a579	GNSIVNRSTLPLCRAQVIVGVDYNCDLKVAKEAVLKAAVEHPLSVQNEERQAAAYITALG					
	130	140	150	160	170	180
	190	200	210	220	230	
m579.pep	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	: : : : : :					
a579	DNAIEITLWAWANEADRWTLCQDLNEQVVENLRKVNINIPFPQORDIHIINSX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1767>:

g579-1.seq

```

1  ATGGACTTCA  AACAAATTGA  TTTTTCACAC  CTGATCAGTG  TTTCCGGTTG
51  GGGGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTCTTGGTC  GGGAAATGGG  CGGCGAAACG  CATTGTCGCC
151 GTAATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTGGG  ACGGTTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGGCGCGG  GTTGGCGGT  GCGTTGTCC  TTAAGAAC  AGCTGTCCAA
351 TTTTGGCGC  GCGCGCTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ACTTTATCCG  TGTGCGCGGT  TTGAAGGAT  ATGTCCGGGA  AATCAAATG
451 GTGCAGACTT  CTTGCGGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTCCAGC  CTGCCGCTTT
551 CCCGCGCCA  AGTGATAGTC  GCGTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGCCG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1768; ORF 008.ng>:

g579-1.pep

```

1  MDFKQDFDLH  LISVSGWGH  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIAALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLTTDN  EEVLPNSVV  MGNSIVNRSS  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAA  EHPLSVQNEE  RQPAAYITAL  GDNAIEITLW  AWANEADRW
251 LQCDLNEQVV  ENLRKVNINI  PFPQORDIHII  NS*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1769>:

m579-1.seq

```

1  ATGGACTTCA  AACAAATTGA  TTTTTCACAC  CTGATCAGTG  TTTCCGGTTG
51  GGAGCATCTG  GCTGAAAAGG  CGTGGGCGTT  CGGGCTGAAC  CTTGCCGCCG
101 CGCTGCTTAT  TTTTTCGGTC  GGAAATGGG  CGGCGAAACG  CATTGTCGCT
151 GTGATGAGGG  CGGCGATGAC  GCGCGCGCAG  GTCGATGCCA  CGCTGATTAG
201 TTTTGTGTGT  AATGTTGCCA  ATATCGGCTT  ATTGATTTTG  GTGATTATTG
251 CCGCATTGGG  CAGATTGGGC  GTTCCACAA  CATCCGTAAC  CGCCTTAATC
301 GCGGCGCGG  GTTGGCGGT  GCGTTGTCC  CTGAAAGACC  AGCTGTCCAA
351 TTTTGGCGC  GCGCGACTGA  TTATCCTGTT  CCGCCCGTTC  AAAGTCGGCG
401 ATTTTATCCG  CGTCGCGGT  TTTGAAGGAT  ATGTCCGAGA  GATTAAGATG
451 GTGCAGACTT  CTTTGGCGAC  GACCGACAAC  GAAGAAGTCG  TGCTGCCCAA
501 CAGCGTGGTG  ATGGGCAACA  GCATCGTCAA  CCGTCCACA  CTGCCGCTGT
551 GCGGCGCCA  AGTGATAGTC  GCGTCGATT  ACAACTGCGA  TTTGAAAGTG
601 GCGAAAGAGG  CGGTGTTGAA  AGCCGCCGTC  GAACACCCCT  TGAGCGTTCA
651 AAACGAAGAG  CGGCAGGCTG  CCGCTACAT  CACCGCCTTG  GCGGACAATG
701 CCATCGAAAT  CACATTATGG  GCTTGGGCAA  ACGAAGCAGA  CCGCTGGACG
751 CTGCAATGCG  ACTTGAACGA  ACAAGTGGTC  GAAACCTCC  GCAAAGTCAA
801 TATCAACATC  CCGTCCCGC  AACGCGACAT  ACACATCATC  AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1770; ORF 579-1>:

m579-1.pep

```

1  MDFKQDFDLH  LISVSGWEHL  AEKAWAFGLN  LAAALLIFLV  GKWAAKRIVA
51  VMRAAMTRAQ  VDATLISFLC  NVANIGLLIL  VIIAALGRLG  VSTTSVTALI
101 GGAGLAVALS  LKDQLSNFAA  GALIILFRPF  KVGDFIRVGG  FEGYVREIKM
151 VQTSRLTTDN  EEVLPNSVV  MGNSIVNRST  LPLCRAQVIV  GVDYNCDLKV
201 AKEAVLKAAV  EHPLSVQNEE  RQAAAYITAL  GDNAIEITLW  AWANEADRW
251 LQCDLNEQVV  ENLRKVNINI  PFPQORDIHII  NS*

```

m579-1/g579-1 98.6% identity in 282 aa overlap

	10	20	30	40	50	60
m579-1.pep	MDFKQDFDLHLISVSGWEHLAEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
g579-1	MDFKQDFDLHLISVSGWGHLEKAWAFGLNLAAALLIFLVGKWAAKRIVAVMRAAMTRAQ					
	10	20	30	40	50	60
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
g579-1	VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA					
	70	80	90	100	110	120
m579-1.pep	GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST					
	130	140	150	160	170	180

900

```

|||||
g579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRSS
          130      140      150      160      170      180
          190      200      210      220      230      240
m579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
g579-1  LPLCRAQVIVGVVDYNDLKVAKAEVLKAAAEHPLSVQNEERQPAAYITALGDNAIEITLW
          190      200      210      220      230      240
          250      260      270      280
m579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          |||||
g579-1  AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX
          250      260      270      280

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1771>:

```

a579-1.seq
1  ATGGACTTCA AACAATTGA TTTTTCAC CTGATAAGTG CTTCCGGCTG
51  GGAGCATCTG GCTGAAAAGG CGTGGGCGTT CGGGCTGAAC CTTGCCGCCG
101 CGCTGCTTAT TTTTTCGTC GGAAATGGG CGGCGAAACG CATGTGCGCC
151 GTGATGAGGG CGCGATGAC GCGCGCGCAG GTCGATGCCA CGCTGATTAG
201 TTTTTCGTC AATGTTGCCA ATATCGGCTT ATTGATTTTG GTGATTATTG
251 CCGCATGGGG CAGATTGGGC GTTCCACAA CATCCGTAAC CGCCTTAATC
301 GGCGGCGCGG GTTGGCGGT GCGGTGTGCC TTGAAAGACC AGCTGTCCAA
351 TTTTGCCGCG GCGCGCTGA TTATCCTGTT CCGCCCGTTC AAAGTCGGCG
401 ATTTTATCCG CGTCGGCGGT TTTGAAGGAT ATGTCCGAGA GATTAAAATG
451 GTGCAGACTT CTTGCGGAC GACCGACAAC GAAGAAGTCG TGCTGCCCAA
501 CAGCGTGGTG ATGGGCAACA GCATCGTCAA CCGTCCACA CTGCCGCTGT
551 GCCGCGCCCA AGTGATAGTC GCGCTCGATT ACAACTGCGA TTTGAAAGTG
601 GCGAAAGAGG CGGTGTTGAA AGCCGCGCTC GAACACCCCT TGAGCGTTCA
651 AAACGAAGAG CGGCAGGCCG CCGCTACAT CACCGCCTTG GCGGACAATG
701 CCATCGAAAT CACATTATGG GCTTGGGCAA ACGAAGCAGA CCGCTGGACG
751 CTGCAATGCG ACTTGAACGA ACAAGTGGTC GAAAACCTCC GCAAAGTCAA
801 TATCAACATC CCGTTCCCGC AACGCGACAT ACACATCATC AATTCTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1772; ORF 579-1.a>:

```

a579-1.pep
1  MDFKQFDLHL LISASGWEHL AEKAWAFGLN LAAALLIFLV GKWAAKRIVA
51  VMRAAMTRAQ VDATLISFLC NVANIGLLIL VIIAALGRLG VSTTSVTALI
101 GGAGLAVALS LKDQLSNFAA GALIILFRPF KVGDFIRVGG FEGYVREIKM
151 VQTSRLRTDN EEVLPNSVV MGNSIVNRST LPLCRAQVIV GVDYNDLKV
201 AKEAVLKAAV EHPLSVQNEE RQAAAYITAL GDNAIEITLW AWANEADRWT
251 LQCDLNEQVV ENLRKVNINI PFPQORDIHI NS*

```

a579-1/m579-1 99.6% identity in 282 aa overlap

```

          10      20      30      40      50      60
a579-1.pep MDFKQFDLHL LISASGWEHLAEKAWAFGLNLAAALLIFLVGKWA AKRIVAVMRAAMTRAQ
          |||||
m579-1  MDFKQFDLHL LISASGWEHLAEKAWAFGLNLAAALLIFLVGKWA AKRIVAVMRAAMTRAQ
          10      20      30      40      50      60
          70      80      90      100     110     120
a579-1.pep VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          |||||
m579-1  VDATLISFLCNVANIGLLILVIIAALGRLGVSTTSVTALIGGAGLAVALSLKDQLSNFAA
          70      80      90      100     110     120
          130     140     150     160     170     180
a579-1.pep GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          |||||
m579-1  GALIILFRPFKVGDFIRVGGFEGYVREIKMVQTSRLRTDNEEVLPNSVVMGNSIVNRST
          130     140     150     160     170     180
          190     200     210     220     230     240
a579-1.pep LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          |||||
m579-1  LPLCRAQVIVGVVDYNDLKVAKAEVLKAAVEHPLSVQNEERQAAAYITALGDNAIEITLW
          190     200     210     220     230     240
          250     260     270     280
a579-1.pep AWANEADRWTLQCDLNEQVVENLRKVNINIPFPQORDIHIINSX

```

901

|||||
m579-1 AWANEADRWTLCQDLNEQVVENLRKVNINIPFPQIDIHIINSX
 250 260 270 280

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1773>:

g580.seq
1 atggattcgc ccaaggtcgg gtgcgggtgg atggttttgc cgatgtctgc
51 cgcgtcgcag ccatttcga tggcaaggca gacttcgccg atcatgtcgc
101 caccgttcgg accgacaatg ccgccgccga tgatgcggcc ggtttcggca
151 tcgaaaatca gcttggtaaa gccgtgtcgc caaccgttgg caatcgcacg
201 accggaagcc gcccatggga agttggcttt ggtaattttg cggcctgatg
251 ctttggcaga caattcgggt tcaccgaccc atgccacttc gggggaagtg
301 tag

This corresponds to the amino acid sequence <SEQ ID 1774; ORF 580.ng>:

g580.pep..
1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPDALADNSV SPTHATSGEV
101 *

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1775>:

m580.seq..
1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATATCGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCGGCA
151 TCAAAAATCA GCTTGGTAAA GCCGTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCC GCCCACGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
251 CTTTGGCGGA CAGTTCGGTT TCGCCACCC ACGCCACTTC GGGGGAAGTG
301 TAG

This corresponds to the amino acid sequence <SEQ ID 1776; ORF 580>:

m580.pep..
1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IISPPFGPTM PPPMMRPVSA
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADSSV SPTHATSGEV
101 *

m580/g580 97.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSP IISPPFGPTM PPPMMRPVSASKISLVKPLS					
g580	MDSPKVGCGWMVLPMASASQPISMARQTSP IMSPPFGPTM PPPMMRPVSASKISLVKPLS					
	10	20	30	40	50	60
	70	80	90	100		
m580.pep	QPLAIARPEAAHGKLALVILRPEALADSSV SPTHATSGEVX					
g580	QPLAIARPEAAHGKLALVILRPDALADNSV SPTHATSGEVX					
	70	80	90	100		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1777>:

a580.seq
1 ATGGATTTCGC CCAAGGTCGG GTGCGGGTGG ATGGTTTTCG CGATGTCTGC
51 CGCGTCGCAG CCCATTTCGA TGGCAAGGCA GACTTCGCCG ATCATGTCTGC
101 CACCGTTTCGG ACCGACAATG CCGCCGCCGA TGATGCGGCC GGTTTCAGCA
151 TCAAAAATCA GCTTGGTGAA ACCATTGTGCG CAACCGTTGG CAATCGCACG
201 GCCGGAAGCA GCCCATGGGA AGTTGGCTTT GGTGATTTTG CGGCCGGAGG
251 CTTTGGCAGA CAATTCGGTT TCGCCACCC ATGCCACTTC AGGAGAAGTG
301 TAA

This corresponds to the amino acid sequence <SEQ ID 1778; ORF 580.a>:

a580.pep
1 MDSPKVGCGW MVLPMASASQ PISMARQTSP IMSPPFGPTM PPPMMRPVSA
51 SKISLVKPLS QPLAIARPEA AHGKLALVIL RPEALADNSV SPTHATSGEV

902

101 *

m580/a580 98.0% identity in 100 aa overlap

	10	20	30	40	50	60
m580.pep	MDSPKVGCGWMVLPMASASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
a580	MDSPKVGCGWMVLPMASASQPISMARQTSPIISPPFGPTMPPPMRPVSASKISLVKPLS					
	10	20	30	40	50	60

	70	80	90	100
m580.pep	QPLAIARPEAAHGKLLVILRPEALADSSVSPHATSSEVX			
a580	QPLAIARPEAAHGKLLVILRPEALADNSVSPHATSSEVX			
	70	80	90	100

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1779>:

g581.seq..

```

1  atgcacttcg cccagcttgt gggcacaacc ggtatagaac aaaatacgtt
51  ctgtcgtcgt ggttttaccg gcatcgatat gggcggaaat accgatgttg
101 cggtagacggc tgatcggggg cttacgagcc attttattag cctttcaaaa
151 ttagaaacgg aagtgcagaga atgctttgtt ggcttcagcc atacgggtga
201 cttcttcacg ttttttcaac gcaccgccac ggcttcggga cgcataatc
251 aactcgctcg ccaaacgcag atccatggat ttctcaccac gtttgcgggc
301 cgcgtcgcga acccaacgca ttgccaaagc cagacggcgt ga

```

This corresponds to the amino acid sequence <SEQ ID 1780; ORF 581.ng>:

g581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVAVQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQLACQTQ IHGFLTTFAG
101 RVANPTHCS QTA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1781>:

m581.seq..

```

1  ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
51  CTGTCGTCGT GGTTTTACCC GCGTCAATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTGTGTT GGCTTCAGCC ATACGGGTGA
201 CTTCTTCACG TTTTTCACAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTCGCCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1782; ORF 581>:

m581.pep..

```

1  MHFAQLVGQT GIEQNTFCRR GFTRVNMGGN TDVTQADRG LTSHFISLSK
51  LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTTFAG
101 RIANPAHCQS QTA*

```

m581 / g581 93.8% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTQADRGGLTSHFISLSKLETEVRECFV					
g581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVAVQADRGGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60

	70	80	90	100	110
m581.pep	GFSHTVYFFTFFQRTATAFGRINQFACQTQVHGFLLTTFAGRIANPAHCQSQTAX				
g581	GFSHTVYFFTFFQRTATAFGRINQLACQTQIHGFLLTTFAGRVANPTHCSQTAX				
	70	80	90	100	110

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1783>:

903

```

a581.seq
  1 ATGCACTTCG CCCAGCTTGT GGGTCAAACC GGTATAGAAC AAAATACGTT
 51 CTGTCGTCGT GGTTTTACCC GCATCGATAT GGGCGGAAAT ACCGATGTTA
101 CGGTACAGGC TGATCGGGGT CTTACGAGCC ATTTTATTAG CCTTCAAAA
151 TTAGAAACGG AAGTGAGAGA ATGCTTTGTT GGCTTCAGCC ATACGGTGTA
201 CTTCTTCACG TTTTTC AAC GCACCGCCAC GGCCTTCGGA CGCATCAATC
251 AATTGCGCTG CCAAACGCAG GTCCATGGAT TTCTCACCAC GTTTGCGGGC
301 CGCATCGCGA ACCCAGCGCA TTGCCAAAGC CAAACGGCGT GA

```

This corresponds to the amino acid sequence <SEQ ID 1784; ORF 581.a>:

```

a581.pep
  1 MHFAQLVGQT GIEQNTFCRR GFTRIDMGGN TDVTVQADRG LTSHFISLSK
 51 LETEVRECFV GFSHTVYFFT FFQRTATAFG RINQFACQTQ VHGFLLTFAG
101 RINPAHCQS QTA*

```

m581/a581 98.2% identity in 113 aa overlap

	10	20	30	40	50	60
m581.pep	MHFAQLVGQTGIEQNTFCRRGFTRVNMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV					
a581	MHFAQLVGQTGIEQNTFCRRGFTRIDMGGNTDVTVQADRGLTSHFISLSKLETEVRECFV					
	10	20	30	40	50	60
	70	80	90	100	110	
m581.pep	GFSHTVYFFTFFQRTATAFG RINQFACQTQVHGFLLTFAGRIANPAHCQSQTAX					
a581	GFSHTVYFFTFFQRTATAFG RINQFACQTQVHGFLLTFAGRIANPAHCQSQTAX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1785>:

```

g582.seq..
  1 atgcgctata ttcttttgac aggactgttg ccgacggcat ccgcttttgg
 51 agagaccgcg ctgcaatgcg ccgctttgac ggacaatggt acgcgtttgg
101 cgtgttacga caggattttt gcggcacagc ttccgtcttc ggcagggcag
151 gaagggcagg agtcgaaagc cgtactcaat ctgacggaaa ccgtccgcag
201 cagcttggat aagggcgagg cggtcattgt tgttgaaaaa ggcggggatg
251 cgcttcctgc cgacagtgcg ggcgaaaccg ccgatatcta tacgcctttg
301 agcctgatgt acgacttggg caaaaacgat ttgcgcgggc tgttgggcgt
351 acgcgaacac aatccgatgt accttatgcc gttttggtat aacaattcgc
401 ccaactatgc cccgagttcg ccgacgcgcg gtacgactgt acaggaaaaa
451 ttccggacagc agaaacgtgc ggaaaccaa ttgcaggttt cgttcaaaag
501 caaaattgcc gaaaatttgt ttaaaacccg ccgagatctg tggttcggct
551 acacccaaag atccgattgg cagatttaca accaaggcag gaaatccgcg
601 ccgttcgcga atacggatta caaacctgaa attttcctga cccagcctgt
651 gaagggcggat ttgccgttcg gcggcaggct gcgtatgctc ggtgcgggtt
701 ttgtccacca gtccaacgga cagagccgtc ccgaatcgcg ttcgtggaac
751 aggatttatg ccatggcagg catggaatgg ggcaaatgga cggtgattcc
801 gcgcgtgtgg gtgcgtgcgt tcgatcagag cggcgataaa aacgacaatc
851 ccgatattgc cgactatatg gggatggcg acgtgaagct gcagtaccgc
901 ctgaacgaca ggcagaatgt gtattccgta ttgcgctaca accccaaaac
951 gggctacggc gcgattgaag ccgcctacac gtttccgatt aagggcaaac
1001 tcaaaggcgt ggtacgcgga ttccacggtt acggcgagag cctgatcgac
1051 tacaaccaca agcagaacgg tatcggtatc gggttgatgt tcaacgactg
1101 ggacggcatc tga

```

This corresponds to the amino acid sequence <SEQ ID 1786; ORF 582.ng>:

```

g582.pep ..
  1 MRYILLTGLL PTASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
 51 EQQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLVREH NPMYLMPPWY NNSPNYAPSS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA ENLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVI PRVW VRAFDQSGDK NDNPDADYM GYGDKVLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGKLGKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMPNDWDGI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1787>:

```
m582.seq ..
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAA CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTTGAAAAA GGCAGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTG
301 AGCCTGATGT ACGACTTGGA CAAAACGAT TTGCGCGGGC TGTGGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAAATTCG
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGACAGC AGAAACGTGC GGAACCAAAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TTAACACCCG CGCGGATCTG TGGTTCGGCT
551 ACAGCAAGAC ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCGCA ATACGGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCGTTCG GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTTAC CCATGGCAGG CATGGAATGG GGCAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCCT TCGATCAGAG CGGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ACCCCAAAAC
951 GGGCTACGCG CCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA
```

This corresponds to the amino acid sequence <SEQ ID 1788; ORF 582>:

```
m582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGQ
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRLLGVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQKRAETK LQVSFASKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYD GYGDVVKLYR
301 LNDQRNVYSV LRYNPKTVYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *
```

m582 / g582 98.6% identity in 370 aa overlap

m582.pep	10	20	30	40	50	60
	MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
g582	MRYILLTGLLPTASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN					
	10	20	30	40	50	60
m582.pep	70	80	90	100	110	120
	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
g582	LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRLLGVREH					
	70	80	90	100	110	120
m582.pep	130	140	150	160	170	180
	NPMYLMPLWYNNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFASKIAEDLFKTRADL					
g582	NPMYLMPLWYNNNSPNYAPSSPTRGTTVQEKFGQKRAETKLQVSFASKIAENLFKTRADL					
	130	140	150	160	170	180
m582.pep	190	200	210	220	230	240
	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
g582	WFGYTQRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNQ					
	190	200	210	220	230	240
m582.pep	250	260	270	280	290	300
	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVVKLYR					
g582	QSRPESRSWNRIYAMAGMEWGKLTVIPRVWVRAFDQSGDKNDNPDADYMGYGDVVKLYR					
	250	260	270	280	290	300
	310	320	330	340	350	360

905

```

m582.pep      LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
|||||
g582          LNDQRNVYSVLRYNPKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
                310      320      330      340      350      360

                370
m582.pep      GLMFNDLDGIX
|||||
g582          GLMFNDWDGIX
                370

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1789>:

```

a582.seq
1  ATGCGCTATA TTCTTTTGAC AGGACTGTTG CCGATGGCAT CCGCTTTTGG
51  AGAGACCGCG CTGCAATGCG CCGCTTTGAC GGACAATGTT ACGCGTTTGG
101 CGTGTTACGA CAGGATTTT GCGGCACAGC TTCCGTCTTC GGCAGGGCAG
151 GAAGGGCAGG AGTCGAAAGC CGTACTCAAT CTGACGGAAG CCGTCCGCAG
201 CAGCCTGGAT AAGGGCGAGG CGGTCATTGT TGTGAAAAA GGCGGGGATG
251 CGCTTCCTGC CGACAGTGCG GCGGAAACCG CCGACATCTA TACGCCTTTC
301 AGCCTGATGT ACGACTTGA CAAAAACGAT TTGCGCGGGC TGTGCGGCGT
351 ACGCGAACAC AATCCGATGT ACCTTATGCC GCTCTGGTAC AACAATTCGC
401 CCAACTATGC CCCGGGTTTC CCGACGCGCG GTACGACTGT ACAGGAAAAA
451 TTCGGACAGC AGAAACGTGC GGAAACCAA TTGCAGGTTT CGTTCAAAAG
501 CAAAATTGCC GAAGATTTGT TAAAACCCG CGCGGATCTG TGGTTCGGCT
551 ACACCCAAAG ATCCGATTGG CAGATTTACA ACCAAGGCAG GAAATCCGCG
601 CCGTTCCGCA ATACGATTA CAAACCTGAA ATTTTCCTGA CCCAGCCTGT
651 GAAGGCGGAT TTGCCGTTTC GCGGCAGGCT GCGTATGCTC GGTGCGGGTT
701 TTGTCCACCA GTCCAACGGA CAGAGCCGTC CCGAATCGCG TTCGTGGAAC
751 AGGATTTACG CCATGGCAGG CATGGAATGG GGCAAATTGA CGGTGATTCC
801 GCGCGTGTGG GTGCGTGCGT TCGATCAGAG CCGCGATAAA AACGACAATC
851 CCGATATTGC CGACTATATG GGGTATGGCG ACGTGAAGCT GCAGTACCGC
901 CTGAACGACA GGCAGAATGT GTATTCCGTA TTGCGCTACA ATCCCAAAC
951 GGGCTACGGC GCGATTGAAG CCGCCTACAC GTTTCGATT AAGGGCAAAC
1001 TCAAAGGCGT GGTACGCGGA TTCCACGGTT ACGGCGAGAG CCTGATCGAC
1051 TACAACCACA AGCAGAACGG TATCGGTATC GGGTTGATGT TCAACGACTT
1101 GGACGGCATC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1790; ORF 582.a>:

```

a582.pep
1  MRYILLTGLL PMASAFGETA LQCAALTDNV TRLACYDRIF AAQLPSSAGO
51  EGQESKAVLN LTETVRSSLD KGEAVIVVEK GGDALPADSA GETADIYTPL
101 SLMYDLKND LRGLLVREH NPMYLMPLWY NNSPNYAPGS PTRGTTVQEK
151 FGQQKRAETK LQVSFKSKIA EDLFKTRADL WFGYTQRSDW QIYNQGRKSA
201 PFRNTDYKPE IFLTQPVKAD LPFGGRLRML GAGFVHQSNQ QSRPESRSWN
251 RIYAMAGMEW GKLTVIPRVW VRAFDQSGDK NDNPDADYM GYGDVKLQYR
301 LNDQRNVYSV LRYNPKTGYG AIEAAYTFPI KGLKGVVRG FHGYGESLID
351 YNHKQNGIGI GLMFNDLDGI *

```

m582/a582 100.0% identity in 370 aa overlap

```

                10      20      30      40      50      60
m582.pep      MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
|||||
a582          MRYILLTGLLPMASAFGETALQCAALTDNVTRLACYDRIFAAQLPSSAGQEGQESKAVLN
                10      20      30      40      50      60

                70      80      90      100     110     120
m582.pep      LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLVREH
|||||
a582          LTETVRSSLDKGEAVIVVEKGGDALPADSAGETADIYTPLSLMYDLKNDLRGLLVREH
                70      80      90      100     110     120

                130     140     150     160     170     180

```

906

```

m582.pep      NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
|||||
a582          NPMYLMPLWYNNSPNYAPGSPTRGTTVQEKFGQKRAETKLQVSFKSKIAEDLFKTRADL
              130      140      150      160      170      180

              190      200      210      220      230      240
m582.pep      WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG
|||||
a582          WFGYTQSRSDWQIYNQGRKSAPFRNTDYKPEIFLTQPVKADLPFGGRLRMLGAGFVHQSNG
              190      200      210      220      230      240

              250      260      270      280      290      300
m582.pep      QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDADIADYMGYGDVKLQYR
|||||
a582          QSRPESRSWNRIYAMAGMEWGKLTVI PRVWVRAFDQSGDKNDNPDADIADYMGYGDVKLQYR
              250      260      270      280      290      300

              310      320      330      340      350      360
m582.pep      LNDQRNVYSVLRYPNKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
|||||
a582          LNDQRNVYSVLRYPNKTGYGAIEAAYTFPIKGLKGVVRGFHGYGESLIDYNHKQNGIGI
              310      320      330      340      350      360

              370
m582.pep      GLMFNDLDGIX
|||||
a582          GLMFNDLDGIX
              370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1791>:

g583.seq..

```

1   atgataattg accaaagcca aatatttacc catcttgcc tctgtgcctt
51  ttgcgggatt ggagccgtaa ctgccggcaa tcgactgcat aatcggatgt
101 ataatgccgc cgccgcgcgc ggtattggaa ggggtaacgg gagccagcag
151 cagttcggaa agagcgagac tgtaaccgat gccacgcgtt tttcttccaa
201 aaacggcgat aaacaaatat ccgatacgca tccccagccc tgttttgagc
251 aaaccgcgcg aatcataaac tgcgatggca atcagccaaa tcaacggatt
301 ggcgaacgca ctcaacgcat cgctcatcgc cgcgcccggt ttgtcggcgg
351 ttacgccggt tactgcgacc aaccgcacgg caataatcga cagcgcgccc
401 aacggcataa ccttgccgat aatggcggca atcacaccga caaacatagc
451 cagcagcgtc caagcctgag gcttgacccc gtcgggtacg ggcagtgcca
501 aaaccagggc gcacaatact gcggcaatgg cgaggggtat cggtttgaaa
551 cccaatttca tcatattgac ctccgtaaaa aagaccgtcc cgaaaaatcg
601 gaaaaataa

```

This corresponds to the amino acid sequence <SEQ ID 1792; ORF 583.ng>:

g583.pep..

```

1   MIIDQSQIFT HLAFAFCGI GAVTAGNRLH NRMYNAAAAR GIGRGNGSQQ
51  QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIAGR RARFVGGYAG YCDQPDGNNR QRAQRHNLAD NGGNHTDKHS
151 QQRPSLRLLD VGYGQCQNGQ AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1793>:

m583.seq..

```

1   ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51  TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCgcgc GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCGGAA AGAGCGAGAC TGTAACCGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTTGAGC
251 AAACCGCGCG AATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCGCCCGGT TTGTGCGCGG
351 TTACGCCGGT TACTGCGACC AACCgcacgg CAATAATCGA CAGCGCGCCC
401 AACGGCATGG CTTGccgat AATGGCGGCA ATCACACCGA CAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACcagggc GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA

```

907

551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1794; ORF 583>:

m583.pep..

1 MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RARFVGGYAG YCDQPDGNNR QRAQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583 / g583 98.5% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
	:					
g583	10	20	30	40	50	60
	MIIDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					
	:					
m583.pep	70	80	90	100	110	120
	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRIGERTQRIahr RARFVGGYAG					
g583	70	80	90	100	110	120
	AQRFSKNGDKQISDTHPQPCFEQTARNHNC DGNQPNQRIGERTQRIahr RARFVGGYAG					
m583.pep	130	140	150	160	170	180
	YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY					
g583	130	140	150	160	170	180
	YCDQPDGNNRQRAQRHNLADNGGNHTDKHSQQRPSLRLLDPVGYGQCQNQGAQYCGNGEGY					
m583.pep	190	200				
	RFETQFHHIDLRRKKDRPEKSEKX					
g583	190	200				
	RFETQFHHIDLRRKKDRPEKSEKX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1795>:

a583.seq

1 ATGATAGTTG ACCAAAGCCA AATATTTACC CATCTTGCCT TCTGTGCCTT
51 TTGCGGGATT GGAGCCGTAA CTGCCGGCAA TCGACTGCAT AATCGGATGT
101 ATAATGCCGC CGCCGCGCGC GGTATTGGAA GGGGTAACGG GAGCCAGCAG
151 CAGTTCCGAA AGAGCGAGAC TGTAAACGAT GCCCAGCGTT TTTCTTCCAA
201 AAACGGCGAT AAACAAATAT CCGATACGCA TCCCCAGCCC TGTTTGAGC
251 AAACCGCGC AAATCATAAC TGCGATGGCA ATCAGCCAAA TCAACGGATT
301 GGCGAACGCA CTCAACGCAT CGCTCATCGC CGCACCCGGT TTGTCCGGCG
351 TTACGCGGT TACTGCGACC AACCCGACGG CAATAATCGA CAGCGCACCC
401 AACGGCATGG CTTGCGGAT AATGGCGGCA ATCACACCGA TAAACATGGC
451 CAGCAGCGTC CAAGCCTGAG GCTTGACCCC GTCGGGTACG GGCAGTGCCA
501 AAACCAAGGC GCACAATACT GCGGCAATGG CGAGGGGTAT CGGTTTGAAA
551 CCCAATTTCA TCATATTGAC CTCCGTAAAA AAGACCGTCC CGAAAAATCG
601 GAAAAATAA

This corresponds to the amino acid sequence <SEQ ID 1796; ORF 583.a>:

a583.pep

1 MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ
51 QFGKSETVTD AQRFSKNGD KQISDTHPQP CFEQTARNHN CDGNQPNQRI
101 GERTQRIahr RTRFVGGYAG YCDQPDGNNR QRTQRHGLAD NGGNHTDKHG
151 QQRPSLRLLDP VGYGQCQNQG AQYCGNGEGY RFETQFHHID LRKKDRPEKS
201 EK*

m583/a583 99.0% identity in 202 aa overlap

m583.pep	10	20	30	40	50	60
	MIVDQSQIFT HLAFC AFCGI GAVTAGNRLH NRMYNAAAAR GIGRNGSQQ QFGKSETVTD					

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```

a583      MIVDQSQIFTHLAFCAFCGIGAVTAGNRLHNRMYNAAAARGIGRNGSQQFGKSETVTD
              10      20      30      40      50      60

              70      80      90      100     110     120
m583.pep  AORFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRARFVGGYAG
            |||
a583      AORFSSKNGDKQISDTHPQPCFEQTARNHNCDGNQPNQRIGERTQRIAHRRTRFVGGYAG
              70      80      90      100     110     120

              130     140     150     160     170     180
m583.pep  YCDQPDGNNRQRAQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
            |||
a583      YCDQPDGNNRQRTQRHGLADNGGNHTDKHGQQRPSLRLDPVGYGQCQNQGAQYCGNGEGY
              130     140     150     160     170     180

              190     200
m583.pep  RFETQFHHIDLRRKKDRPEKSEKX
            |||
a583      RFETQFHHIDLRRKKDRPEKSEKX
              190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1797>:

g584.seq..

```

1  atgtgcggtt ctattttggc ggcttccctg ctggcggtat cttttccggc
51  ggcggctgag gcattgaatt acaatattgt cgaattttcc gaatcggcgg
101 gtatcgaggt ggctcaggat acaatgtccg cgcgtttcca ggtggcggcg
151 gaaggacggg acaaaaatgc cgtcaatgcc gagtttggtt aaaaattcaa
201 caatttcacc agaaaatcga aaaatggtag ctttaaaacc gaattggtat
251 cgcgcgagtgc gatgccgcgc tatcaatata ccaacggcag acgcattcaa
301 acaggctggg aggagcgtgc ggaatttaag gcggaggcca gggattttga
351 tgctttaaac cgttttattg ctgatgttca gacggatgct tcgcttgaag
401 ataccgattt cagcgtgtcg cgcgaacgcc gaaacgaggt catcgatcag
451 gtcagcaagg atgccgtttt gcgtttcaag gcgcgtgccg aaaaactggc
501 gggcgttctg ggtgcgtccg gttataaaat cgtcaaattg aattttgggc
551 aaatcggcag ccatattgcg ggcgatgggg ctgttcgggc aaaaatgctg
601 cgcgcgatgc cgatggcggc aagcgtcaat atgaagggtg cggattcagc
651 cgcaccgggt gtggaggaaa tcagcatcag catcaatggg acggttcagt
701 tctaa

```

This corresponds to the amino acid sequence <SEQ ID 1798; ORF 584.ng>:

g584.pep Length:..

```

1  MLRSILAASL LAVSFPAAAE ALNYNIVEFS ESAGIEVAQD TMSARFQVAA
51  EGRDKNAVNA EFVKKFNNFT RSKKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK AEGRDFDALN RFIADVQTD SLEDTDFSVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAGVL GASGYKIVKL NFGQIGSHIA GDGAVRAKML
201 RAMPMAASVN MKGTDSAAPG VEEISISING TVQF*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1799>:

m584.seq..

```

1  ATGTTGCGTC TTGTTTGGC GGCTTCGCTG TCGGCGGTAT CTTTCCGGC
51  AGCGGCTGAA GCATTGAATT ACAATATTGT CGAATTTTCC GAATCGGCGG
101 GTGTCGAGGT GGCTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG ACAAAAATGC CGTCAATGCT GAGTTTGTTA AAAAAATCAA
201 CAAGTTCATC AGAAAAATCGA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGCATTCAA
301 ACAGGCTGGG AGGAGCGTGC GGAATTAAAG GTCGAAGGTA GAGATTTTGA
351 TGAGTTAAAC CGTTTTATTG CCGATATTCA AGCAGATGCC GCGTTGGMAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCKATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCGCG
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1800; ORF 584>:

m584.pep..

```

1  MLRLVLAASL SAVSFPAAAE ALNYNIVEFS ESAGVEVAQD TMSARFQVTA
51  EGRDKNAVNA EFVKKFNKFI RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRDFDELN RFIADIQADA ALXYTDFHVS RERRNEVIXQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584 / g584 89.7% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep    MLRLVLAASLSAVSFPAAAEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584        MLRSILAASLLAVSFPAAAEALNYNIVEFSSESAGIEVAQDTMSARFQVAAEGRDKNVNA
              10      20      30      40      50      60

              70      80      90      100     110     120
m584.pep    EFVKKFNKFIKRSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEEAEFKVEGRDFDELN
              ||||| : | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584        EFVKKFNNTFRKSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEEAEFKAEGRDFDALN
              70      80      90      100     110     120

              130     140     150     160     170     180
m584.pep    RFIADIQADAALXYTDFHVSERRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL
              ||||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584        RFIADVQTDASLEDTFVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL
              130     140     150     160     170     180

              190     200     210     220     230
m584.pep    NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVEEISISVNGTVQFX
              | : | |||| | |||| | |||| | |||| | |||| | |||| | |||| |
g584        NFGQIGSHIAGDGAVRAKMLRAMPMAASVNMKGTDGSAAPGVEEISISINGTVQFX
              190     200     210     220     230

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1801>:

a584.seq

```

1  ATGTTGCGTT CTATTTTGGC GGCTTCCTCG CTG.....
51  .....ATTGT CGAATTTTCT GAATCGGCGG
101 GTGTCGAGGC GGTTCAGGAT ACAATGTCCG CACGTTTCCA AGTGACGGCG
151 GAAGGACGGG AAAAAATGC CGTCAATGCC GAGTTTGTTA AAAAATTCAA
201 CAATTTTACC AGAAAATCAA AAAATGGTAG CTTTAAACC GAATTGGTAT
251 CGCGCAGTGC GATGCCGCGC TATCAATATA CCAACGGCAG ACGATTCAA
301 ACAGGTTGGG AGGAGCGTGC GGAATTTAAG GTCGAGGGTA GGAATTTTGA
351 TGC GTTGAAC CGTTTATTG CCGATGTTCA GGCAGATGCC GCGTTGGAAT
401 ATACGGATTT CCATGTGTCG CGCGAACGCC GCAACGAGGT CATCGATCAG
451 GTCAGCAAGG ATGCCGTTTT GCGTTTCAAG GCGCGTGCCG AAAAGTTGGC
501 GGGCGTTTTG GGTGCGTCCG GTTATAAAAT CGTCAAATTG AATTTGGGAC
551 ACATCGGCAG CCATATCGCG GGAGGGGGAG CTGCTCAGGC AAAAATGCTT
601 CGTGCCATGC CGATGGCGGC AAGCGTCAAT ATGGAGGGTG CGGATTCCGC
651 CGCGCCTGGT GTGGAGGAAA TCAGCATCAG CGTCAATGGG ACGGTTTCAGT
701 TCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1802; ORF 584.a>:

a584.pep

```

1  MLRSILAASL L..... IVEFS ESAGVEAVQD TMSARFQVTA
51  EGRDKNAVNA EFVKKFNFT RSKNGSFKT ELVSRSAMPR YQYTNRRRIQ
101 TGWEERAEFK VEGRNFDALN RFIADVQADA ALEYTDFHVS RERRNEVIDQ
151 VSKDAVLRFK ARAEKLAVL GASGYKIVKL NLGHIGSHIA GGGAAQAKML
201 RAMPMAASVN MEGADSAAPG VEEISISVNG TVQF*

```

m584/a584 88.9% identity in 234 aa overlap

```

              10      20      30      40      50      60
m584.pep    MLRLVLAASLSAVSFPAAAEALNYNIVEFSSESAGVEVAQDTMSARFQVTAEGRDKNVNA
              ||| : |||| | |||| | |||| | |||| | |||| | |||| | |||| |
a584        MLRSILAASLL-----IVEFSSESAGVEAVQDTMSARFQVTAEGRDKNVNA
              10      20      30      40

```

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	70	80	90	100	110	120
m584.pep	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEERAEFKVEGRDFDELN					
a584	EFVKKFNKFIRKSKNGSFKTELVSRSAMPYQYTNRRRIQTGWEERAEFKVEGRNFDALN					
	50	60	70	80	90	100
	130	140	150	160	170	180
m584.pep	RFIADIQADAALXYTDFHVSRRRNEVIXQVSKDAVLRFKARAELAGVLGASGYKIVKL					
a584	RFIADVQADAALXYTDFHVSRRRNEVIDQVSKDAVLRFKARAELAGVLGASGYKIVKL					
	110	120	130	140	150	160
	190	200	210	220	230	
m584.pep	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
a584	NLGHIGSHIAGGGAAQAKMLRAMPMAASVNMEGADSAAPGVVEEISISVNGTVQFX					
	170	180	190	200	210	220

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1803>:

g585.seq..

```

1  atgaaactgt  tccaacgcat  tttcgccaca  ttttgcgcgg  ttatcgctctg
51  cgcaatcttt  gtggcgagtt  tttctttttg  gctggtgcag  aacacccttg
101  ccgaaaacca  attcaaccaa  cgccgcacca  tcgaaaccac  attgatgggc
151  agcattattt  ccgcattcaa  gacacggggc  gacaacggcg  cgcgcgaaat
201  cctgaccgaa  tggaaaaaca  gccccgtctc  atccgcggtt  tacgtcatac
251  agggcgacga  gaaaaaagac  atcttaaac  gctatatcga  caattacacc
301  atagaacgcg  cccggctgtt  tgccgcgaac  aacccccatt  ccaaccttgt
351  ccgcatacga  tacgaccgtt  tcggcggaaga  atacctgttc  ttcattaaag
401  gctgggacaa  ccaccaggca  caacgcctgc  ccagcccgct  gtttatcccg
451  ggccctgcgc  ttgccccgat  ttggcacgaa  ttcacatcat  tctccttcac
501  catcattgtc  ggactgctga  tggcatatat  ccttgccggc  aacattgcca
551  aaccatcag  aatcttaggc  aacggcatgg  acagggtggc  agaacgagaa
601  cttgaagacc  gcgtttgcca  acaggttcgc  gaccgcgacg  acgaattggc
651  cgatgttgcc  atgcaattcg  acacaatggt  ggaaaaactg  gaataa

```

This corresponds to the amino acid sequence <SEQ ID 1804; ORF 585.ng>:

g585.pep..

```

1  MKLFORIFAT  FCAVIVCAIF  VASFSFWLVQ  NTLAENQFNQ  RRTIETTLMG
51  SIISAFKTRG  DNGAREILTE  WKNSPVSSAV  YVIQGDDEKD  ILNRYIDNYT
101  IERARLFAAN  NPHSNLVRIE  YDRFGEEYLF  FIKGWDNHQA  QRLPSPLFIP
151  GLPLAPIWHE  FIILSFIIIV  GLLMAYILAG  NIAKPIRILG  NGMDRVAERE
201  LEDRVCQQVR  DRDDELADVA  MQFDTMVEKL  E*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1805>:

m585.seq..

```

1  ATGAACTGT  TCCAACGCAT  TTTCCGCCACA  TTTTGCGCGG  TTATCGTCTG
51  TGCAATCTTT  GTGGCGAGTT  TTTCTTTCTG  GCTGGTGCGA  AACACCCTTG
101  CCGAAAACCA  GTTCAACCAA  CGCCGCACCA  TCGAAACCAC  TTTGATGGGC
151  AGCATCATTT  CCGCATTCG  GGCACGCGGG  GACGCGGGTG  CGCGCGAAAT
201  CCTGACGGAA  TGGAAAAGCA  GCCCCGTCTC  ATCGGGCGTG  TACGTTATAC
251  AGGGCGACGA  GAAAAAGAT  ATCCTGAACC  GGTATATCGA  CAGCTATACC
301  ATCGAACGCG  CCCGGCTTTT  CGCCGCCGGA  CACCCGCATT  CCAACCTCGT
351  CCATATCGAA  TACGACCGCT  TCGGCGAAGA  ATACCTGTTC  TTCACCAAAG
401  ACTGGGACAA  ACTCCAAGCC  CGCCGCCCTG  CCAGCCCCCT  GTTGATCCCC
451  GGCCTGCCGC  TCGCCCCGAT  TTGGCACGAA  CTCATCATAT  TGTCTTCAT
501  CATCATCGTC  GGACTGCTGA  TGGCATATAT  CCTCGCCGGC  AACATTGCCA
551  AACCCATCAG  AATCTTAGGC  AACGGCATGG  ACAGGGTGGC  AAACGGAGAA
601  CTTGAAACCC  GTATCTCCCA  ACAGGTCGAC  GACCGCGACG  ACGAATTGTC
651  CCATCTTGCC  ATCCAATTCT  ACAAAATGGT  GGAAAAACTC  GAAAAACTCG
701  TTGCCAAGA  ACGCCACCTG  CTCCATCACG  TCTCCCATGA  AATGCGTTCT
751  CCCCTTGCGC  GCATGCAGGC  AATTGTCGGA  CTGATTCAGG  CGCAGCCCCA
801  AAAACAGGAG  CAATATCTCA  AACGGCTGGA  AGGCGAACTG  ACCCGCATGG
851  ATACGCTGGC  CGGGGAACCT  TTAACCCCTG  CCCGTCTCGA  AACTTCCAAT
901  ATGGCTTTGG  AAAAAGAAAG  CCTGAAACTC  CTGCCCTTCC  TGGGCAACCT
951  GGTAGAAGAC  AATCAAAGCA  TTGCCCAGAA  AAACGGACAA  ACGGTTACCC
1001  TGTCTGCCGA  CGGAAAAATC  CCCGAAACA  CAACCATCCT  TGCCAACGAA

```



```

1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGACTGGGGC TTGCATTGAC CCAACATATT ATGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCCAAGAA AAAAACCAGT TCCAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1806; ORF 585>:

m585.pep..

```

1 MKLFQIRIFAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGGDEKDD ILNRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLIP
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDDELSHLA IQFDKMVEKL EKLVAKERHL LHHVSHEMRS
251 PLARMQAIIV LIQAQPKQKE QYLKRLEGEL TRMDTLAGE LTLRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTSLADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNYSPG GSTILINIGQ DHKHIIIDVT DNGPGVDEMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHCGKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585 / g585 88.3% identity in 231 aa overlap

```

          10      20      30      40      50      60
m585.pep  MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFRARG
          |||
g585       MKLFQIRIFATFCAVIVCAIFVASFSFWLVQNTLAENQFNQRTIETTLMGSIISAFKTRG
          10      20      30      40      50      60

          70      80      90      100     110     120
m585.pep  DAGAREILTEWKDSPVSSGVYVIQGGDEKDDILNRYIDSYTIERARLFAAGHPHNSNLVHIE
          | |||
g585       DNGAREILTEWKNSPVSSAVYVIQGGDEKDDILNRYIDNYTIERARLFAANNPHNSNLVRIE
          70      80      90      100     110     120

          130     140     150     160     170     180
m585.pep  YDRFGEEYLFFTKDWKQLQARRLPSPLLIPGLPLAPIWHELIILSFIIIVGLLMAYILAG
          |||
g585       YDRFGEEYLFYIKGWDNHQAQRLPSPLFIPGLPLAPIWHEFIILSFIIIVGLLMAYILAG
          130     140     150     160     170     180

          190     200     210     220     230     240
m585.pep  NIAKPIRILGNGMDRVANGELETRISQQVDDRDDELSHLAIQFDKMVEKLEKLVAKERHL
          |||
g585       NIAKPIRILGNGMDRVAERELEDRCVQQRDRDDELADVAMQFDTMVEKLEX
          190     200     210     220     230

          250     260     270     280     290     300
m585.pep  LHHVSHEMRSPLARMQAIIVGLIQAQPKQKEQYLKRLEGELTRMDTLAGE LTLRLETSN

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1807>:

a585.seq

```

1 ATGAAACTGT TCCAACGCAT CTTCGCCACA TTTTGCGCGG TTATCGTCTG
51 TGCAATCTTT GTGGCGAGTT TTTCTTTCTG GCTGGTGCAG AACACCCTTG
101 CCGAAAACCA GTTCAACCAA CGCCGCACCA TCGAAACCAC TTTGATGGGC
151 AGCATCATT CCGCATTCCG GGCACGCGGG GACGCGGGTG CGCGCGAAAT
201 CCTGACGGAA TGGAAAGACA GCCCCGTCTC ATCGGGCGTG TACGTTATAC
251 AGGGCGACGA GAAAAAGAT ATCCTGCACC GGTATATCGA CAGCTACACC
301 ATCGAACGCG CCCGGCTTTT CGCCGCCGGA CACCCGCATT CCAACCTCGT
351 CCATATCGAA TACGACCGCT TCGGCGAAGA ATACCTGTTC TTCACCAAAG
401 ACTGGGACAA ACTCCAAGCC CGCCGCCTGC CCAGCCCCCT GTTGATCCCC
451 GGCCTGCCGC TCGCCCGAT TTGGCACGAA CTCATCATAT TGTCCTTCAT
501 CATCATCGTC GGA CTGCTGA TGGCGTACAT CCTCGCCGGC AACATTGCCA
551 AATCCATCAG AATCTTAGGC AACGGCATGG ACAGGGTGGC AAACGGAGAA
601 CTTGAAACCC GTATCTCCCA ACAGGTCGAC GACCGCGACG ACGAATTGTC

```

```

651 CCATCTTGCC ATCCAATTCC ACAAATGGT GGAAAACTC GAAAACTCG
701 TTGCCAAGA ACGCCACCTG CTCCATCAG TCTCCCATGA AATGCGTTCT
751 CCCCTTGCGC GCATGCAGGC AATTGTCGGA CTGATTCAGG CGCAGCCCCA
801 AAAACAGGAG CAATATCTCA AACGGCTGGA AGGCGAACTG ACCCGCATGG
851 ATACGCTGGC CGGGGAAGT TTAACCCTGT CCCGTCTCGA AACTTCCAAT
901 ATGGCTTTGG AAAAAGAAAG CCTGAACTC CTGCCCTTCC TGGGCAACCT
951 GGTAGAAGAC AATCAAAGCA TTGCCAGAA AAACGGACAA ACGGTTACCC
1001 TGTCTGCCGA CGGAAAAATC CCCGAAAACA CAACCATCCT TGCCAACGAA
1051 AGCTACCTGT ACCGCGCCTT CGACAACGTC ATCCGCAACG CCGTCAACTA
1101 CAGTCCCGAA GGCAGCACCA TCCTGATCAA CATCGGACAA GACCACAAAC
1151 ACTGGATAAT CGACGTTACC GACAACGGCC CCGGCGTGGA CGAAATGCAG
1201 CTCCCGCACA TCTTCACCGC TTTCTACCGT GCAGACTCCA GTGCCAACAA
1251 ACCCGGAACA GGAAGGGGCG TTGCATTGAC CCAACATATT ATTGAACAGC
1301 ACTGCGGCAA AATCATCGCC GAAAACATCA AACCGAACGG TCTGCGGATG
1351 CGCTTTATCC TGCCAAGAA AAAAACCGGT TCCAAAACAG AAAAAAGTGC
1401 GAACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1808; ORF 585.a>:

a585.pep

```

1 MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG
51 SIISAFRARG DAGAREILTE WKDSPVSSGV YVIQGDEK KD ILHRYIDSYT
101 IERARLFAAG HPHSNLVHIE YDRFGEEYLF FTKDWDKLQA RRLPSPLLI P
151 GLPLAPIWHE LIILSFIIIV GLLMAYILAG NIAKPIRILG NGMDRVANGE
201 LETRISQQVD DRDEL SHLA IQFDKMVEKL EKLVA KERHL LHHVSHEMRS
251 PLARMQAIVG LIQAQPQKQE QYLRLEGE LTRMDTLAGE L LTLSRLETSN
301 MALEKESLKL LPFLGNLVED NQSIAQKNGQ TVTLSADGKI PENTTILANE
351 SYLYRAFDNV IRNAVNY SPE GSTILINIGQ DHKHWIIDVT DNGPGVD EMQ
401 LPHIFTAFYR ADSSANKPGT GLGLALTQHI IEQHC GKIIA ENIKPNGLRM
451 RFILPKKKTG SKTEKSAN*

```

m585/a585 99.8% identity in 468 aa overlap

	10	20	30	40	50	60
m585.pep	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
a585	MKLFQRI FAT FCAVIVCAIF VASFSFWLVQ NTLAENQFNQ RRTIETTLMG SIISAFRARG					
	10	20	30	40	50	60
	70	80	90	100	110	120
m585.pep	DAGAREILTEWKDSPVSSGVYVIQGDEK KDILNRYIDSYTIERARLFAAGHPHSNLVHIE					
a585	DAGAREILTEWKDSPVSSGVYVIQGDEK KDILHRYIDSYTIERARLFAAGHPHSNLVHIE					
	70	80	90	100	110	120
	130	140	150	160	170	180
m585.pep	YDRFGEEYLF FTKDWDKLQARRLPSPLLI PGLPLAPIWHE LIILSFIIIVGLLMAYILAG					
a585	YDRFGEEYLF FTKDWDKLQARRLPSPLLI PGLPLAPIWHE LIILSFIIIVGLLMAYILAG					
	130	140	150	160	170	180
	190	200	210	220	230	240
m585.pep	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKERHL					
a585	NIAKPIRILGNMGMDRVANGELETRISQQVDDRDEL SHLA IQFDKMVEKLEKLVAKERHL					
	190	200	210	220	230	240
	250	260	270	280	290	300
m585.pep	LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLRLEGE LTRMDTLAGE L LTLSRLETSN					
a585	LHHVSHEMRSPLARMQAIVGLIQAQPQKQE QYLRLEGE LTRMDTLAGE L LTLSRLETSN					
	250	260	270	280	290	300
	310	320	330	340	350	360
m585.pep	MALEKESLKL LPFLGNLVEDNQSIAQKNGQ TVTLSADGKI PENTTILANESYLYRAFDNV					
a585	MALEKESLKL LPFLGNLVEDNQSIAQKNGQ TVTLSADGKI PENTTILANESYLYRAFDNV					

	310	320	330	340	350	360
m585.pep	370	380	390	400	410	420
	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
a585	IRNAVNYSPEGSTILINIGQDHKHWIIDVTDNGPGVDEMQLPHIFTAFYRADSSANKPGT					
	370	380	390	400	410	420
m585.pep	430	440	450	460	469	
	GLGLALTQHIIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
a585	GLGLALTQHIIIEQHCGKIIAENIKPNGLRMRFILPKKKTGSKTEKSANX					
	430	440	450	460		

g586.seq..

g586.pcp..

m586.seq

m586.pcp

m586.pep 10 20 30 40 50 60
MAAHLEEQQELDNFKYFWKTTGKWLFALLILAAALGYLGTYVQNRKVSONQEAAAVLANI
| | | | | | | | | | | | | | | | | | | | | | | | | | | | : |

914

```

g586      MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

m586.pep  70      80      90      100     110     120
VEKAQSKAPQSEINAELTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
g586      VEKAQNKAPQSEINAELSKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120

m586.pep  130     140     150     160     170     180
QKDSLILQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
g586      QKDSLILQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQKSQEA
           130     140     150     160     170     180

m586.pep  190     200     210
LKNYGQALEKMPQDSVGRELQMKLDSLKX
g586      LKNYGQALEKMPQDSVGRELLQMKLDSLKX
           190     200     210

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1813>:

```

a586.seq
1   ATGGCAGCCC ATTTGGAAGA ACAACAAGAG TTGGACAACT TTAAATATTT
51  TTGGAAAACC ACGGGCAAAT GGCTGTTTGC CGTGCTGATT TTGGCGGCAC
101 TCGGCTACTT GGGATACACG GTTTACCAAA ACCGTGCGGC TTCCCAAAAT
151 CAGGAAGCGG CGGCGGTGCT GGCAACATC GTGGAAAAGG CGCAAAACAA
201 AGCCCCGCAA AGCGAAATCA ATGCCGAATT GGCCAAGCTC CAACAAGACT
251 ACCCCCATT CATTTCGCC GCGCAAGCCA CGCTGATGGC GCGAGCAACC
301 GAATTTGACG CGCAGCGTTA CGATGTTGCC GAAGGCCATT TGAAATGGGT
351 ATTGTC AAC CAAAAAGACA GCCTGATCCA GCGTGTGGCG GCGCAGCGTC
401 TGGGCGTTGT GTTGTGCAA CAAAAAAAT ACGATGCCGC GCTTGCCGCA
451 CTCGACACGC CGGTTGAAGC GGACTTCGCC CCCCTGCTGA TGGAAACCAA
501 AGGCGATGTC TATGCCGCAC AGGGAAAAAG CCAGGAAGCC TTAATAAACT
551 ACGGACAGGC TTTAGAAAAA ATGCCTCAAG ATTCTGTCGG TCGCGAATTG
601 GTTCAAATGA AACTTGATTC GCTGAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1814; ORF 586.a>:

```

a586.pep
1   MAAHLEEQQE LDNFKYFWKT TGKWLFAVLI LAALGYLGYT VYQNRAASON
51  QEAAAVLANI VEKAQNKAPQ SEINAELAKL QSYPHSISA AQATLMAAAT
101 EFDAQRYDVA EGHKLKWLNSN QKDSLILQALA AQLGVVLLQ QKKYDAALAA
151 LDTPVEADFA PLLMETKGDV YAAQGSQEA LKNYGQALEK MPQDSVGREL
201 VQMKLDSLK*

m586/a586 97.6% identity in 209 aa overlap

           10      20      30      40      50      60
m586.pep  MAAHLEEQQEELDNFKYFWKTTGKWLFAALLILAAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60
a586      MAAHLEEQQEELDNFKYFWKTTGKWLFAVLI LAALGYLGYTVYQNRAASQNQEAAAVLANI
           10      20      30      40      50      60

           70      80      90      100     110     120
m586.pep  VEKAQSKAPQSEINAELTKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120
a586      VEKAQNKAPQSEINAELAKLQSYPHSISAAQATLMAAAATEFDAQRYDVAEGHLKWLNSN
           70      80      90      100     110     120

           130     140     150     160     170     180
m586.pep  QKDSLILQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180
a586      QKDSLILQALAAQRLGVVLLQKKYDAALALDTPVEADFAPLLMETKGDVYAAQGSQEA
           130     140     150     160     170     180

```

915

```

                190      200      210
m586.pep      LKNYGQALEKMPQDSVGRELVMKLDLKLX
                |||
a586          LKNYGQALEKMPQDSVGRELVMKLDLKLX
                190      200      210

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1815>:

```

g587.seq..
1  atgaaacgta tctttttgcc cgccttgccc gccatcctgc ctttatccgc
51 ttatgccgac ctgcccttga cgattgaaga cataatgacc gacaagggaa
101 aatggaaact ggaaacttcc cttacctatc tgaatagcga aaacagccgc
151 gccgcacttg ccgcaccggt ttacattcaa accggcgcaa cctcgtttat
201 ccccatctcg accgaaattc aagaaaacgg cagcaatacc gatatgctcg
251 ccggcacgct cggtttgccg tacggactga ccggcaatac cgacatttac
301 ggacgaggca gctatctgtg gcacgaagaa cgcaaactcg acggcaacgg
351 caaaacccgc aacaaacgga tgtccgacat atccgcggcg atcagccaca
401 ccttccttaa agacggcaaa aaccccgccc taatcagctt tcttgaaagc
451 acggtttacg aaaaatcgcg caacaaagcc tcgttaatca aaaaaagggg
501 gctttgcccc tttataact taaggataaa ttatgaatat taa

```

This corresponds to the amino acid sequence <SEQ ID 1816; ORF 587.ng>:

```

g587.pep..
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNS
51 AALAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLAGTLGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDISAG ISHTFLKDGK NPALISFLES
151 TVYEKSRNKA SLIKRGLCP FYNLRINYEY *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1817>:

```

m587.seq..
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCAC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGAA
101 AATGGAAACT GGAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACCTG CCGCACCGGT TTACATTCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCGG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TCGGCACGCT CGGTTTGCGC TACGGACTGA CCGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTG ACGGCAACAG
351 CAAAACCCGC AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CTTTCCTTAA AGACGACAAA AACCCCGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATAGA TCCGATTGTC CTTTCCCTCA
551 CCGCCGCTA CCGCATCAAC GGCAGCAAAA CCCTTTCAGA CGGCATCCGC
601 TACAAATCGG GCAACTACCT GCTGCTCAAC CCCAACATCT CATTGCTGTC
651 CAACGACAGA ATCAGCCTGA CCGGAGGCAT CCAATGGCTG GGCAGGCAGC
701 CCGACCGGAC GGACGGCAAA CGGGAATCCT CCAGAAACAC ATCCACCTAC
751 GCCCATTTTC GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTCCGAA CTGAAATTTG
851 GCGTACAGCA TACATTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1818; ORF 587>:

```

m587.pep..
1  MKRIFLPALP AILPLSTYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNS
51 AELAAPVYIQ TGATSFIPIP TEIQENGSTNT DMLVGTGLR YGLTGNTDIY
101 GSGSYLWHEE RKLDGNSKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPIV LSLTAAYRIN GSKTSLSDGIR
201 YKSGNYLLN PNISFAANDR ISLTGGIQWL GRQPDRTDGK RESSRNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m587 / g587 95.0% identity in 161 aa overlap

10 20 30 40 50 60

916

```

m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          ||||||||||||||||:||||||||||||||||||||||||||||||:|| |||||
g587       MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          ||||||||||||||||:||||||||||||||||||||||||||||||:|||
g587       TGATSFIPTEIQENGSDMLAGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

          130     140     150     160     170     180
m587.pep  NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV
          |||||:| ||||| ||||| ||||| ||||| ||||| ||||| |||||
g587       NKRMSDISAGISHTFLKDGKNPALISFLESTVYEKSRNKASLIKKRGLCPFYNLIRINYEY
          130     140     150     160     170     180

          190     200     210     220     230     240
m587.pep  LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK
g587       X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1819>:

```

a587.seq
1  ATGAAGCGCA TCTTTTGGCC CGCCTTGCCC GCCATCCTGC CTTTATCCGC
51 TTATGCCGAC CTGCCCTTGA CGATTGAAGA CATAATGACC GACAAGGGCA
101 AATGGAAACT GGAAACTTCC CTTACCTACC TGAACAGCGA AAACAACCGC
151 GCCGAACTTG CCGCACCGGT TTACATCCAA ACCGGCGCAA CCTCGTTTAT
201 CCCCATTCCG ACCGAAATCC AAGAAAACGG CAGCAATACC GATATGCTCG
251 TTGGCAGGCT CGGTTTGGCG TACGGACTGA CCGGGAATAC CGACATTTAC
301 GGCAGCGGCA GCTATCTGTG GCACGAAGAA CGCAAACCTCG ACGGCAACGG
351 CAAAACCCGA AACAAACGGA TGTCCGACGT ATCCCTCGGC ATCAGCCACA
401 CCTTCCTTAA AGACGACAAA AACCCTGCCC TAATCAGCTT TCTTGAAAGC
451 ACGGTTTACG AAAAATCGCG CAACAAAGCC TCGTCGGGAA AATCCTGGCT
501 CATCGGCGCC ACCACCTACA AAGCCATCGA CCCCCTCGTC CTCTCATTGA
551 CCGCTGCCTA CCGTATCAAC GGCAGCAAAA CCCTTTCAAG CAACACCAAA
601 TACAAAGCAG GCAATTACTG GATGCTGAAT CCCAATATAT CCTTCGCCGC
651 CAACGACAGA ATCAGCCTCA CGGGCGGCAT CCAATGGCTG GGCAAGCAGC
701 CCGACCGTCT GGACGGCAAA AAAGAATCCG CAAGAAACAC ATCCACCTAT
751 GCCCATTTCT GCGCAGGTTT CGGTTTCACC AAAACCACGG CTTTAAACGC
801 ATCCGCACGT TTCAACGTTT CAGGGCAAAG CAGTTCGAA CTGAAATTTG
851 GCGTACAGCA TACGTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1820; ORF 587.a>:

```

a587.pep
1  MKRIFLPALP AILPLSAYAD LPLTIEDIMT DKGKWKLETS LTYLNSENNR
51 AELAAPVYIQ TGATSFIPTE IQENGSDML VGTGLRLY YGLTGNTDIY
101 GSGSYLWHEE RKLDGNGKTR NKRMSDVSLG ISHTFLKDDK NPALISFLES
151 TVYEKSRNKA SSGKSWLIGA TTYKAIDPVV LSLTAAYRIN GSKTLSSNTK
201 YKAGNYWMLN PNISFAANDR ISLTGGIQWL GKQPDRLDGK KESARNTSTY
251 AHFGAGFGFT KTTALNASAR FNVSGQSSE LKFGVQHTF*

```

m587/a587 95.2% identity in 289 aa overlap

```

          10      20      30      40      50      60
m587.pep  MKRIFLPALPAILPLSTYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          ||||||||||||||||:||||||||||||||||||||||||||||||:|||
a587       MKRIFLPALPAILPLSAYADLPLTIEDIMTDKGKWKLETSLTYLNSENNAELAAPVYIQ
          10      20      30      40      50      60

          70      80      90      100     110     120
m587.pep  TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNSKTR
          ||||||||||||||||:||||||||||||||||||||||||||||||:|||
a587       TGATSFIPTEIQENGSDMLVGTGLRLYGLTGNTDIYSGSYLWHEERKLDGNGKTR
          70      80      90      100     110     120

```

917

	130	140	150	160	170	180
m587.pep	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPIV					
a587	NKRMSDVSLGISHTFLKDDKNPALISFLESTVYEKSRNKASSGKSWLIGATTYKAIDPVV					
	130	140	150	160	170	180
	190	200	210	220	230	240
m587.pep	LSLTAAYRINGSKTLSDGIRYKSGNYLLNPNISFAANDRISLTGGIQWLGRQPDRTDGK					
a587	LSLTAAYRINGSKTLSSNTKYKAGNYWMLNPNISFAANDRISLTGGIQWLKGQPDRLDGK					
	190	200	210	220	230	240
	250	260	270	280	290	
m587.pep	RESSRNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
a587	KESARNTSTYAHFGAGFGFTKTALNASARFNVSGQSSSELKFGVQHTFX					
	250	260	270	280	290	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1821>:

```

g588.seq
1  atgcttaaac atctcgcat cctactgccc gccatgatgt tcgccctccc
51  cgcccagacc gccgtcctaa gcccctatca ggaaaccggc tgcacctacg
101 aaggcgggat cggaagac gggcttcctt caggcaaagg catatggcgt
151 tgccgggatg ggcgcggtta taccggttca ttcaaaaacg gcaaattcga
201 cgggcaaggc gtttataacc ttgccgcggt ccgcgaagta tttctcgagc
251 cgttcaattc cgacagtacc aaattccgca atatggcatt gtcgggcacg
301 ttcaacaag gcttggcaca cggcaggttc gccgcctcgc aaaacggcga
351 aaccctcttt tattatgaaa tgcgaacacg gcatgattaa

```

This corresponds to the amino acid sequence <SEQ ID 1822; ORF 588.ng>:

```

g588.pep..
1  MLKHLAFLLP AMMFALPAQT AVLSPYQETG CTYEGGIGKD GLPSGKGIWR
51  CRDGRGYTGS FKNGKFDGQG VYTVAAGREV FLEPFNSDST KFRNMALSGT
101 FKQGLAHGRF AASQNGETLF YYEMRTRHD*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1823>:

```

m588.seq..
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51  CACTTCGGCC GCCGTCCTGA CTCCTATCA AGAACCAGGC TGCACCTACG
101 ACGGCAATGT CGGCAAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCTG TTTAAAAACG GCAAATTCGA
201 CGGGCAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCCGCA ACATGGTACT CTCGGGCACG
301 TTCAAAAAAG GCTTGGCACA CCGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAC
401 TGCCCAAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1824; ORF 588>:

```

m588.pep..
1  MLKHLAFLLP AMMFALPTSA AVLTSYQEPG CTYDGNVGKD GKPAKGKTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FLEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m588 / g588 82.5% identity in 120 aa overlap

10 20 30 40 50 60

918

```

m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||
g588         MLKHLAFLLPAMMFALPAQTAVLSPYQETGCTYEGGIGKDGKPSGKGIWRCRDGRGYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             |||||
g588         FKNGKFDGQGVYTVAAAGREVLFEPFNSDSTKFRNMALSGTFKQGLAHGRFAASQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMIKEVKLPKNKX
g588         YYEMRTRHDX
             130

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1825>:

```

a588.seq
1  ATGCTTAAAC ATCTCGCATT CCTACTGCCC GCCATGATGT TCGCCCTCCC
51 CGCCGCGTCC GCCGTTCTGA CTTCTATCA AGAACCCGGC TGCACCTACG
101 AAGGCGATGT CGGCAAGAC GGTAAACCCG CCGGCAAAGG CACATGGCGC
151 TGCCAAGACG GCGCAACTA TACCGGTTCTG TTAAAAATG GCAAATTCGA
201 CGGACAAGGC GTTTATACCG TTGCCGCCAA CCGCGAAATA TTTATCGAAC
251 CGTTCAATTC CGACAGTACC AAATTCGCA ACATGGTACT CTCGGGCACA
301 TTCAAAAAG GCTTGGCACA CGGCAGATTT ACCGTCTCGC AAAACGGCGA
351 AACCCTCTTC ATTATGAAAT GCGAAAACGG CATGATTAAA GAAGTGAAGC
401 TGCCCCAAAA CAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1826; ORF 588.a>:

```

a588.pep
1  MLKHLAFLLP AMMFALPAAS AVLTSYQEPG CTYEGDVGKD GKPAGKGTWR
51  CQDGRNYTGS FKNGKFDGQG VYTVAANREI FIEPFNSDST KFRNMVLSGT
101 FKKGLAHGRF TVSQNGETLF IMKCENGMIK EVKLPKNK*

m588/a588    96.4% identity in 138 aa overlap

             10      20      30      40      50      60
m588.pep    MLKHLAFLLPAMMFALPTSAAVLTSYQEPGCTYDGNVGKDGKPKAGKGTWRCQDGRNYTGS
             |||||
a588         MLKHLAFLLPAMMFALPAASAVLTSYQEPGCTYEGDVGKDGKPKAGKGTWRCQDGRNYTGS
             10      20      30      40      50      60

             70      80      90      100     110     120
m588.pep    FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             |||||
a588         FKNGKFDGQGVYTVAAANREIFIEPFNSDSTKFRNMVLSGTFKKGLAHGRFTVSQNGETLF
             70      80      90      100     110     120

             130     139
m588.pep    IMKCENGMIKEVKLPKNKX
             |||||
a588         IMKCENGMIKEVKLPKNKX
             130

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1827>:

```

g589.seq..
1  atgcaacaaa aaatccggtt ccaaatcgag gcgatgacct gtcaggcatg
51  tgcttcgctg attgaaaaag tggtgaacaa aaaagatttt gtcgaatcgg
101 cgggagtgaa ctttgccagt gaggaagcgc aggttacgtt tgacggcagc
151 aaaacctcgg ttgccgacat tgccaaaatc attgagaaaa ccggttacgg
201 cgcgaaggaa aaaacggaag atacattgcc gcaacctgaa gcagaacacc
251 atatcgctg gcggttgctg cttttgctga ccatcaatat cccgttcctt

```



```

301 atcgggatgg tagggatgat gctaaaaggg ctgaattgga caccggcacga
351 ttggatgatt ccgcctgtat ggcagtttgt actggcaagc atagtgaac
401 tttggctggc aatcccgttt tacaaaagcg cgtgggcaag cattaaggc
451 gggctggcga atatggacgt actcgttacc atcggcacgg tgctgattta
501 cctgtattcc gtttatatgc tgtttttcag ttcgcatgcg gcgcacggta
551 tggcgcatgt gtattttgaa gcgggcggtga tggatgacgg ttttgtgtcg
601 ctgggtaagt ttttggaaca ccgcacaaaa aaatccagcc tgaacagctt
651 gggcttactg ctaaaactca cgccgaccca agtcaacgtg caacgcaacg
701 gcgaatggaa acaactgccc atcgaccaag tgcaaatcgg cgaccttacc
751 cgcaccaacc acggcggaacg catcgctgcc gacggcatta tcgaaagcgg
801 cagcgggttg gcggacgaaa gccaccttac cggcgaatcc aatcccgaag
851 agaaaaaggc gggcggaaca gtgttgccgg gcgcgctgat gaccgaaggc
901 agcgtggtgt accgcgccgc gcagctcggc agccaaaccc tgctcggcga
951 catgatgaac gcgctctctg aagcacaagg cagttaaagca ccgattgcgc
1001 gcgtggccga taaagcggcg gcggtatttg tgccaaactgt cgtgggcatc
1051 gcgcttctga cttttatcgt tgcttggtcg attaaggcg attggacggt
1101 cgcactgatg cagcgcgttg ccgttttggg gattgcctgc ccgtgcgcgc
1151 tcggtctggc gacccctgcc gcgattatgg tcggcatggg caaagcgggtg
1201 aaacacggca tttggtttta agacgcggcg gcaatggagg aagcagccca
1251 cgtcgatgcc gtcgtatttg acaaaaccgg tacgctgacc gaaggcaggc
1301 cgcaggttg cgccgtttat tacgttccc acagcggctt tgacgaagac
1351 gctttgtacc gcatcgccgc cgccgtcgag caaaacgcgc cccaccgct
1401 cgcccgccgc atcgtctccg ccgcacaagc gcgcggtttg gagattcccg
1451 ctgcacaaaa tgcgcaaac gttgtcggag caggcattac cgccgaagtg
1501 gaaggcgtgg gtttggtgaa atcaggcaaa gccgaatttg ccgaactgac
1551 cttgccgaag ttttcagacg gcgtttggga aatcgccagt gcggttaccg
1601 tatctgtaaa cggcaaacgc atcggcgcat tcgcactctc cgacgcgttg
1651 aaagccgata ccgccgaagc cataggccgt ctgaaaaaac acaatatcga
1701 tgtctatatt atgagcggcg ataaccaaaag tacggctcga tacgtcgcca
1751 aacaactggg catcgcacac gccttcggta atatgagtc gtgcgacaaa
1801 gccgccgaag tgcagaaaact caaagccgcc ggcaaaaccc tggcgatggt
1851 cggcgacggc atcaacgacg cgcccgcgct tgccgcgcgc aacgtcagct
1901 tcgccatgaa aggcgggtgc gacgttgccg aacacaccgc ctccgccacg
1951 ctgatgcagc attcgggtcaa tcagctcgcc gatgccctgc tgatatcgca
2001 ggcaacgttg gaaaacatca agcaaaacct atttttcgcc ttcttctaca
2051 atatattggg cattccgctc gccgcgctcg gctttttaaa tcccgtcata
2101 gcaggcgcgg caatggcggc aagctcggtt tcggtatttg gcaatgccct
2151 gcgcctgaaa tgggtaaaaa tcgattga

```

This corresponds to the amino acid sequence <SEQ ID 1828; ORF 589.ng>:

g589.pep..

```

1  MQQKIRFQIE AMTCQACASR IEKVLNKKDF VESAGVNFAS EEAQVTFDGS
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLTINIPFL
101 IGVMGMLKLG LNWTRHDWMI PPVWQFVLAS IVQLWLAIPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSSHA AHGMAHVYFE AGVMVIGFVS
201 LGKFLHRTK KSSLNSLGLL LKLTPTQVNV QRNGEWKQLP IDQVQIGDLI
251 RTNHGERIAA DGIIESGSGW ADESHLTGES NPEEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMMN ALSEAQGSKA PIARVADKAA AVFVPTVVGI
351 ALLTFIVAWL IKGDWTVAlM HAVAVLVIAc PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGRPQVAAYV YVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPAAQNAQT VVGAGITAEV
501 EGVGLVKSGK AEFAELTLPK FSDGVWEIAS AVTVSVNGKP IGAFALSDAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQSTVE YVAKQLGIAH AFGNMSPCDK
601 AAEVOKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGK DVAEHTASAT
651 LMQHSVNQLA DALLISQATL ENIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLGNALRLK WVKID*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1829>:

m589.seq..

```

1  ATGCAACAAA AAATCCGTTT CCAAATCGAA GGCATGACCT GCCAGGCCTG
51  CGCTTCGCGC ATTGAAAAAG TGTGTAACAA AAAAGATTTT GTCGAATCGG
101 CGGGGGTAAA CTTCGCCAGC GAAGAGGCGC AGGTAGTGTT TGACGACAGC
151 AAAACCTCAG TAGCCGACAT TGCCAAAATC ATTGAGAAAA CCGGTTACGG
201 CGCGAAGGAA AAAACGGAAG ATACATTGCC GCAACCCGAA GCAGAACACC
251 ATATCGGCTG GCGGCTGTGG CTGCTGTTCA CCATCAACGT CCCGTTCTTT

```

920

```

301 ATCGGCATGG CGGGGATGAT GATCGGCAGA CACGATTGGA TGATTCCGCC
351 GTTGTGGCAG TTCGCATTGG CAAGCGTGGT GCAGCTTTGG CTGGCAATCC
401 CGTTTTACAA AAGCGCGTGG GCGAGCATT AAGGCGGACT GGCGAATATG
451 GACGTGCTGG TTACCATCGG CACGGTCTCG ATTTACCTGT ATTCCGTCTA
501 TATGCTGTTT TTCAGCCCGC ACGCGGCGTA CGGTATGGCG CATGTGTATT
551 TTGAAGTGGG CGTGATGGTG ATCGGTTTTG TGTCACGGG TAAATTTTTG
601 GAACACCGTA CCAAAAAATC CAGCCTCAAC AGCTTGGGCT TGCTGCTCAA
651 ACTTACACCA ACCCAAGTCA ACGTGCAACG CAACGCGGAA TGGAAACAGC
701 TTCCCATCGA CCAAGTGCAA ATCGGCGACC TTATCCGCGC CAACCACGGC
751 GAACGCATTG CCGCAGACGG CATCATTGAA AGCGGCAGCG GTTGGGCGGA
801 CGAGAGCCAT CTTACCGGCG AATCCAATCC TGAAGAAAAA AAGGCGGGCG
851 GCAAAGTGTT GCGGCGGCGG TTAATGACCG AAGGCAGTGT GGTGTACCGC
901 GCCACGCAGC TCGGCAGCCA AACCAGCTC GGCACATGA TGAACGCGCT
951 CTCTGAAGCA CAAGGCAGTA AAGCACCGAT TGCGCGCGTA GCCGATAAAG
1001 CGGCTGCGGT ATTCGTGCCT GCCGTCGTGG GCATTGCGTT GTTGACTTTT
1051 ATTGTTACTT GGCTGATTAA GGGCGATTGG ACGGTTGCGC TGATGCACGC
1101 CGTCGCCGTT TTGGTGATTG CCTGCCCGTG CGCGCTGGGT CTGGCAACCC
1151 CTGCCGCGAT TATGGTCGGT ATGGGCAAAG CGGTAAACA CGGTATTTGG
1201 TTTAAAGACG CGGCAGCAAT GGAGGAAGCC GCCCACGTCG ATGCCGTCGT
1251 GTTGGACAAA ACCGGTACGC TGACCGAAGG CAGCCCGCAG GTTGCCGCGC
1301 TTTATTGCGT TCCCGACAGC GGCTTTGACG AAGACGCTTT GTACCGCATC
1351 GCCGCCGCCG TCGAACAAAA CGCCGCCCAT CCGCTCGCCC GTGCCATCGT
1401 CTCCGCCGCC CAAGCGCGCG GTTGGACAT TCCCGCGCA CAAAACGCAC
1451 AAACCGTTGT CGGCGCAGGC ATTACCGCCG AAGTGGAAGG CGTGGGTTTG
1501 GTGAAAGCAG GCAAAGCCGA ATTTGCCGAA CTGGCCTTGC CGAAGTTTTT
1551 AGACGGCGTT TGGGATATTG CAAGCATTGT TCGGCTCTCA GTCCGCATCA
1601 AACCATCGG CGCATTGCGA CTTGCCGACG CGTTGAAAGC CGATACCGCC
1651 GAAGCCATAG GCCGTCTGAA AAAACACAAT ATCGATGTCT ATATTATGAG
1701 CGGCGACAAC CAAGGCACGG TCGAATACGT CGCCAAACAA CTGGGCATCG
1751 CACACGCCTT CGGCAACATG AGTCCGCGCG ATAAAGCTGC CGAAGTGCAA
1801 AAACCTCAAAG CCGCCGGCAA AACCGTGCGG ATGGTCGGCG ACGGCATCAA
1851 CGACGCGCCC GCGCTTGCCG CCGCTAACGT CAGCTTCGCC ATGAAAGGCG
1901 GAGCGGACGT TGCCGAACAT ACCGCATCCG CCACGCTGAT GCAGATTTCG
1951 GTCAACCAAC TCGCCGATGC TCTGCTGGTG TCGCAAGCCA CTTTGAAAAA
2001 CATCAAGCAA AACCTGTTTT TCGCCTTCTT CTACAATATT TTGGGCATTC
2051 CTCTCGCCGC GCTTGGCTTT TTAAATCCCG TCATCGCTGG CGCGGCAATG
2101 GCGGCAAGCT CGGTTTCCGT GTTGAGCAAT GCCTTGCGCC TGAACGGGT
2151 AAAATCGAT TAG

```

This corresponds to the amino acid sequence <SEQ ID 1830; ORF 589>:

m589.pep..

```

1  MQQKIRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLFTINVPFLL
101 IGMAGMMIGR HDWMIPPLWQ FALASVVQLW LAIPFYKSAW ASIKGGLANM
151 DVLVTIGTVS IYLYSVYMLF FSPHAAYGMA HVYFEVGMVM IGFVSLGKFL
201 EHRTKKSSLN SLGLLLKLTP TQVNVQRNGE WKQLPIDQVQ IGDILIRANHG
251 ERIAADGIIE SGSGWADESH LTGESNPEEK KAGGKVLAGA LMTEGSVVYR
301 ATQLGSQTQL GDMMNALSEA QGSKAPIARV ADKAAAVFVP AVVGIALLTFL
351 IVTWLIKGDW TVALMHAVAV LVIACPCALG LATPAAIMVG MGKAVKHGIW
401 FKDAAMEEAA AHVDAVVLDK TGTLTEGSPQ VAAVYCVFDS GFDEDALYRI
451 AAAVEQNAAH PLARAIVSAA QARGLDIPAA QNAQTVVGAG ITAEVEGVGL
501 VKAGKAEFAE LALPKFLDGV WDIASIVAVS VDNKPIGAFA LADALKADTA
551 EAIGRLKKHN IDVYIMSGDN QGTVEYVAKO LGIAHAFGNM SPRDKAAEVQ
601 KLKAAGKTVA MVGDGINDAP ALAAANVSFA MKGGADVAEH TASATLMQHS
651 VNQLADALLV SQATLKNIKQ NLFFAFFYNI LGIPLAALGF LNPVIAGAAM
701 AASSVSVLSN ALRLKRVKID *

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m589 / g589 94.2% identity in 725 aa overlap

```

              10      20      30      40      50      60
m589.pep  MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANKI
            |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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921

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g589      MQQKIRFQIEAMTCQACASRIEKVLNKKDFVESAGVNFASEEAQVTFDGSKTSVADIAKI
           10      20      30      40      50      60

           70      80      90      100     1      110
m589.pep  IEKTGYGAKEKTEDTLQPQEAHHIGWRLWLLFTINVPFLIGMAGMMIG-----RHDWMI
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IEKTGYGAKEKTEDTLQPQEAHHIGWRLWLLLTINIPFLIGMVGMMMLKGLNWTNRHDWMI
           70      80      90      100     110     120

           120     130     140     150     160     170
m589.pep  PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
           ||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||
g589      PPVWQFVLASIVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSSHA
           130     140     150     160     170     180

           180     190     200     210     220     230
m589.pep  AYGMAHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           |:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      AHGMAHVYFEAGVMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
           190     200     210     220     230     240

           240     250     260     270     280     290
m589.pep  IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      IDQVQIGDLIRTNHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG
           250     260     270     280     290     300

           300     310     320     330     340     350
m589.pep  SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFFIVTWL
           |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
g589      SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPTVVVGIALLTFFIVAWL
           310     320     330     340     350     360
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922

	360	370	380	390	400	410
m589.pep	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
g589	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
	370	380	390	400	410	420
	420	430	440	450	460	470
m589.pep	VVLDKTGTLTEGSPQVAAYVCVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
g589	VVLDKTGTLTEGRPQVAAYVVPDSGFDEDALYRIAAVEQNAAHPLARAIVSAAQARGL					
	430	440	450	460	470	480
	480	490	500	510	520	530
m589.pep	DIPAAQNAQTVVGAGITAEVEGVGLVKAGKAFAELALPKFLDGVWDIASIVAVSVDNKP					
g589	EIPAAQNAQTVVGAGITAEVEGVGLVKSAGKAFAELTLPKFSDGVWEIASAVTVSVNGKP					
	490	500	510	520	530	540
	540	550	560	570	580	590
m589.pep	IGAFALADALKADTAEAIIGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
g589	IGAFALSDALKADTAEAIIGRLKKHNIDVYIMSGDNQSTVEYVAKQLGIAHAFGNMSPCDK					
	550	560	570	580	590	600
	600	610	620	630	640	650
m589.pep	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
g589	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
	610	620	630	640	650	660
	660	670	680	690	700	710
m589.pep	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
g589	DALLISQATLENIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLGNALRLK					
	670	680	690	700	710	720
	720					
m589.pep	RVKIDX					
g589	WVKIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1831>:

a589.seq	1	ATGCAACAAA	AAGTCCGTTT	CCAAATCGAA	GGCATGACCT	GCCAGGCATG
	51	TGCTTCGCGC	ATTGAAAAAG	TGTTGAACAA	AAAAGATTTT	GTGCAATCGG
	101	CGGGGGTAAA	CTTCGCCAGC	GAAGAGGCTC	AGGTAGTGTT	TGACGACAGC
	151	AAAACCTCAG	TAGCCGACAT	TGCCAAATC	ATTGAGAAAA	CCGGTTACGG
	201	CGCGAAGGAA	AAAACGGAAG	ATACATTGCC	GCAACCCGAA	GCAGAACACC
	251	ATATCGGCTG	GAGGTTGTGG	CTTTTGCTGG	CCATCAATAT	CCCGTTCCTT
	301	ATCGGTATGG	TAGGGATGAT	GCTAAAAGGG	CTGAATTGGA	CACGGCATGA
	351	TTGGATGTTG	TCGCCCTTGT	TGCAGTTTGC	ATTGGCGAGT	GTGGTGCAGC
	401	TTTGGCTGGC	GGTGCCATTT	TACAAAAGCG	CGTGGGCGAG	CATTAAAGGC
	451	GGGCTGGCGA	ATATGGACGT	ACTCGTTACC	ATCGGCACGG	TCTCGATTTA
	501	CCTGTATTCC	GTCTATATGC	TGTTTTTCAG	CCCGCACGCG	GCGTACGGTA
	551	TGGCGCATGT	GTATTTTGAA	GTAGGCATAA	TGGTGATTGG	TTTTGTGTCA
	601	CTGGGTAAAT	TTTTGGAACA	CCGCACAAA	AAATCCAGCC	TGAACAGCTT
	651	GGGCTTGCTG	CTCAAACCTCA	CGCCAACCCA	AGTCAACGTG	CAACGCGATG
	701	GCGAATGGCG	GCAGCTACCC	ATCGACCAAG	TGCAATCGG	CGACCTAATC
	751	CGCGCCAATC	ACGGCGAACG	CATTGCCGCC	GACGGCATCA	TAGAAAGCGG
	801	CAGCGGCTGG	GCGGACGAAA	GCCATCTTAC	CGGCGAATCC	AATCCCGAAG
	851	AGAAAAAGGC	AGGCGGCAAA	GTATTGGCGG	GCGCGCTGAT	GACTIONAGGC
	901	ACGCTGGTGT	ACCGCGCCGC	GCAGCTCGGC	AGCCAAACCC	TGCTCGGCGA
	951	CATGATGAAC	GCGCTCTCCG	AAGCGCAAGG	CAGTAAAGCA	CCGATTGCGC
	1001	GTGTGGCGGA	CAAGGCGGCG	GCGGTATTCG	TGCCTGCCGT	TGTGGGCATC
	1051	GCACTTTTGA	CTTTTATCGC	TACTTGGCTG	ATTAAGGGCG	ATTGACGCT
	1101	CGCATTGATG	CACGCCGTCG	CCGTTTTGGT	GATTGCCTGC	CCGTGTGCAC

923

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1151 TCGGTTTGGC AACCCCTGCT GCGATTATGG TCGGTATGGG CAAAGCGGTT
1201 AAACACGGTA TTTGGTTTAA AGACGCGGCA GCAATGGAAG AAGCCGCCCA
1251 CGTTGATGCC GTCGTGCTGG ACAAACCGG CACGCTGACC GAAGGCAAGC
1301 CGCAGGTTGC CGCCGTTTAT TGTGTTCCCG ACAGCGGCTT TGACGAAGAC
1351 GCTTTGTACC GCATCGCCGC CGCCGTCGAA CAAAACGCCG CCCATCCGCT
1401 CGCCCGTGCC ATCGTCTCCG CCGCCCAGGC GCGCGGTTTG GAGATTCCCA
1451 CCGCACAAAA TGCCCAAACC ATTGTCGGCG CGGGCATTAC CGCCGAAGTA
1501 AAAGGCGCGG GTTGGTAAA AGCAGGCAAA GCCGAATTTG CCGAACTGAC
1551 CTTGCCGAAG TTTTCAGACG GCGTTTGGGA AATCGCCAGT GTGGTTGCCG
1601 TATCTGTAAG CGGCAACCT ATCGGCGCAT TCGCACTCGC CGACGCGTTG
1651 AAAGCCGATA CCGCCGAAGC CATAGGCCGT CTGAAAAAAC ACAATATCGA
1701 TGCTATATT ATGAGCGGCG ATAACCAAGG CACGGTCGAG TACGTCGCCA
1751 AACAACTGGG CATCGCACAC GCCTTCGGTA ATATGAGTCC GCGCGACAAA
1801 GCGCCCGAAG TGCAGAAACT CAAAGCCGCC GGCAAACCG TGCGATGGT
1851 CGGCGACGGC ATCAACGACG CGCCGCGGCT CGCCGCCGCC AACGTCAGCT
1901 TCGCCATGAA AGCGGTGCA GACGTTGCCG AACACACCGC ATCCGCCACA
1951 CTGATGCAGC ATTCGGTCAA CCAGCTCGCC GATGCGCTAT CGGTATCGCG
2001 AGCGACGTTG AAAAACATCA AGCAAAACCT GTTTTTCGCC TTCTTCTACA
2051 ATATTTTGGG CATTCCGCTC GCCGCGCTCG GCTTTTTTAA CCCCCTCATC
2101 GCAGGCGCGG CAATGGCGGC AAGCTCGGTT TCCGTGTTGA GCAACGCCTT
2151 GCGCCTGAAA CGGGTAAAAA TCGATTGA

```

This corresponds to the amino acid sequence <SEQ ID 1832; ORF 589.a>:

a589.pep

```

1  MQQKVRFQIE GMTQCACASR IEKVLNKKDF VESAGVNFAS EEAQVVFDDSD
51  KTSVADIANK IEKTGYGAKE KTEDTLPQPE AEHHIGWRLW LLLAINIPFL
101 IGMVGMMLKG LNWTRHDWML SPLLQFALAS VVQLWLAVPF YKSAWASIKG
151 GLANMDVLVT IGTVSIYLYS VYMLFFSPHA AYGMHVYFE VGIMVIGFVS
201 LGKFLEHRTK KSSLNSLGLL LKLTPTQVNV QRDGEWRQLP IDQVQIGDLI
251 RANHGERIAA DGIIESGSW ADESHLTGES NPEKKAGGK VLAGALMTEG
301 SVVYRAAQLG SQTLLGDMN ALSEAQGSKA PIARVADKAA AVFVPAVVGI
351 ALLTFIATWL IKGDWTLALM HAVAVLVIAC PCALGLATPA AIMVGMGKAV
401 KHGIWFKDAA AMEEAAHVDA VVLDKTGTLT EGKQPQAAVY CVPDSGFDED
451 ALYRIAAAVE QNAAHPLARA IVSAAQARGL EIPTAQNAQT IVGAGITAEV
501 KGAGLVKAGK AEFAELTLPK FSDGVWEIAS VVAVSVNGKP IGAFALADAL
551 KADTAEAIGR LKKHNIDVYI MSGDNQGTVE YVAKQLGIAH AFGNMSPRDK
601 AAEVQKLKAA GKTVMVGDG INDAPALAAA NVSFAMKGGG DVAEHTASAT
651 LMQHSVNQLA DALSVSRATL KNIKQNLFFA FFYNILGIPL AALGFLNPVI
701 AGAAMAASSV SVLSNALRLK RVKID*

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m589/a589 94.9% identity in 725 aa overlap

```

10 20 30 40 50 60
m589.pep MQQKIRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||
a589 MQQKVRFQIEGMTQCACASRIEKVLNKKDFVESAGVNFASEEAQVVFDDSKTSVADIANK
10 20 30 40 50 60

70 80 90 100 1 110
m589.pep IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLFTINVPFLIGMAGMMIG----RHDWMI
|||||||||||||||||||||||||||||||||||||||||:|||||:|||||:|||||
a589 IEKTGYGAKEKTEDTLPQPEAEHHIGWRLWLLLAINIPFLIGMVGMMMLKGLNWTRHDWML
70 80 90 100 110 120

120 130 140 150 160 170
m589.pep PPLWQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
|| |||||||||||||||||||||||||||||||||||||||||||||||||||
a589 SPLLQFALASVVQLWLAIPFYKSAWASIKGGLANMDVLVTIGTVSIYLYSVYMLFFSPHA
130 140 150 160 170 180

180 190 200 210 220 230
m589.pep AYGMHVYFEVGMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRNGEWKQLP
|||||||||||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a589 AYGMHVYFEVGIMVIGFVSLGKFLEHRTKKSSLNSLGLLLKLTPTQVNVQRDGEWRQLP
190 200 210 220 230 240

```

924

m589.pep	240	250	260	270	280	290
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
a589	250	260	270	280	290	300
	IDQVQIGDLIRANHGERIAADGIIESGSGWADESHLTGESNPEEKKAGGKVLGALMTEG					
m589.pep	300	310	320	330	340	350
	SVVYRATQLGSQTQLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFIIVTWL					
a589	310	320	330	340	350	360
	SVVYRAAQLGSQTLLGDMMNALSEAQGSKAPIARVADKAAAVFVPAVVGIALLTFIATWL					
m589.pep	360	370	380	390	400	410
	IKGDWTVALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
a589	370	380	390	400	410	420
	IKGDWTLALMHAVAVLVIAACPCALGLATPAAIMVGMGKAVKHGIWFKDAAAMEEAAHVDA					
m589.pep	420	430	440	450	460	470
	VVLDKTGTLTGEGSPQVAAYVCVPDSGFEDDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
a589	430	440	450	460	470	480
	VVLDKTGTLTGEGKQVAAYVCVPDSGFEDDALYRIAAAVEQNAAHPLARAIVSAAQARGL					
m589.pep	480	490	500	510	520	530
	DIPAAQNAQTIVGAGITAEVEGVGLVKAGKAEFAELALPKFLDGVWDIASIVAVSVDNKP					
a589	490	500	510	520	530	540
	EIPTAQNQTIVGAGITAEVKGAGLVKAGKAEFAELTLPKFSDGVWEIASVAVSVNGKP					
m589.pep	540	550	560	570	580	590
	IGAFALADALKADTAEAGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
a589	550	560	570	580	590	600
	IGAFALADALKADTAEAGRLKKHNIDVYIMSGDNQGTVEYVAKQLGIAHAFGNMSPRDK					
m589.pep	600	610	620	630	640	650
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
a589	610	620	630	640	650	660
	AAEVQKLKAAGKTVAMVGDGINDAPALAAANVSFAMKGGADVAEHTASATLMQHSVNQLA					
m589.pep	660	670	680	690	700	710
	DALLVSQATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
a589	670	680	690	700	710	720
	DALSVSRATLKNIKQNLFFAFFYNILGIPLAALGFLNPVIAGAAMAASSVSVLSNALRLK					
m589.pep	720					
	RVKIDX					
a589						
	RVKIDX					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1833>:

g590.seq..

```

1  atgaaaaaac ctttgatttc agttgcggca gtattgctcg gcgttgcttt
51  ggggtacacct tattatttgg gtgtcaaagc agaagaaagt ctgacgcagc
101 agcaaaaaat attgcagaaa acgggctttt tgaccgtcga atcgaccag
151 tatgatcgag gctggtttac ctctacggaa acgacgggtca tccgtctgaa
201 acccgagttg ctgcataatg cgcagaaata cctgccggat aacttgaaaa
251 tagtgttgga acagccggtt acgctggtaa accatatcac gcacggccct
301 ttcgccggcg gattcggcac gcaggcgcac attgaaaccg agttcaaata
351 cgcgctcgaa acggaaaaag ttttggaaacg cttttttggg aaacaagtcc
401 cggtttccct tgccaatacc gtttatttca acggcagcgg taaaatggaa
451 gtcagtggtc cgcgtttcga ttatgaagaa ctgtcgggca tcaggctgca

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501 ctgggaagggc ctgacggggg aaacgggttta tcaaaaaggt ttcaaaagct
551 accgcaacag ctatgatgcg cccttggttca aaatcaagct ggcagacaaa
601 ggcgatgccc cgtttgaaaa agcgcatctt gattcggaat cttcagacgg
651 catcaatccc cttgctttgg gcagcagcaa tctgactttg gaaaaatttt
701 cgctcgaatg gaaagagggg gtcgattaca acgtcaaatt gaacgaactg
751 gtcaaccctcg ttaccgattt gcagatcggc gcgtttatca atcccaacgg
801 cagcatcgca ccttccaaaa tcgaagtcgg caagctggct ttttcaacca
851 agaccggggg atcgggcgcg tttatcgaca gcgaagggcg gttccggttc
901 gatacgttgg tgtacggcga tgaaaaatac ggcccgtg acatccatat
951 cgctgccgaa cacctcgatg cttctgcctt aaccgtattg aaacgcaagt
1001 ttgcacaaat ttctgccaaa aaaatgactg aggaacaaat ccgcaatgat
1051 ttgattgccc cagtcaaaag cgatgccttc ggattattta cccatgaccc
1101 ggtactaaat atcaaaattt tccgtttcac cctgcctcag gaaaaaattg
1151 atgtggggcg aaaaatcatg tttaaaggca tgaagaagga agatttgaac
1201 caattgggac tgatgttaaa gaaaaccgag gcaaacatca gaatgagtat
1251 tccctaaaaa atgttggaag atttggcggg aagtcaggct ggaatatatt
1301 tcagtgtaaa tgccgaagat gaggcggaag ccagagcaag cattgccgat
1351 attaatgaaa cattgcgcct gatgggtggc agtacgggtc aaagtatggc
1401 aagggaaaaa tatcttactt tagacggtaa tcagattgat acggctcattt
1451 cctttaaaaa caacgcctcg aagttaaacc ggaaaacgct gcaaaatgaa
1501 cccgatcctg attttgacga gggagatatg gtttccggcc agccgcatta
1551 a

```

This corresponds to the amino acid sequence <SEQ ID 1834; ORF 590.ng>:

g590.pep..

```

1 MKKPLISVAA VLLGVALGTP YYLGVKAES LTQQKILQK TGFLTVESHQ
51 YDRGWFTSTE TTVIRLKPEL LHNAQKYLDP NLKIVLEQPV TLVNHITHGP
101 FAGGFGTQAH IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFYDYE LSGIRLHWEG LTGETVYQKG FKSYSNSYDA PLFKIKLADK
201 GDAAFEKAHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGRFRF
301 DTLVYGEKEY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTTEEQIRND
351 LTAAVKGDAE GLFTHDPVLN IKIFRFTLPQ GKIDVGGKIM FKGMMKEDLN
401 QLGLMLKKTF ANIRMSIPQK MLEDLAVSQA GNIFSUNAED EAEARASIAE
451 INETLRLMVD STVQSMAREK YLTLDGNQID TVISLKNNAL KLNKGTLLQNE
501 PDPDFDEGDM VSGQPH*

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1835>:

m590.seq (partial) ..

```

1 ..TGGTTTACCT CTATGGAAC GACGGTCATC CGTCTGAAAC CCGAGTTGCT
51 GAATAATGCC CGAAATACC TGCCGGATAA CCGTGAACAA GTGTTTGAAC
101 AGCCGGTTAC GCTGGTTAAC CATATCACGC ACGGCCCTTT CGCCGGCGGA
151 TTCGGCAGC AGGCGTACAT TGAACCCGAG TTCAAATACG CGCCTGAAAC
201 GGAATAAGTT CTGGAACGCT TTTTGGAAA ACAAGTCCCG GCTTCCCTTG
251 CCAATACCGT TTATTTTAAC GGCAGCGGTA AAATGGAAGT CAGTGTTCCT
301 GCCTTCGATT ATGAAGAGCT GTCGGGCATC AG.CTGCACT GGGAAKGCCT
351 GACGGGAGAA ACGGTTTATC AAAAAGGTTT CAAAAGTAC CGGAACGGCT
401 ATGATGCCCC CTTGTTTAAA ATCAAGCTGG CAGACAAAGG CGATGCCGCG
451 TTTGAAAAAG TGCAATTCGA TTCGGAAACT TCAGACGGCA TCAATCCGCT
501 TGCTTTGGGC AGCAGCAATC TGACCTTGA AAAATTCTCC CTAGAATGGA
551 AAGAGGGTGT CGATTACAAC GTCAAGTTAA ACGAACTGGT CAATCTGTGT
601 ACCGATTGTC AGATTGGCGC GTTTATCAAT CCAACGGCA GCATCGCACC
651 TTCCAAAATC GAAGTCGGCA AACTGGCTTT TTCAACCAAG ACCGGGGAAT
701 CAGGCGCGTT TATCAACAGT GAAGGGCAGT TCCGTTTCGA TACACTGGTG
751 TACGGCGATG AAAAATACGG CCCGCTGGAC ATCCATATCG CTGCCGAACA
801 CCTCGATGCT TCTGCCTTAA CCGTATTGAA ACGCAAGTTT GCACAAATTT
851 CCGCCAAAAA AATGACCGAG GAACAAATCC GCAATGATTT GATTGCCGCC
901 GTCAAAGGAG AGGCTTCCGG ACTGTTTACC AACAATCCCG TATTGGACAT
951 TAAAACTTTC GATTTCACGC TGCCATCGGG AAAAAATCGAT GTGGGCGGAA
1001 AAATCATGTT TAAAGACATG AAGAAGGAAG ATTTGAATCA ATTGGGTTTG
1051 ATGCTGAAGA AAACCGAAGC CGACATCAGA ATGAGTATTC CCAAAAAAAT
1101 GCTGGAAGAC TTGGCGGTCA GTCAAGCAGG CAATATTTTC AGCGTCAATG
1151 CCGAAGATGA GCGGGAAGGC AGGGCAAGTC TTGACGACAT CAACGAGACC
1201 TTGCGCCTGA TGGTGGACAG TACGGTTCAG AGTATGGCAA GGGAAAAATA
1251 TCTGACTTTG AACGCGCACC AGATTGATAC TGCCATTTC CTGAAAAACA
1301 ATCAGTTGAA ATTGAACGGT AAAACGTTGC AAAACGAACC GGAGCCGGAT
1351 TTTGATGAAG GCGGTATGTT TTCAGAGCCG CAGCAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1836; ORF 590>:

m590 / g590 93.1% identity in 462 aa overlap

[illegible]

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1837>:

```
a590.seq
1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGCG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA GCGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTACGGA ACGACGGTCA TCCGCTTGAA
201 ACCCGAGTTG CTGCATAATG CGCAGAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTGGA ACAGCCGGTT ACGCTGGTAA ACCATATCAC GCACGGTCCT
301 TTTGCCGGCG GATTTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGTTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCCG CGTTTGAAAA AGTGCATTTT GATTCGGAAA CTTCAGACGG
651 CATCAACCCG CTTGCTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTTT
701 CCTTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAAGCT
751 GTCAATCTTG TTACCGATTT GCAGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAAA TCGAAGTCGG CAAGCTGGCT TTTTCAACCA
851 AGACCGGGGA ATCGGGCGCG TTTATCGATA GCGAAGGGCA GTTCCGTTTT
901 GGCACGCTGG TTTACGGCGA TGAAAAATAC GGCCCTCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACGAAT TTCTGCCAAA AAAATGACTG AAGAACAAAT CCGCAATGAT
1051 TTGATTGCGG CAGTCAAAGG CGAGGCTTCC GGATTATTTA CCCATAACCC
1101 AGTATTGGAC ATTAAACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTTGAAC
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT
1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCGCCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAACGTT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A
```

This corresponds to the amino acid sequence <SEQ ID 1838; ORF 590.a>:

```
a590.pep
1  MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE AGFLTVESHO
51  YERGWTSTE TTVIRLKP EL LHNAQKYL PD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPVSLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNGSIA PSKIEVGKLA FSTKTGESGA FIDSEGQFRF
301 GTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFARISAK KMTEEQIRND
351 LIAAVKGEAS GLFTHNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRLMVD STVQSMAREK YLTLNGDQID TAISLKNNQL KLNKRTLQNE
501 PEPDFDEGGM VSEPQQ*

m590/a590 97.8% identity in 462 aa overlap

m590.pep
10 20 30
WFTSMETTVIRLKPPELLNNARKYLPDNLKT
|||||

a590
30 40 50 60 70 80
VKAEE SLTQQQKILQEAGFLTVESHOYERGWTSTETTVIRLKPPELLHNAQKYL PDNLKT

m590.pep
40 50 60 70 80 90
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPASLANTVYFN
|||||

a590
90 100 110 120 130 140
VLEQPVTLVNHITHGPFAGGFGTQAYIETEFKYAPETEKVLERFFGKQVPVSLANTVYFN

m590.pep
100 110 120 130 140 150
GSGKMEVSVPAFDYEELSGIXLHWEXLTGETVYQKGFKSyrNGYDAPLFKIKLADKGDA
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928

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|||||
a590      GSGKMEVSVPAFDYEEELSGIRLHWEGLTGETVYQKGFKSYRNGYDAPLFKIKLADKGDAA
          150      160      170      180      190      200

          160      170      180      190      200      210
m590.pep  FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          |||||
a590      FEKVHFDSETSDGINPLALGSSNLTLEKFSLEWKEGVDYNVKLNELVNLVTDLQIGAFIN
          210      220      230      240      250      260

          220      230      240      250      260      270
m590.pep  PNGSIAPSKIEVGKLAFFSTKTGESGAFINSEGQFRFDLTVYGDEKYGPLDIHIAAEHLDA
          |||||
a590      PNGSIAPSKIEVGKLAFFSTKTGESGAFIDSEGQFRFGTLVYGDEKYGPLDIHIAAEHLDA
          270      280      290      300      310      320

          280      290      300      310      320      330
m590.pep  SALTVLKRKFAQISAKKMTTEEQIRNDLIAAVKGEASGLFTNNPVLDIKTFRFTLPSGKID
          |||||
a590      SALTVLKRKFARISAKKMTTEEQIRNDLIAAVKGEASGLFTHNPVLDIKTFRFTLPSGKID
          330      340      350      360      370      380

          340      350      360      370      380      390
m590.pep  VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          |||||
a590      VGGKIMFKDMKKEDLNQLGLMLKKTEADIRMSIPQKMLEDLAVSQAGNIFSVNAEDEAEAG
          390      400      410      420      430      440

          400      410      420      430      440      450
m590.pep  RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQNLKLNKTLQNEPEPD
          |||||
a590      RASLDDINETLRLMVDSTVQSMAREKYLTNLNGDQIDTAISLKNQNLKLNKTLQNEPEPD
          450      460      470      480      490      500

          460
m590.pep  FDEGGMVSEPQQX
          |||||
a590      FDEGGMVSEPQQX
          510

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The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1839>:

m590-1.seq

```

1  ATGAAAAAAC CTTTGATTTC GGTGCGGCA GCATTGCTCG GCGTTGCTTT
51  GGGCACGCCT TATTATTGCG GTGTCAAAGC CGAAGAAAGC TTGACGCAGC
101 AGCAAAAAAT ATTGCAGGAA ACGGGCTTCT TGACCGTCGA ATCGCACCAA
151 TATGAGCGCG GCTGGTTTAC CTCTATGGAA ACGACGGTCA TCCGCTCGAA
201 ACCCGAGTTG CTGAATAATG CCCGAAAATA CCTGCCGGAT AACCTGAAAA
251 CAGTGTTGGA ACAGCCGGTT ACGCTGGTTA ACCATATCAC GCACGGCCCT
301 TTCGCCGCGG GATTCGGCAC GCAGGCGTAC ATTGAAACCG AGTTCAAATA
351 CGCGCCTGAA ACGGAAAAAG TTCTGGAACG CTTTTTTGGA AAACAAGTCC
401 CGGCTTCCCT TGCCAATACC GTTTATTTTA ACGGCAGCGG TAAAAATGGAA
451 GTCAGTGTTC CCGCCTTCGA TTATGAAGAG CTGTCGGGCA TCAGGCTGCA
501 CTGGGAAGGC CTGACGGGAG AAACGGTTTA TCAAAAAGGT TTCAAAAGCT
551 ACCGGAACGG CTATGATGCC CCCTTGTTTA AAATCAAGCT GGCAGACAAA
601 GGCGATGCGG CGTTTGAAAA AGTGCATTTC GATTCGGAAA CTTCAGACGG
651 CATCAATCCG CTGCTTTTGG GCAGCAGCAA TCTGACCTTG GAAAAATTCT
701 CCCTAGAATG GAAAGAGGGT GTCGATTACA ACGTCAAGTT AAACGAACTG
751 GTCAATCTTG TTACCGATT TACGATTGGC GCGTTTATCA ATCCCAACGG
801 CAGCATCGCA CCTTCCAAA TCGAAGTCGG CAAACTGGCT TTTTCAACCA
851 AGACCGGGGA ATCAGGCGCG TTTATCAACA GTGAAGGGCA GTTCCGTTTC
901 GATACACTGG TGTACGGCGA TGAAAAATAC GGCCCGCTGG ACATCCATAT
951 CGCTGCCGAA CACCTCGATG CTTCTGCCTT AACCGTATTG AAACGCAAGT
1001 TTGCACAAAT TTCCGCCAAA AAAATGACCG AGGAACAAAT CCGCAATGAT
1051 TTGATTGCCG CCGTCAAAGG AGAGGCTTCC GGACTGTTCA CCAACAATCC
1101 CGTATTGGAC ATTAAAACTT TCCGATTAC GCTGCCATCG GGAAAAATCG
1151 ATGTGGGCGG AAAAATCATG TTTAAAGACA TGAAGAAGGA AGATTGTAAT
1201 CAATTGGGTT TGATGCTGAA GAAAACCGAA GCCGACATCA GAATGAGTAT

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1251 TCCCCAAAAA ATGCTGGAAG ACTTGGCGGT CAGTCAAGCA GGCAATATTT
1301 TCAGCGTCAA TGCCGAAGAT GAGGCGGAAG GCAGGGCAAG TCTTGACGAC
1351 ATCAACGAGA CCTTGCCTCT GATGGTGGAC AGTACGGTTC AGAGTATGGC
1401 AAGGGAAAAA TATCTGACTT TGAACGGCGA CCAGATTGAT ACTGCCATTT
1451 CTCTGAAAAA CAATCAGTTG AAATTGAACG GTAAAAACGT GCAAAACGAA
1501 CCGGAGCCGG ATTTTGATGA AGGCGGTATG GTTTCAGAGC CGCAGCAGTA
1551 A

```

This corresponds to the amino acid sequence <SEQ ID 1840; ORF 590-1>:

m590-1.pep

```

1 MKKPLISVAA ALLGVALGTP YYLGVKAEES LTQQQKILQE TGFLTVESHO
51 YERGWFTSME TTVIRLKPPEL LNNARKYLPD NLKTVLEQPV TLVNHITHGP
101 FAGGFGTQAY IETEFKYAPE TEKVLERFFG KQVPASLANT VYFNGSGKME
151 VSVPAFDYEE LSGIRLHWEG LTGETVYQKG FKSyrNGYDA PLFKIKLADK
201 GDAAFEKVHF DSETSDGINP LALGSSNLTL EKFSLEWKEG VDYNVKLNEL
251 VNLVTDLQIG AFINPNNGSIA PSKIEVGKLA FSTKTGESGA FINSEGQFRF
301 DTLVYGDEKY GPLDIHIAAE HLDASALTVL KRKFAQISAK KMTEEQIRND
351 LIAAVKGEAS GLFTNNPVLD IKTFRFTLPS GKIDVGGKIM FKDMKKEDLN
401 QLGLMLKKTE ADIRMSIPQK MLEDLAVSQA GNIFSVNAED EAEGRASLDD
451 INETLRMLVD STVQSMAREK YLTNGDQID TAISLKNQNL KNGKTLQNE
501 PEPDFDEGGM VSEPQQ*

```

m590-1/g590 93.6% identity in 516 aa overlap

	10	20	30	40	50	60
m590-1.pep	MKKPLISVAA	ALLGVALGTP	YYLGVKAEES	LTQQQKILQE	TGFLTVESHO	YERGWFTSME
g590	MKKPLISVAA	VLLGVALGTP	YYLGVKAEES	LTQQQKILQKT	TGFLTVESHO	YDRGWFTSTE
	10	20	30	40	50	60
m590-1.pep	70	80	90	100	110	120
m590-1.pep	TTVIRLKPPEL	LNNARKYLPD	NLKTVLEQPV	TLVNHITHGP	FAGGFGTQAY	IETEFKYAPE
g590	TTVIRLKPPEL	LHNAQKYL	PDNLKIVLEQ	PVTLVNHITH	GP	FAGGFGTQAH
	70	80	90	100	110	120
m590-1.pep	130	140	150	160	170	180
m590-1.pep	TEKVLERFFG	KQVPASLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
g590	TEKVLERFFG	KQVPVSLANT	VYFNGSGKME	VSVPAFDYEE	LSGIRLHWEG	LTGETVYQKG
	130	140	150	160	170	180
m590-1.pep	190	200	210	220	230	240
m590-1.pep	FKSYRNGYDA	PLFKIKLADK	GDAAFEKVHF	DSETSDGINP	LALGSSNLTL	EKFSLEWKEG
g590	FKSYRNSYDA	PLFKIKLADK	GDAAFEKAH	FDSETSDGIN	PALGSSNLTL	EKFSLEWKEG
	190	200	210	220	230	240
m590-1.pep	250	260	270	280	290	300
m590-1.pep	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FINSEGQFRF
g590	VDYNVKLNEL	VNLVTDLQIG	AFINPNNGSIA	PSKIEVGKLA	FSTKTGESGA	FIDSEGRFRF
	250	260	270	280	290	300
m590-1.pep	310	320	330	340	350	360
m590-1.pep	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGEAS
g590	DTLVYGDEKY	GPLDIHIAAE	HLDASALTVL	KRKFAQISAK	KMTEEQIRND	LIAAVKGDAS
	310	320	330	340	350	360
m590-1.pep	370	380	390	400	410	420
m590-1.pep	GLFTNNPVLD	IKTFRFTLPS	GKIDVGGKIM	FKDMKKEDLN	QLGLMLKKTE	ADIRMSIPQK
g590	GLFTHDPV	LNKIFRFTLP	QKIDVGGKIM	FKGMMKKEDLN	QLGLMLKKTE	ANIRMSIPQK
	370	380	390	400	410	420
m590-1.pep	430	440	450	460	470	480
m590-1.pep	MLEDLAVSQA	GNIFSVNAED	EAEGRASLDD	INETLRMLVD	STVQSMAREK	YLTNGDQID
g590	MLEDLAVSQA	GNIFSVNAED	EAEARASIAD	INETLRMLVD	STVQSMAREK	YLTLDGNQID
	430	440	450	460	470	480
m590-1.pep	490	500	510			
m590-1.pep	TAISLKNQNL	KNGKTLQNE	PEPDFDEGGM	VSE	EPQQX	

	100	200	300	400	500	600	700	800	900	1000	1100	1200	1300	1400	1500	1600	1700	1800	1900	2000	2100	2200	2300	2400	2500	2600	2700	2800	2900	3000	3100	3200	3300	3400	3500	3600	3700	3800	3900	4000	4100	4200	4300	4400	4500	4600	4700	4800	4900	5000	5100	5200	5300	5400	5500	5600	5700	5800	5900	6000	6100	6200	6300	6400	6500	6600	6700	6800	6900	7000	7100	7200	7300	7400	7500	7600	7700	7800	7900	8000	8100	8200	8300	8400	8500	8600	8700	8800	8900	9000	9100	9200	9300	9400	9500	9600	9700	9800	9900	10000	10100	10200	10300	10400	10500	10600	10700	10800	10900	11000	11100	11200	11300	11400	11500	11600	11700	11800	11900	12000	12100	12200	12300	12400	12500	12600	12700	12800	12900	13000	13100	13200	13300	13400	13500	13600	13700	13800	13900	14000	14100	14200	14300	14400	14500	14600	14700	14800	14900	15000	15100	15200	15300	15400	15500	15600	15700	15800	15900	16000	16100	16200	16300	16400	16500	16600	16700	16800	16900	17000	17100	17200	17300	17400	17500	17600	17700	17800	17900	18000	18100	18200	18300	18400	18500	18600	18700	18800	18900	19000	19100	19200	19300	19400	19500	19600	19700	19800	19900	20000	20100	20200	20300	20400	20500	20600	20700	20800	20900	21000	21100	21200	21300	21400	21500	21600	21700	21800	21900	22000	22100	22200	22300	22400	22500	22600	22700	22800	22900	23000	23100	23200	23300	23400	23500	23600	23700	23800	23900	24000	24100	24200	24300	24400	24500	24600	24700	24800	24900	25000	25100	25200	25300	25400	25500	25600	25700	25800	25900	26000	26100	26200	26300	26400	26500	26600	26700	26800	26900	27000	27100	27200	27300	27400	27500	27600	27700	27800	27900	28000	28100	28200	28300	28400	28500	28600	28700	28800	28900	29000	29100	29200	29300	29400	29500	29600	29700	29800	29900	30000	30100	30200	30300	30400	30500	30600	30700	30800	30900	31000	31100	31200	31300	31400	31500	31600	31700	31800	31900	32000	32100	32200	32300	32400	32500	32600	32700	32800	32900	33000	33100	33200	33300	33400	33500	33600	33700	33800	33900	34000	34100	34200	34300	34400	34500	34600	34700	34800	34900	35000	35100	35200	35300	35400	35500	35600	35700	35800	35900	36000	36100	36200	36300	36400	36500	36600	36700	36800	36900	37000	37100	37200	37300	37400	37500	37600	37700	37800	37900	38000	38100	38200	38300	38400	38500	38600	38700	38800	38900	39000	39100	39200	39300	39400	39500	39600	39700	39800	39900	40000	40100	40200	40300	40400	40500	40600	40700	40800	40900	41000	41100	41200	41300	41400	41500	41600	41700	41800	41900
--	-----	-----	-----	-----	-----	-----	-----	-----	-----	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------	-------

g591.seq

1	TTGCAAAACC	TTCTAGCTTT	TATCTTCGCC	ATCCTGATTT	TGGTCAGCCT
51	GCACGAATTC	GGACACTACA	TCGTGCGCCG	GTTGTGCGCG	GTCAAGGTTG
101	TGCGTTTTTC	GCTCGGTTTC	GGCAAAACCGT	TTTTTACC	AAAGCGCGCG
151	GACACCGAAT	GGTGCCCTCGC	CCCGATTCCG	TTGGGCGGCT	ACGTCAAAAT
201	GGTCGATACG	CGCGAAGGCG	AAGTATCAGA	AGCCGATTTA	CCCTACGCTT
251	TTGACAAACA	ACACCCCGCG	AAGCGCATCG	CCATCGTGCg	CGCCGGTCCG
301	CTGACCAACC	TCGCActggc	ggTTTTTGCTG	TACGGACTGa	gctTttctct
351	cggcqttaaC	GAACTGCGGC	Cctatgtcgg	cacagtccaA	cccgacacc

931

```

401 ttgccgCCCG CACCGGCTTC caaagcggcg acaaAATACa atccgtcaac
451 ggcgtTtccg tCCAAGACTG GAGCAGCGCG CAAACCGAAA TCGTcctcAA
501 CCTCGAAGCC Ggcaaagtcg ccgtcggcgT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCAtcgAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC cteaTGGCAG
751 GAATGggcaa acctgACccg cCAAAGCCGg ggcAAAAAAA Tcaccctgac
801 ctacgAaCGC GCcggacaaa cccaTAccgc CGACATCCGC CccgATactg
851 TCGAAcagcc cgACCACACC CTGATCgggc gcgTCGGCCT CCGtcggcaG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCTGTCAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCGTTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGTCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTGATGATG CTGATGATGG
1301 CGGCCGCCTT CTTCAACGAC GTTACCCGGC TGATCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1842; ORF 591.ng>:

g591.pep..

```

1 LQTLAIFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFTRKRK
51 DTEWCLAPIP LGGYVKMVDI REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTVE PDTVAARTGF QSGDKIQSVN
151 GVSVDWSSA QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTYER AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVR AFGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVLNLL PVPVLDGGHL
401 VFYTVIEWIRG KPLGERVQNI GLRFLGALMM LMMAAAFFND VTRLIG*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1843>:

m591.seq

```

1 TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51 GCACGAGTTC GGACACTACA TCGTTGCCAG ATTGTGCGGC GTCAAAGTCG
101 TACGCTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAT
201 GGTGATACG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCA
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CCGCGTAACC GAACTGCGCC CCTACGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCG CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTCAAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTAAAATC
601 GCAAAAAACC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCCTCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAA TCACCCTGAA
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATCTG
851 TCGAACAGTC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCCTTTCC CACTCGTGGA
1001 CAACCCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCGTGAGC
1051 CATATTTCCG GGCCGCTGAC CATTGCCGAC ATTGCCGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGGAATTTT AGCACTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTACTG CCCGTCCCTG TTTTGGACGG CGGGCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 CCAAAACATC GGTTCGCGCT TCGGGCTCGC CCTCATGATG CTGATGATGG
1301 CGGTGCGCCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1844; ORF 591>:

m591.pep..

932

```

1  LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFFFTRKRG
51 DTEWCLAPIP LGGYVKMVDV REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV E PDTIARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITT VAGG VEKGS PAEKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLNYER AGQTH TADIR PDTVEQSDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMGWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNLL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFG LALMM LMMAVAFFND VTRL LG*

```

Computer analysis of this amino acid sequence gave the following results:
Homology with a predicted ORF from *N. gonorrhoeae*

m591 / g591 97.3% identity in 446 aa overlap

	10	20	30	40	50	60
m591.pep	LHTLLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
g591	LQTLAFIFA	ILILVSLHEF	GHYIVARLCG	VKVVRFSVGF	GKPFFFTRKRG	DTEWCLAPIP
	10	20	30	40	50	60
m591.pep	LGGYVKMVDV	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
g591	LGGYVKMVDV	REGEVSEADL	PYAFDKQHPA	KRIAIVAAGP	LTNLALAVLL	YGLSFSFGVT
	70	80	90	100	110	120
m591.pep	ELRPYVGTV	EPDTIARAGF	QSGDKIQSVN	GTPVADWGS	AQTEIVLNLEA	GKVAVGVQTA
g591	ELRPYVGTV	EPDTVAARTG	FQSGDKIQSVN	GVSVQDWSSA	QTEIVLNLEA	GKVAVGVQTA
	130	140	150	160	170	180
m591.pep	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITT VAGG	VEKGS PAEKA	GLKPGDRLTA
g591	SGAQTVRTID	AAGTPEAGKI	AKNQGYIGLM	PFKITT VAGG	VEKGS PAEKA	GLKPGDRLTA
	190	200	210	220	230	240
m591.pep	ADGKPIASWQ	EWANLTRQSP	GKKITLNYER	AGQTH TADIR	PDTVEQSDHT	LIGRVGLRPQ
g591	ADGKPIASWQ	EWANLTRQSP	GKKITLTYER	AGQTH TADIR	PDTVEQPDHT	LIGRVGLRPQ
	250	260	270	280	290	300
m591.pep	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
g591	PDRAWDAQIR	RSYRPSVVRA	FGMGWEKTVS	HSWTTLKFFG	KLISGNASVS	HISGPLTIAD
	310	320	330	340	350	360
m591.pep	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTAEWIRG	KPLGERVQNI
g591	IAGQSAELGL	QSYLEFLALV	SISLGVNLNLL	PVPVLDGGHL	VFYTVIEWIRG	KPLGERVQNI
	370	380	390	400	410	420
m591.pep	GLRFG LALMM	LMMAVAFFND	VTRL LGX			
g591	GLRFG LALMM	LMAAAFFND	VTRL LIGX			
	430	440				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1845>:
a591.seq

933

```

1   TTGCACACCC TTCTAGCTTT TATCTTCGCC ATCCTGATTT TGGTCAGCCT
51  GCACGAATTC GGACACTACA TCGTCGCCAG ATTGTGCGGC GTCAAGGTTG
101 TGCCTTTTTC CGTCGGCTTC GGCAAACCGT TTTTCACCCG AAAGCGCGGC
151 GACACCGAAT GGTGCCTCGC CCCGATTCCG TTGGGCGGTT ACGTCAAAAT
201 GGTGACACAG CGCGAAGGCG AAGTATCAGA AGCCGATTTA CCCTACGCTT
251 TTGACAAACA ACACCCCGCC AAGCGCATCG CCATCGTCGC CGCCGGCCCG
301 CTGACCAACC TCGCACTGGC GGTTTTGCTG TACGGACTGA GCTTTTCCTT
351 CGGCGTTACC GAACTGCGCC CCTATGTCGG CACAGTCGAA CCCGACACCA
401 TTGCCGCCCC CGCCGGCTTC CAAAGCGGCG ACAAATACA ATCCGTC AAC
451 GGCACACCCG TTGCAGATTG GGGCAGCGCG CAAACCGAAA TCGTCCTCAA
501 CCTCGAAGCC GGCAAAGTCG CCGTCGGCGT TCAGACGGCA TCGGGCGCGC
551 AAACCGTCCG CACCATCGAT GCCGCAGGCA CGCCGGAAGC CGGTA AAATC
601 GCAAAAACCC AAGGCTACAT CGGACTGATG CCCTTTAAAA TCACAACCGT
651 TGCCGGCGGC GTGGAAAAAG GCAGCCCCGC CGAAAAAGCA GGCCTGAAAC
701 CGGGCGACAG GCTGACTGCC GCCGACGGCA AACCATCGC CTCATGGCAA
751 GAATGGGCAA ACCTGACCCG CCAAAGCCCC GGCAAAAAAA TCACCCTGAC
801 CTACGAACGC GCCGGACAAA CCCATACCGC CGACATCCGC CCCGATACTG
851 TCGAACAGCC CGACCACACC CTGATCGGGC GCGTCGGCCT CCGTCCGCAG
901 CCGGACAGGG CGTGGGACGC GCAAATCCGC CGCAGCTACC GTCCGTCTGT
951 TGTCCGCGCA TTCGGCATGG GCTGGGAAAA AACCGTTTCC CACTCGTGGA
1001 CAACCTCAA ATTTTTCGGC AAATAATCA GCGGCAACGC CTCCTGACG
1051 CATATTTCCG GTCCGCTGAC CATTGCCGAT ATTGCCGGAC AGTCCGCCGA
1101 ACTCGGCTTG CAAAGTTATT TGAATTTT GGCCTGGTC AGCATCAGCC
1151 TCGGCGTGCT GAACCTGCTG CCCGTCCCCG TTTTGGACGG CGGCCACCTC
1201 GTGTTTTATA CTGCCGAATG GATACGCGGC AAACCTTTGG GCGAACGCGT
1251 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
1301 CGGTGCGCTT CTTCAACGAC GTTACCCGGC TGCTCGGTTA G

```

This corresponds to the amino acid sequence <SEQ ID 1846; ORF 591.a>:

```

a591.pep
1   LHTLLAFIFA ILILVSLHEF GHYIVARLCG VKVVRFSVGF GKPFTRKRK
51  DTEWCLAPIP LGGYVKMVD T REGEVSEADL PYAFDKQHPA KRIAIVAAGP
101 LTNLALAVLL YGLSFSFGVT ELRPYVGTV PDTIAARAGF QSGDKIQSVN
151 GTPVADWGS A QTEIVLNLEA GKVAVGVQTA SGAQTVRTID AAGTPEAGKI
201 AKNQGYIGLM PFKITTVAGG VEKGSPEAKA GLKPGDRLTA ADGKPIASWQ
251 EWANLTRQSP GKKITLTyer AGQHTADIR PDTVEQPDHT LIGRVGLRPQ
301 PDRAWDAQIR RSYRPSVVRA FGMWEKTVS HSWTTLKFFG KLISGNASVS
351 HISGPLTIAD IAGQSAELGL QSYLEFLALV SISLGVNLNL PVPVLDGGHL
401 VFYTAEWIRG KPLGERVQNI GLRFGALMM LMMAVAFFND VTRLLG*

```

m591/a591 99.6% identity in 446 aa overlap

```

          10      20      30      40      50      60
m591.pep  LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSVGF GKPFTRKRGDTEWCLAPIP
          |||||||
a591      LHTLLAFIFAILILVSLHEFGHYIVARLCGVKVVRFSVGF GKPFTRKRGDTEWCLAPIP
          10      20      30      40      50      60

          70      80      90      100     110     120
m591.pep  LGGYVKMVD TREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
          |||||||
a591      LGGYVKMVD TREGEVSEADLPYAFDKQHPAKRIAIVAAGPLTNLALAVLLYGLSFSFGVT
          70      80      90      100     110     120

          130     140     150     160     170     180
m591.pep  ELRPYVGTV PDTIAARAGFQSGDKIQSVNGTPVADWGS AQTEIVLNLEAGKVAVGVQTA
          |||||||
a591      ELRPYVGTV PDTIAARAGFQSGDKIQSVNGTPVADWGS AQTEIVLNLEAGKVAVGVQTA
          130     140     150     160     170     180

          190     200     210     220     230     240
m591.pep  SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA
          |||||||
a591      SGAQTVRTIDAAGTPEAGKIAKNQGYIGLMPFKITTVAGGVEKGSPEAKAGLKPGDRLTA
          190     200     210     220     230     240

```

934

	250	260	270	280	290	300
m591.pep	ADGKPIASWQEWANLTRQSPGKKITLNYERAGQHTADIRPDTVEQSDHTLIGRVGLRPQ					
a591	ADGKPIASWQEWANLTRQSPGKKITLTYERAGQHTADIRPDTVEQPDHTLIGRVGLRPQ					
	250	260	270	280	290	300
	310	320	330	340	350	360
m591.pep	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
a591	PDRAWDAQIRRSYRPSVVRAFGMGWEKTVSHSWTTLKFFGKLISGNASVSHISGPLTIAD					
	310	320	330	340	350	360
	370	380	390	400	410	420
m591.pep	IAGQSAELGLQSYLEFLALVSIISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
a591	IAGQSAELGLQSYLEFLALVSIISLGVNLLPVPVLDGGHLVFYTAEWIRGKPLGERVQNI					
	370	380	390	400	410	420
	430	440				
m591.pep	GLRFGALMMLMMAVAFFNDVTRLLGX					
a591	GLRFGALMMLMMAVAFFNDVTRLLGX					
	430	440				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1847>:

g592.seq..

```

1  atgattccgg acgtgttcgg tcagattttt tcgggcgcggt tcaaattcga
51  cgcggcagca ggcggccttac tcggcggtct gatttcgcaa acgatgatga
101 tgggcatcaa acgcggcctg tattccaacg aggcgggtat gggttccgcg
151 ccgaacgccc ccgcccgcgc cgaagtgaag caccctgttt cgcaaggat
201 gattcaaatg ctgggcgtgt ttgtcgatac catcatcggt tgttcttgca
251 ccgccttcat catcttgatt taccaacagc cttatggcga tttgagcggg
301 gcggcgctga cgcaggcggc gattgtcagc caagtggggc aatggggcgc
351 gggtttcctc gccgtcatcc tgtttatggt tgccttttcc accgttatcg
401 gcaactatgc ctatgccgag tccaacgtcc aattcatcaa aagccattgg
451 ctgattaccg ccgttttccg tatgctgggt ttggcgtggg tctatttcgg
501 cgcggttgcc aatgtgcctt tggctcggga tatggcggat atggcgatgg
551 gcatcatggc gtggatcaac ctgctcgcca tcctgctgct ctgcgcattg
601 gcgtttatgc tgctgcgcga ttacaccgcc aagctgaaaa tgggcaaaga
651 ccccgagttc aaactttccg aacatccggg cctgaaacgc cgcatacaat
701 ccgatgttg gtaa

```

This corresponds to the amino acid sequence <SEQ ID 1848; ORF 592.ng>:

g592.pep ..

```

1  MIPDVFGQIF SGAFKFDAAA GGLLGLISQ TMMGIKRL YSNEAGMGSA
51  PNAAAAAEVK HPVSQGMQM LGVFVDIIIV CSCTAFIILI YQQPYGDLG
101 AALTQAIVS QVGQWAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1849>:

m592.seq ..

```

1  ATGATTCCGG ACGTGTTCGG TCAGATTTT TCGGGCGCGT TCAAATTCGA
51  CGCGGCAGCA GCGCGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
101 TGGGCATCAA ACGCGGCTGT TATTCCAACG AGGCGGGTAT GGGTTCGCG
151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTCTGCA
251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
301 GCGGCGCTGA CGCAGCGGCG GATTGTCAGC CAAGTGGGGC AATGGGCGC
351 GGGCTTCCTC GCCGTCATCC TGTTTATGTT TGCCTTTTCC ACCGTTATCG
401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTATCAA AAGCCATTGG
451 CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG

```


935

601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1850; ORF 592>:

m592.pep ..
 1 MIPDVFGQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQOPYGDLG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592 / g592 100.0% identity in 237 aa overlap

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAA	GLLGLISQTMMGIKRL	YSNEAGMGS	APNAAAAAEVK		
g592	MIPDVFGQIFSGAFKFDAAA	GLLGLISQTMMGIKRL	YSNEAGMGS	APNAAAAAEVK		
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMQIMLGVFVDTIIV	CSCTAFIILIYQOPYGDL	SGAALTQAAIVSQVGQW	GAGFL		
g592	HPVSQGMQIMLGVFVDTIIV	CSCTAFIILIYQOPYGDL	SGAALTQAAIVSQVGQW	GAGFL		
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAE	SNVQFIKSHWLITAVFRML	VLAWVYFGAVANVPLVW	DMAD		
g592	AVILFMFAFSTVIGNYAYAE	SNVQFIKSHWLITAVFRML	VLAWVYFGAVANVPLVW	DMAD		
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLLSPL	AFMLLRDYTAKLKM	GKDPEFKLSEHPGLKR	RIKSDVW		
g592	MAMGIMAWINLVAILLLSPL	AFMLLRDYTAKLKM	GKDPEFKLSEHPGLKR	RIKSDVW		
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1851>:

a592.seq
 1 ATGATTCCGG ACGTGTTCGG TCAGATTTTT TCGGGCGCGT TCAAATTCGA
 51 CGCGGCAGCA GGCGGCTTAC TCGGCGGTCT GATTTCGCAA ACGATGATGA
 101 TGGGCATCAA ACGCGGCCCTG TATTCCAACG AGGCGGGTAT GGGTCCGCG
 151 CCGAACGCCG CCGCCGCCGC CGAAGTGAAA CACCCTGTTT CGCAAGGTAT
 201 GATTCAAATG CTGGGCGTGT TTGTCGATAC CATCATCGTT TGTCTTGCA
 251 CCGCCTTCAT CATCTTGATT TACCAACAGC CTTACGGCGA TTTGAGCGGT
 301 GCGGCGCTGA CGCAGGCGGC GATTGTCAGC CAAGTGGGGC AATGGGGCGC
 351 GGGCTTCCTC GCCGTCATCC TGTATTATGTT TGCCTTTTCC ACCGTTATCG
 401 GCAACTATGC CTATGCCGAG TCCAACGTCC AATTCATCAA AAGCCATTGG
 451 CTGATTACCG CCGTTTTCCG TATGCTGGTT TTGGCGTGGG TCTATTTCCG
 501 CGCGGTTGCC AATGTGCCTT TGGTCTGGGA TATGGCGGAT ATGGCGATGG
 551 GCATTATGGC GTGGATCAAC CTTGTCGCCA TCCTGCTGCT CTCGCCCTTG
 601 GCGTTTATGC TGCTGCGCGA TTACACCGCC AAGCTGAAAA TGGGCAAAGA
 651 CCCCAGTTTC AAACCTTCCG AACATCCGGG CCTGAAACGC CGTATCAAAT
 701 CCGACGTTTG GTAA

This corresponds to the amino acid sequence <SEQ ID 1852; ORF 592.a>:

a592.pep
 1 MIPDVFGQIF SGAFKFDAAA GLLGLISQ TMMGIKRL YSNEAGMGS
 51 PNAAAAAEVK HPVSQGMQIM LGVFVDTIIV CSCTAFIILI YQOPYGDLG
 101 AALTQAAIVS QVGQWGAGFL AVILFMFAFS TVIGNYAYAE SNVQFIKSHW
 151 LITAVFRMLV LAWVYFGAVA NVPLVWDMAD MAMGIMAWIN LVAILLLSPL
 201 AFMLLRDYTA KLKMGKDPEF KLSEHPGLKR RIKSDVW*

m592/a592 100.0% identity in 237 aa overlap

936

	10	20	30	40	50	60
m592.pep	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
a592	MIPDVFGQIFSGAFKFDAAAGLLGGLISQTMMMGIKRGLYSNEAGMGSAPNAAAAAEVK					
	10	20	30	40	50	60
	70	80	90	100	110	120
m592.pep	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
a592	HPVSQGMIOQLGVFVDTIIVCSCTAFIILIYQQPYGDLSGAALTQAAIVSQVGQWGAGFL					
	70	80	90	100	110	120
	130	140	150	160	170	180
m592.pep	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFERMLVLAWVYFGAVANVPLVWDMAD					
a592	AVILFMFAFSTVIGNYAYAESNVQFIKSHWLITAVFERMLVLAWVYFGAVANVPLVWDMAD					
	130	140	150	160	170	180
	190	200	210	220	230	
m592.pep	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
a592	MAMGIMAWINLVAILLSPLAFMLLRDYTAKLMGKDPEFKLSEHPGLKRRIKSDVWX					
	190	200	210	220	230	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1853>:

```

g593.seq..
1  atgcttgaac tgaacggact ctgcaaatgc ttcggcggca aaacggtcgc
51  cgacaacatc tgcctgactg tcgggcgcgg caaaatactc gccgtactgg
101 ggcggtcggg ctgcggcaaa tccaccctgc tgaatatgat tgcgggcatc
151 gtccggccgg acggcggcga aattcggctg aacggggaaa acattacctg
201 tatgccgccc gaaaaacgcc gtatctcgct gatgtttcaa gattacgcgc
251 tgtttcccca tatgagtgcg ctggaaaata cggcattcgg tttgaaaatg
301 caaaaaatgc cgaaagccga agccgaacgc ctcgccttgt cggcacttgc
351 cgaagtcggg ctggaaaacg aggcgcaccg caagcctgaa aaactttccg
401 gaggcgagaa gcaacggttg gcactggcgc gcgctttggt tgtccgcctc
451 tccctgctgt tgetggatga atcgttttcc agtttggaca cgcatttgcg
501 cgaccggctg cgccgtatga ccgccgaacg catccgcaag ggcggcatcc
551 ctgccgtttt ggtaacgcac tcgcccgaag aggcctgcac ggcggcggac
601 gaaatcgccg tcatgcacga ggggaaaatc cttcaatgcg gtacgcccga
651 aaccttgatt caaacgcctg ccggcgtgca ggtcgcccgt ctgatggggc
701 tgcccaatac cgacgatgac cgccatattc cgcaaaatgc cgtgtgcttg
751 gacaatcatg gaacggaatg ccgtctgctg tccctcgtec gcctgcccga
801 ctcgctccgg ctttcgcccg tccatcccga acacggcgag ctgaccttaa
851 acctgactgt cggacaacat acggacggta tttccggaaa cggtagcgtc
901 cgcattccgc tcgatgaagg gcgtatcgtc cgtttccgat ga

```

This corresponds to the amino acid sequence <SEQ ID 1854; ORF 593.ng>:

```

g593.pep..
1  MLELNLCKC FGGKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIRL NGENITCMPP EKRRISLMFQ DYALFPHMSA LENTAFGLKM
101 QKMPKAEAER LALSALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI LQCGTPETLI QTPAGVQVAR LMGLPNTDDD RHIPQNAVCL
251 DNHGTECRLL SLVRLPDSL RLSAVHPEHGE LTLNLTVGQH TDGISNGTV
301 RIRVDEGRIV RFR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1855>:

```

m593.seq
1  ATGCTTGAAC TGAACGGACT CTGCAAACGC TTCGGAATA AAACCGTCGC
51  CGACAACATC TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTGG
101 GCGGTCGGG CTGCGGAAAA TCCACCCTGC TGAATATAAT TGCGGGGATT
151 GTCCGGCCGG ACGGCGGGGA AATATGGCTG AACGGAGAAA ACATTACCCG

```

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```

201 TATGCCGCC GAAAAACGCC GTATCTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCA TATGAGTGCG CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC CGAAAGCCGA AGCCGAACGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA CTGGAAAACG AGGCGCACCG CAAGCCTGAA AAACTTTCCG
401 GAGGCGAGAA GCAACGGCTG GCGTTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTGCGT
501 CGGCACGCTG CGCCGTATGA CTGCCGAACG TATCCGAAAC GCGGCATCC
551 CTGCCGTTTT GGTAAACGCAT TCGCCGAAG AAGCCTGTAC GACGGCAGAC
601 GAAATCGCCG TGATGCATAA AGGGAGGATT CTACAATACG GTACGCCCGA
651 AACATTGGTC AAAACACCAT CCTGCGTGCA GGTGCCCCGA CTGATGGGTT
701 TGCCCAATAC CGACGATAAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT GCGGCACGCC GGGGCGGTAT CGGGCAAGGA TACGGTACGC
901 ATCCATATCG AAGAACGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1856; ORF 593>:

```

m593.pep ..
   1 MLELNLCKR FGNKTVADNI CLTVGRGKIL AVLGRSGCGK STLLNIIAGI
  51 VRPDGGEIWL NGENITRMPP EKRRISLMFQ DYALFPHMSA LENAAGFLKM
101 QKMPKAEAEER LAMAALAEVG LENEHRKPE KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS SLDTHLRGTL RRMTAERIRN GGIPAVLVTH SPEEACTTAD
201 EIAVMHKGRI LQYGPETLV KTPSCVQVAR LMGLPNTDDN RHIPQHAVRF
251 DQDGMCECVL SRTCLPESFS LSVLHPEHGI LWNLDMRHA GAVSGKDTVR
301 IHIEEREIVR FR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m593 / g593 83.4% identity in 313 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICLTVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
g593	MLELNLCKCFGGKTVADNICLTVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIRL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAGFLKMQKMPKAEAEERLAMAALAEVG					
g593	NGENITCMPPEKRRISLMFQDYALFPHMSALENTAFGLKMQKMPKAEAEERLALSALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRGTLRRMTAERIRN					
g593	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFS SLDTHLRDLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIIVMHKGRIQLQYGPETLVKTPSCVQVARLMGLPNTDDN					
g593	GGIPAVLVTHSPEEACTTADEIIVMHKGRIQLQYGPETLVKTPSCVQVARLMGLPNTDDD					
	190	200	210	220	230	240

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	250	260	270	280	290	299
m593.pep	RHIPQHAVRFDQDGMCECVLSRTCLPESFSLSVLHPEHGILWLNLDLDM-RHAGAVSGKDTV					
	: : : : : : : : :					
g593	RHIPQNAVCLDNHGTECRLLSLVRLPDSLRLSAVHPEHGELTLNLTVGQHTDGLSGNGTV					
	250	260	270	280	290	300
	300	310				
m593.pep	RIHIEEREIVRFRX					
	:: :					
g593	RIRVDEGRIVRFRX					
	310					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1857>:

```

a593.seq
1  ATGCTTGAAC  TGAACGGA CTGCAAACGC TTCGCGCGCA AAACGGTTGC
51  CGACGATATC  TGCCTGACTG TCGGGCGCGG CAAAATACTC GCCGTTTTGG
101 GCGCGTTCGGG CTGCGGCAAA TCCACCCTGC TGAATATGAT TGCGGGCATC
151 GTCCGGCCGG  ACGGCGGGGA AATATGGCTG AATGGGGAAA ACATTACCCG
201 TATGCCGCCC  GAAAAACGCC GTATTTCGCT GATGTTTCAA GATTACGCGC
251 TGTTTCCCCA  TATGAGTGCA CTGGAAAATG CGGCATTCCG TTTGAAAATG
301 CAAAAAATGC  CGAAAGCCGA AGCCGAAAGC CTCGCCATGG CGGCACTTGC
351 CGAAGTCGGA  CTGGAAAACG AGGCGCACCG CAAGCCTGAN AAACTTTCCG
401 GAGGCGAAAA  GCAACGGTTG GCACTGGCGC GCGCTTTGGT TGTCCGCCCT
451 TCCCTGCTGC  TGTGGACGA ATCGTTTTC AGTTTGGACA CGCATTTGCG
501 CGACCGGCTG  CGCCGCATGA CTGCCGAACG TATCCGCAAG GGCGGCATCC
551 CTGCCGTTTT  GGTAAACGCAT TCGCCGAAG AGGCCTGCAC GGCGGCAGAC
601 GAAATCGCCG  TCATGCACGA GGGGAAAATC CTTCAATGCG GTACGCCCGA
651 AACCTTGTT  CAAACGCCTG CCGGCGTGCA GGTGCGCCAT CTGATGGGGC
701 TGCCCAATAC  CGACGATGAC CGCCATATTC CGCAACATGC GGTGCGTTTC
751 GACCAAGACG  GCATGGAGTG CCGCGTATTA TCCCGTACCT GTTTGCCCGA
801 ATCGTTCAGC  CTGTCCGTCC TCCATCCGGA ACACGGCATC CTGTGGCTGA
851 ACCTCGATAT  GCCGCACGCC GGTGAAATAT CGGGAAACGA TACGGTACGC
901 ATCCATATCG  AAGACAGGGA AATCGTCCGC TTCCGCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1858; ORF 593.a>:

```

a593.pep
1  MLELNLCKR  FGGKTVADDI CLTVGRGKIL AVLGRSGCGK STLLNMIAGI
51  VRPDGGEIWL NGENITRMP  EKRRISLMFQ DYALFPHMSA LENAFLGLKM
101 QKMPKAEAES  LAMAALAEVG LENEHRKPX  KLSGGEKQRL ALARALVVRP
151 SLLLLDESFS  SLDTHLRDRL RRMTAERIRK GGIPAVLVTH SPEEACTAAD
201 EIAVMHEGKI  LQCGTPETLV QTPAGVQVAH LMGLPNTDDD RHIPQHAVRF
251 DQDGMCECVL  SRTCLPESFS LSVLHPEHGI LWLNLDMPHA GEISGNDTVR
301 IHIEDREIVR  FR*

```

m593/a593 92.9% identity in 312 aa overlap

	10	20	30	40	50	60
m593.pep	MLELNLCKRFGNKTVDNICTLVGRGKILAVLGRSGCGKSTLLNIIAGIVRPDGGGEIWL					
	:					
a593	MLELNLCKRFGGKTVADDICTLVGRGKILAVLGRSGCGKSTLLNMIAGIVRPDGGGEIWL					
	10	20	30	40	50	60
	70	80	90	100	110	120
m593.pep	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAEERLAMAALAEVG					
	:					
a593	NGENITRMPPEKRRISLMFQDYALFPHMSALENAAFGLKMOKMPKAEAESLAMAALAEVG					
	70	80	90	100	110	120
	130	140	150	160	170	180
m593.pep	LENEHRKPEKLSGGEKQRLALARALVVRPSLLLLDESFSLLDTHLRGTLRRMTAERIRN					
	:					
a593	LENEHRKPXKLSGGEKQRLALARALVVRPSLLLLDESFSLLDTHLRDRLRRMTAERIRK					
	130	140	150	160	170	180
	190	200	210	220	230	240
m593.pep	GGIPAVLVTHSPEEACTTADEIAVMHKGRILQYGTPELVKTPSCVQVARLMGLPNTDDD					

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```

|||||:|||||:|:| | |||||:|:| | |||:|||||:
a593  GGIPAVLVTHSP EEACTAADEIAVMHEGKILQCGTPETLVQTPAGVQVAHLMGLPNTDDD
      190      200      210      220      230      240

      250      260      270      280      290      300
m593.ppep RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLDMRHAGAVSGKDTV
|||||:|||||:|:| | |||||:|:| | |||:|||||:
a593  RHIPQHAVRFDQDGM ECRVLSRTCLPESFSLSVLHPEHGILWLNLDMPHAGEISGNDTV
      250      260      270      280      290      300

      310
m593.ppep IHIEEREIVRFRX
||||:|||||
a593  IHIEDREIVRFRX
      310

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1859>:

```

g594.seq..
1  atgggtgcag ataccgatgg cgacaaggat gttcggctta atcgaacggg
51  tctcgTTTTT agcatactcc ggctgctgtt ccgcacgcga attgggatcg
101 gtaagttcgc cgttcaggcc tttcaggtct ttaagctgct gatctgtacg
151 gttgagcacc caaatcgggt tgccttgcca ctccgcggtc agcagctgac
201 ccgcttcgat tttactgaca tccacctcga cggcagcacc ggaggccttg
251 gctttttccg aagggaAAAA actggccaca aacggcggtg ccacacccaa
301 tgctgccact ccgcccgccg cgcaggtcgc aagtgtcagg aaacggcggc
351 ggccgttggt gatttcttga ttatccatta ttcagtcgtc ctaatatTTT
401 gggaatgccg agccattaaa cattgcaatt ttaccaggtt tgcagtgata
451 ctcaaagcat tatttaaaat aaggtaa

```

This corresponds to the amino acid sequence <SEQ ID 1860; ORF 594.ng>:

```

g594.ppep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR KCQETAAAVV DFLIIHYSVV LIFWECRAIK HCNFTQFAVI
151 LKALFKIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1861>:

```

m594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAGCTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCGGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTGAGG AAACGGCGGC
351 GGCCGTGTGT GATTCTTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 GGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1862; ORF 594>:

```

m594.ppep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFRREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSVV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m594 / g594 98.1% identity in 158 aa overlap

940

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
g594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
g594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRKQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
g594	DFLIHYSVVLIFWECRAIKHCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1863>:

```
a594.seq
1  ATGGGTGCAG ATACCGATGG CGACAAGGAT GTTCGGCTTA ATCGAACGGG
51  TCTCGTTTTT AGCATACTCC GGCTGCTGTT CCGCATCGGA ATTGGGATCG
101 GTAAGTTCGC CGTTCAGGCC TTTCAGGTCT TTAAGCTGCT GATCTGTACG
151 GTTGAGCACC CAAATCGGTT TGCCTTGCCA CTCGGCGGTC AGCAACTGAC
201 CCGCTTCGAT TTTACTGACA TCCACCTCGA CGGCAGCACC GGCAGCCTTG
251 GCTTTTCCG AAGGGAAAAA ACTGGCCACA AACGGCGTTG CCACACCCAA
301 TGCTGCCACT CCGCCCGCGC CGCAGGTGCG GAGTGTCAGG AAACGGCGGC
351 GGCCGTGTT GATTTCCTGA TTATCCATTA TTCAGTCGTC CTAATATTTT
401 CGGAATACCG AGCCATTAAA CGTTGCAATT TTACCCAGTT TGCAGTGATA
451 CTCAAAGCAT TATTTAAAT AAGGTAA
```

This corresponds to the amino acid sequence <SEQ ID 1864; ORF 594.a>:

```
a594.pep
1  MGADTDGDKD VRLNRTGLVF SILRLLFRIG IGIGKFAVQA FQVFKLLICT
51  VEHPNRFALP LGGQQLTRFD FTDIHLDGST GGLGFFREK TGHKRRCHTQ
101 CCHSARAAGR ECQETAAAVV DFLIIHYSV LIFWEYRAIK RCNFTQFAVI
151 LKALFKIR*
```

m594/a594 100.0% identity in 158 aa overlap

	10	20	30	40	50	60
m594.pep	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
a594	MGADTDGDKDVRLNRTGLVFSILRLLFRIGIGIGKFAVQAFQVFKLLICTVEHPNRFALP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m594.pep	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
a594	LGGQQLTRFDFTDIHLDGSTGGLGFFRREKTGHKRRCHTQCCHSARAAGRECQETAAAVV					
	70	80	90	100	110	120
	130	140	150	159		
m594.pep	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
a594	DFLIHYSVVLIFWEYRAIKRCNFTQFAVILKALFKIRX					
	130	140	150			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1865>:

```
g595.seq.
1  atgagaaaat tcaatttgac cgcattgtcc gtgatgcttg ccttggtttt
51  gaccgcgtgc cagccgccgg aggcggagaa agccgcgccg gccgcgtccg
101 gtgagaccca atccgccaa cgaaggcggtt cggtcggtat cgccgtcaac
```

```
151 gacaatgcct gcgaaccgat gaatctgacc gtgccgagcg gacaggttgt
201 gttcaatatt aaaaacaaca gcggccgcaa gctcgaatgg gaaatcctga
251 agggcggtgat ggtggtggac gaacgcgaaa atatcgcccc ggggctttcc
301 gacaaaatga accgtaacct gctgccgggc gaatacgaaa tgacctgcgg
351 ccttttgacc aatccgcgcg gcaagctggt ggtagccgac agcggcttta
401 aagacaccgc caacgaagcg gatttgaaa aactgcccc accgctcgcc
451 gactataaaag cctacgttca aggcgaggtt aaagagctgg cggcgaaaac
501 caaaccttt accgaagccg tcaaagcagg cgacattgaa aaggcgaaat
551 ccctgtttgc cgccaccgc gtccattacg aacgcacga accgattgcc
601 gagcttttca gcgaactcga ccccgtcac gatgctgtg aagacgactt
651 caaagacggt gcgaaagatg ccgggtttac cggcttcac cgtatcgaac
701 acgccctttg ggtggaaaaa gacgtatccg gcgtgaagga aaccgcggcc
751 aaactgatga ccgatgtcga agccctgcaa aaagaaatcg acgcattggc
801 gttccctccg ggcaaagtgg tcggcggcgc gtccgaactg attgaagaag
851 cggcggggcag taaaatcagc ggcgaagaag accgttacag ccacaccgat
901 ttgagcgact tccaagctaa tgcggacgga tctaaaaaaa tcgtcgattt
951 gttccgtccg ttgattgagg caaaaaaca agccttggtg gaaaaaacg
1001 ataccaactt caaacaggtc aacgaaatc tggcgaaata ccgcacaaaa
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942

1051 gacgggttttg aaacctacga caagctgagc gaagccgacc gcaaagcatt
 1101 acaggctcct attaacgcgc ttgccgaaga ccttgcccaa cttcgcgga
 1151 tactcggtt gaaataa

This corresponds to the amino acid sequence <SEQ ID 1866; ORF 595.ng>:

g595.pep ..
 1 MRKFNLTA L S VMLALGLTAC QPPEAEKAAP AASGETQSAN EGGSVGIAVN
 51 DNACEPMNLT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMNRNLLPG EYEMTCGLLT NPRGKLVVAD SGFKDTANEA DLEKLPOPLA
 151 DYKAYVQGEV KELA AKTKTF TEAVKAGDIE KAKSLFAATR VHYERIEPIA
 201 ELFSELDPVI DACEDDFKDG AKDAGFTGFH RIEHALWVEK DVSGVKETAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEAAGSKIS GEEDRYSHTD
 301 LSDFQANADG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLS EADR KALQAP INALAE DLAQ LR GILGLK*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1867>:

m595.seq
 1 ATGAGAAAAT TCAATTTGAC CGCATGTGCC GTGATGCTTG CCTTAGGTTT
 51 GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
 101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCA GTAT CGCCGTCAAC
 151 GACAATGCCT GCGAACCGAT GGAAC TGACC GTGCCGAGCG GACAGGTTGT
 201 GTTCAATATT AAAACAACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
 251 AAGCGGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
 301 GATAAAATGA CCGTCACCCCT GTTGCCGGGC GAATACGAAA TGACTTGCGG
 351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
 401 AAGACACCGC CAACGAAGCG GATTGGAAA AACTGTCCCA ACCGCTCGCC
 451 GACTATAAAG CCTACGTTCA AGGCGAGGTT AAAGAGCTGG TGGCGAAAAC
 501 CAAAAC TTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGCGGAAAT
 551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
 601 GAGCTTTTCA GCGAACTCGA CCCCGTCATC GATGCGCGTG AAGACGACTT
 651 CAAAGACGGC GCGAAAGATG CCGGATTAC CCGCTTTCAC CGTATCGAAT
 701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
 751 AAAGTATGA CCGATGTCGA AGCCCTGCAA AAAGAAATCG ACGATTGGC
 801 GTTTCCTCCG GGCAAGGTGG TCGGCGGCGC GTCCGAACTG ATTGAAGAAG
 851 TGGCGGGCAG TAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
 901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCTAAAAAAA TCGTCGATTT
 951 GTTCCGTCCG CTGATCGAGG CCAAAAACAA AGCCTTGTTG GAAAAAACCG
 1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
 1051 GACGGTTTTG AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
 1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
 1151 TACTCGGCTT GAAATAA

This corresponds to the amino acid sequence <SEQ ID 1868; ORF 595>:

m595.pep
 1 MRKFNLTA L S VMLALGLTAC QPPEAEKAAP AASGEAQ TAN EGGSVSIAVN
 51 DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGVMVVD ERENIAPGLS
 101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
 151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
 201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
 251 KLMTDVEALQ KEIDALAFPP GKVVGGASEL IEEVAGSKIS GEEDRYSHTD
 301 LSDFQANVDG SKKIVDLFRP LIEAKNKALL EKTDTNFKQV NEILAKYRTK
 351 DGFETYDKLG EADR KALQAS INALAE DLAQ LR GILGLK*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m595 / g595 95.4% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNLTA	LSVMLALGLTAC	QPPEAEKAAP	AASGEAQ TAN	EGGSVSIAVN	DNACEPMELT
g595	MRKFNLTA	LSVMLALGLTAC	QPPEAEKAAP	AASGETQSAN	EGGSVGI	AVNDNACEPMNLT
	10	20	30	40	50	60
	70	80	90	100	110	120

943

m595.pep	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT
g595	VPSGQVVFNIKNNSGRKLEWEILKGMVVDERENIAPGLSDKMNRNLLPGEYEMTCGLLT
	70 80 90 100 110 120
m595.pep	130 140 150 160 170 180
	NPRGKLVVTD SGFKDTANEADLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE
g595	NPRGKLVVAD SGFKDTANEADLEKLQPLADYKAYVQGEVKELAAKTKTFTEAVKAGDIE
	130 140 150 160 170 180
m595.pep	190 200 210 220 230 240
	KAKSLFADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK
g595	KAKSLFAATRVHYERIEPIAELFSELDPVIDACEDDFKDGAKDAGFTGFHRIEHALWVEK
	190 200 210 220 230 240
m595.pep	250 260 270 280 290 300
	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHD
g595	DVSGVKETAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEAAGSKISGEEDRYSHD
	250 260 270 280 290 300
m595.pep	310 320 330 340 350 360
	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLG
g595	LSDFQANADGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDGFTYDKLS
	310 320 330 340 350 360
m595.pep	370 380 389
	EADRKALQASINALAEDLAQLRGILGLKX
g595	EADRKALQAPINALAEDLAQLRGILGLKX
	370 380

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1869>:

```

a595.seq
1  ATGAGAAAAT TCAATTTGAC CGCATTGTCC GTGATGCTTG CCTTAGGTTT
51  GACCGCGTGC CAGCCGCCGG AGGCGGAGAA AGCTGCGCCG GCAGCGTCCG
101 GTGAGGCGCA AACCGCCAAC GAGGGCGGTT CGGTCAGTAT CGCCGTC AAC
151 GACAATGCCT GCGAACCGAT GGAAC TGACC GTGCCGAGCG GACAGGTTGT
201 GTTCAATATT AAAAACACA GCGGCCGCAA GCTCGAATGG GAAATCCTGA
251 AAGGCGTGAT GGTGGTGGAC GAGCGCGAAA ACATCGCCCC CGGACTTTCC
301 GATAAAATGA CCGTCACCCT GTTGCCGGGC GAATACGAAA TGACTTGC GG
351 TCTTTTGACC AATCCGCGCG GCAAGCTGGT GGTAACCGAC AGCGGCTTTA
401 AAGACACCGC CAACGAAGCG GATTTGGAAA AACTGTCCCA ACCGCTCGCC
451 GACTATAAAG CCTATGTTC AAGCGAAGTC AAAGAGCTGG TGGCGAAAAC
501 CAAAACCTTT ACCGAAGCCG TCAAAGCAGG CGACATTGAA AAGGCGAAT
551 CCCTGTTTGC CGACACCCGC GTCCATTACG AACGCATCGA ACCGATTGCC
601 GAGCTTTTCA GCGAACTCGA CCCCCTCATC GATGCGCGTG AAGACGACTT
651 CAAAGACGGC GCGAAAGATG CCGGATTTAC CGGCTTCCAC CGTATCGAAT
701 ACGCCCTTTG GGTGGAAAAA GACGTGTCCG GCGTGAAGGA AATTGCAGCG
751 AAAGTATGAT CCGATGTCTG AGCCCTGCAA AAAGAAATCG ACGCATTGGC
801 GTTTCTCTCG GGCAAGGTGG TCGGCGGCGC GTCCGAAGT ATTGAAGAAG
851 TGGCGGGCAG TAAAATCAGC GGCGAAGAAG ACCGGTACAG CCACACCGAT
901 TTGAGCGACT TCCAAGCCAA TGTGGACGGA TCGAAAAAAA TCGTCGATTT
951 GTTCCGTCCT TTGATCGAGA CCAAAAACAA AGCCTTGTTG GAAAAAACCG
1001 ATACCAACTT CAAACAGGTC AACGAAATTC TGGCGAAATA CCGGACTAAA
1051 GACGGTTTGA AAACCTACGA CAAGCTGGGC GAAGCCGACC GCAAAGCGTT
1101 ACAGGCCTCT ATTAACGCGC TTGCCGAAGA CCTTGCCCAA CTTGCGGGCA
1151 TACTCGGCTT GAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1870; ORF 595.a>:

```

a595.pep
1  MRKFNLALS VMLALGLTAC QPPEAEKAAP AASGEAQTAN EGGSVSIAVN
51  DNACEPMELT VPSGQVVFNI KNNSGRKLEW EILKGMVVVD ERENIAPGLS

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944

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101 DKMTVTLLPG EYEMTCGLLT NPRGKLVVTD SGFKDTANEA DLEKLSQPLA
151 DYKAYVQGEV KELVAKTKTF TEAVKAGDIE KAKSLFADTR VHYERIEPIA
201 ELFSELDPVI DAREDDFKDG AKDAGFTGFH RIEYALWVEK DVSGVKEIAA
251 KLMTDVEALQ KEIDALAFPP GKVVGASEL IEEVAGSKIS GEEDRYSHTD
301 LSDFQANVDG SKKIVDLFRP LIETKNKALL EKTDNFKQV NEILAKYRTK
351 DGFETYDKLG EADRKALQAS INALAEDLAQ LRGILGLK*

```

m595/a595 99.7% identity in 388 aa overlap

	10	20	30	40	50	60
m595.pep	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIAVNDNACEPMELT				
a595	MRKFNL	TALSVMLALGLTACQPPEAEKAAPASGEAQTANEGGSVSIAVNDNACEPMELT				
	10	20	30	40	50	60
	70	80	90	100	110	120
m595.pep	VPSGQV	VFNIKNN	SGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT			
a595	VPSGQV	VFNIKNN	SGRKLEWEILKGMVVDERENIAPGLSDKMTVTLLPGEYEMTCGLLT			
	70	80	90	100	110	120
	130	140	150	160	170	180
m595.pep	NPRGKL	VVTD	SGFKDTANEA	DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE		
a595	NPRGKL	VVTD	SGFKDTANEA	DLEKLSQPLADYKAYVQGEVKELVAKTKTFTEAVKAGDIE		
	130	140	150	160	170	180
	190	200	210	220	230	240
m595.pep	KAKSLF	ADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
a595	KAKSLF	ADTRVHYERIEPIAELFSELDPVIDAREDDFKDGAKDAGFTGFHRIEYALWVEK				
	190	200	210	220	230	240
	250	260	270	280	290	300
m595.pep	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
a595	DVSGVKEIAAKLMTDVEALQKEIDALAFPPGKVVGASELIEEVAGSKISGEEDRYSHTD					
	250	260	270	280	290	300
	310	320	330	340	350	360
m595.pep	LSDFQANVDGSKKIVDLFRPLIEAKNKALLEKTDNFKQVNEILAKYRTKDG	FETYDKLG				
a595	LSDFQANVDGSKKIVDLFRPLIETKNKALLEKTDNFKQVNEILAKYRTKDG	FETYDKLG				
	310	320	330	340	350	360
	370	380	389			
m595.pep	EADRKALQASINALAEDLAQLRGILGLKX					
a595	EADRKALQASINALAEDLAQLRGILGLKX					
	370	380				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1871>:

g596.seq. (partial).

```

1 ..atgctgctct tggacgagcc gaccaaccac ttggatgctg aatcggtgga
51 atggctggag caattcctcg tgcgcttccc cggcacagtg gtcgcggtaa
101 cgcacgaccg ctacttctc gacaacgccg ccgaatggat tttggaactc
151 gaccgctggac acggcattcc gtggaaaggc aattactcgt cttggctgga
201 gcagaaagaa aaacgcttgg aaaacgaggc gaaatccgaa gccgcgcgcg
251 tgaaggcgat gaagcaggaa ttggaatggg tgcgccaaaa tgccaaaggc
301 cgccaagcca agcccaaagc gcgtttggcg cgttttgaag aaatgagcaa
351 ctacgaatac caaaaacgca acgaaactca ggaaatcttt atccctgttg
401 ccgagcggtt gggtaacgaa gtgattgaat ttgtgaatgt ttccaaatcg

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945

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451      ttcggcgata aagtgtctgat tgacggtttg agcttcaaaag tgccggcgagg
501      cgcgattgtc ggcatcatcg gcccgaacgg cgcggtgaaa tcgacgctgt
551      tcaaaatgat tcggggcaaa gagcagcccg attcgggcca agtgaaaatc
601      gggcaaacgg tgaaaatgag cttgattgac caaagccgag aaggtttgca
651      aaacgacaaa accgtgttcg acaacattgc cgaaggtcgc gatattttgc
701      aggtcggaca gtttgaaatc cccgcccggc aatatttggg acgcttcaac
751      tttaaaggca gcgaccaaag caaaatcgca aggcagcttt ccggcgcgca
801      acgcgccgct ctgcacttgg caaaaacctt gttgggaggc ggcaatgtgt
851      tgctgctgga cgaaccgtcc aacgatctcg acgtggaaac cctgcgcgag
901      ttggaagacg cattgttggg atttgccggc agcgtgatgg tgatttcgca
951      cgaccgctgg tttctcgacc gcatagccac gcatatcttg gcgtgtgaag
1001     gcgactccaa atgggtgttc ttcgacggca actatcaaga atacgaagcc
1051     gacaagaaac gccgactcgg caaagaaggc gcgaaaccga aacgcatcaa
1101     atacaaaccg gtaacgcgtt aa

```

This corresponds to the amino acid sequence <SEQ ID 1872; ORF 596.ng>:

g596.pep (partial).

```

1      ..MLLLDEPTNH LDAESVEWLE QFLVRFPGTV VAVTHDRYFL DNAAEWILEL
51     DRGHGIPWKG NYSSWLEQKE KRLNEAKSE AARVKAMKQE LEWVRONAKG
101    RQAKPKARLA RFEEMSNEYE QKRNETQEIF IPVAERLGNE VIEFVNVSKS
151    FGDKVLIDGL SFKVPAGAIV GIIGPNGAGK STLFKMIAGK EQPDSGEVKI
201    GQTVKMSLID QSREGLQNDK TVFDNIAEGR DILQVQFEI PARQYLGRFN
251    FKGSQSKIA RQLSGGERGR LHLAKTLLGG GNVLLLDDEPS NDLDVETLRA
301    LEDALLEFAG SVMVISHDRW FLDRIATHIL ACEGDSKWVF FDGNYQEYEA
351    DKRRLGKEG AKPKRIKYKP VTR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1873>:

m596.seq..

```

1      ATGTCCCAAC AATACGTCTA TTCTATGCTG CGCGTGAGCA AGGTTGTGCC
51     GCCGCAGAAA ACCATCATTA AAGATATTTT CCTTCTTTT TTCCCCGGCG
101    CGAAAATCGG CCTGCTCGGT TTGAACGGCG CGGGCAAGTC CACCGTGCTG
151    CGGATTATGG CGGGCGTGGA TAAGGAATTT GAGGGCGAAG CCGTGCCGAT
201    GGGCGGCATC AAAATCGGCT ACCTGCCGCA AGAGCCTGAG CTGTATCCGG
251    AAAAAACCGT GCGCGAGGAA GTGGAAAGCG GTTGGGGCGA AGTGGCTGCC
301    GCGCAGAAAC GTTTGGAAGA AGTGTATGCC GAGTACGCCA ATCCTGATGC
351    GGATTTTGAC GCGTTGGCAG AAGAGCAGGG CCGCTTGGA GCGATTATTG
401    CGGCAGGTTT GTCCACGGGC GCGGGTGCGG AACACGAATT GGAAATCGCC
451    GCCGACGCGC TGCGCCTGCC GGAATGGGAT GCCAAAATCG ATAATTGTCT
501    CGGCGGTGAA AAACGCGCGG TTGCCTTGTG CAAACTCTTG TTGAGCAAGC
551    CCGATATGCT TTTGCTGGAC GAGCCGACCA ACCACTTGGG TGCGGAATCG
601    GTCGAGTGGC TGGAGCAATT TCTCGTGCGC TCCCCGGCA CAGTCGTTGC
651    GGTAACGCAC GACCGCTACT TCCTCGACAA CGCCGCCGAA TGGAATTTGG
701    AACTCGACCG CGGCCATGGT ATTCCGTGGA AAGGCAATTA CTCGTCTTGG
751    CTGGAGCAGA AAGAAAAACG CTTGGAACAA GAGGCAAAAT CCGAAGCCGC
801    GCGCGTGAAG GCGATGAAGC AGGAATTGGA ATGGGTGCGC CAAAATGCCA
851    AAGGCCGCCA AGCCAAGTCC AAAGCGCGTT TGGCTCGTTT TGAAGAAATG
901    AGCAACTACG AATACCAAAA ACGCAATGAA ACGCAGGAAA TCTTTATTCC
951    CGTTGCCGAG CGTTTGGGTA ACGAAGTGAT TGAATTTGTA AATGTTTCCA
1001   AATCGTTTCG CGATAAAGTG CTGATTGACG ATTTGAGCTT CAAAGTGCC
1051   GCGGGCGCGA TTGTCGGCAT CATCGGCCCG AACGGCGCGG GTAAATCTAC
1101   GCTGTTCAAA ATGATTTTCG GCAAAGAGCA GCCTGATTCC GCGGAGGTGA
1151   AAATCGGACA AACCGTGAAG ATGAGCTTGA TTGACCAAAG CCGCGAAGGT
1201   TTGCAAAACG ACAAACCGT GTTCGACAA ATTGCCGAAG GCCGCGACAT
1251   TTTGCAGGTT GGTCAAGTTT AAATTCCCGC CCGCCAATAT TTGGGCGGTT
1301   TCAACTTCAA AGGCAGCGAC CAAAGCAAAA TTGCAGGTCA ATTGTCTGGC
1351   GCGCAACGCG GTCGTCTGCA CTTGGCAAAA ACCTTGTTGA GCGGCGGCAA
1401   TGTATTGCTG CTGGATGAAC CGTCTAACGA CCTTGACGTG GAAACCTGTC
1451   GCGCGTTGGA AGACGCATTG TTGGAATTTG CCGGCAGCGT GATGGTGATT
1501   TCGCACGACC GTTGGTTCCG CGACCGCATC GCCACGCATA TCTTGGCGTG
1551   TGAAGGCGAC TCTAAATGGG TGTTCTTCGA CGGCAACTAT CAGGAATACG
1601   AAGCCGACAA GAAACGCCGT TTGGGCGAAG AAGGCGCGAA ACCGAAACGC
1651   ATCAATACA AACCGGTAAC GCGTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1874; ORF 596>:

m596.pep..

946

```

1  MSQQYVYSML RVSKVVPQK TIIKDISLSF FPGAKIGLLG LNGAGKSTVL
51 RIMAGVDKEF EGEAVPMGGI KIGYLPQEPE LDPEKTVREE VESGLGEVAA
101 AQKRLEEVYA EYANPDADF ALAEEQGRLE AIIAAGSSTG GGAEHELEIA
151 ADALRLPEWD AKIDNLSGGE KRRVALCKLL LSKPDMLLLD EPTNHLD AES
201 VEWLEQFLVR FPGTVVAVTH DRYFLDNAAE WILELDRGHG IPWKGNYSW
251 LEQKEKRLN EAKSEAARVK AMQOELEWVR QNAKGRQAKS KARLARFEEM
301 SNYEYQKRNE TQEIFIPVAE RLGNEVIEFV NVSKSFGDKV LIDDLSEFKVP
351 AGAIVGIIGP NGAGKSTLFK MISGKEQPDG GEVKIGQTVK MSLIDQSREG
401 LQNDKTVFDN IAEGRDILQV GQFEIPARQY LGRFNFKGSD QSKIAGQLSG
451 GERGLHLAK TLLSGGNVLL LDEPSNDLDV ETLRALEDAL LEFAGSVMVI
501 SHDRWFLDRI ATHILACEGD SKWVFFDGN YQEYADKRRR LGEEGAKPKR
551 IKYKPVTR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

```

m596 g596 98.4% identity in 373 aa overlap

      160      170      180      190      200      210
m596.pep LPEWDAKIDNLSGGEKRRVALCKLLLSKPDMLLLDEPTNHLD AESVEWLEQFLVRFP GTV
g596                                     MLLLDEPTNHLD AESVEWLEQFLVRFP GTV
                                     10      20      30

      220      230      240      250      260      270
m596.pep VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
g596 VAVTHDRYFLDNAAEWILELDRGHGIPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQE
      40      50      60      70      80      90

      280      290      300      310      320      330
m596.pep LEWVRQNAKGRQAKSKARLARFEEMS NYEYQKRNETQEIFIPVAERLGN EVIEFVNVSKS
g596 LEWVRQNAKGRQAKPKARLARFEEMS NYEYQKRNETQEIFIPVAERLGN EVIEFVNVSKS
      100      110      120      130      140      150

      340      350      360      370      380      390
m596.pep FGDKVLIDDLSEFKVPAG AIVGIIGPNGAGKSTLFKMISGKEQPDGSEVKIGQTVKMSLID
g596 FGDKVLIDGLSFKVPAG AIVGIIGPNGAGKSTLFKMIAGKEQPDGSEVKIGQTVKMSLID
      160      170      180      190      200      210

      400      410      420      430      440      450
m596.pep QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIAGQLSGGERGR
g596 QSREGLQNDKTVFDNIAEGRDILQVGQFEIPARQYLGRFNFKGSDQSKIARQLSGGERGR
      220      230      240      250      260      270

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	460	470	480	490	500	510
m596.pep	LHLAKTLLSGGNVLLLD	EPSNDLDVETLRALED	ALLEFAGSVMVISHDRW	FLDRIATHIL		
	:					
g596	LHLAKTLLGGGNVLLLD	EPSNDLDVETLRALED	ALLEFAGSVMVISHDRW	FLDRIATHIL		
	280	290	300	310	320	330
	520	530	540	550	559	
m596.pep	ACEGDSKWVFFD	GNVQEY	EADKKRRLG	EAGAKPKRIK	YPVTRX	
g596	ACEGDSKWVFFD	GNVQEY	EADKKRRLG	EAGAKPKRIK	YPVTRX	
	340	350	360	370		

a596.seq

1	ATGTCCCAAC	AATACGTCTA	TTCTATGCTG	CGCGTGAGCA	AGGTTGTGCC
51	GCCGCAGAAA	ACCATCATT	AAGATATTTT	CCTTTCTTTT	TTCCCCGGCG
101	CGAAAATCGG	TTGGCTCGGT	TTGAACGGCG	CGGGCAAGTC	CACCGTGCCT
151	CGGATTATGG	CGGGCGTGG	TAAAGAATTT	GAGGGCGAAG	CCGTGCCATG
201	GGGCGGTATT	AAAATCGGCT	ACCTGCCGCA	AGAGCCTGAG	CTTGATCCGG
251	AAAAAACCGT	GCGTGAGGAA	GTGGAAAGCG	GTTTGGGCGA	AGTGGCTGCC
301	GCGCAGAAAC	GTTTGGAGGA	AGTGTATGCC	GAGTACGCCA	ATCCCGATGC
351	GGATTTTGAC	GCGTTGGCGG	AAGAGCAGGG	CGGTTTGGAA	GCGATTATTG
401	CGCGGGGTTT	GTCACGGGG	GGCGGTGCGG	AACACGAATT	GGAATTCGCT
451	GCCGACGCGC	TGCGCCTGCC	GGAATGGGAT	GCCAAAATCG	ATAATTTGTC
501	CGGCGGTGAA	AAACGCCGCG	TCGCTTTGTG	CAAACCTCTT	TTGAGCAAGC
551	CCGATATGCT	TTTGCTGGAC	GAGCCGACCA	ACCACCTGGA	TGCGGAAATCG
601	GTCGAGTGGC	TGGAGCAATT	TCTCGTCGCG	TTCCCTGGTA	CAGTCGTTGC
651	CGTAACACAC	GACCGCTACT	TCTCTGACAA	CGCCGCCGAA	TGGATTTTGG
701	AACTCGACCG	CGGGCACGGT	ATTCCGTGGA	AAGGAAATTA	CTCGTCTTGG
751	TTGGAGCAGA	AAGAAAAACG	TTTGGA AAAAC	GAGGCGAAAT	CCGAAGCCGC
801	GCGCGTGAAA	GCGATGAAG	AGGAATTGGA	ATGGGTGCGC	CAAAATGCCA
851	AAGGCGCTCA	AGCCAAGTCC	AAAGCGCGTT	TGGCGCGTTT	TGAAGAAATG
901	AGCAACTATG	AATACCAAAA	ACGCAATGAA	ACGCAAGAAA	TCTTCATTCC
951	CGTCGCCGAG	CGTTTGGGTA	ACGAAGTGAT	TGAATTTGTG	AATGTTTCCA
1001	AATCGTTTCG	CGACAAAGTG	CTGATTGACG	ATTTGAGCTT	CAAAGTGCCT
1051	GCGGGCGCGA	TTGTCCGGAT	CATCGGTCCG	AACGGCGCGG	GTAATTCGAC
1101	ACTGTTTAAA	ATGATTTCGG	GC AAGAGCA	GCCCGATTCC	GGTGAAGTGA
1151	AAATCGGGCA	AACCGTGAAA	ATGAGCTTGA	TTGACCAAAG	CCCGCAAGGT
1201	TTGCAAAACG	ACAAAACCGT	GTTCGACAAC	ATTGCCGAAG	GTGCGGATAT
1251	TTTACAGGTC	GGGCAGTTTG	AAATCCCCGC	CCGCCAATAT	TTGGGACGCT
1301	TCAATTTCAA	AGGCACGCAC	CAAAGCAAAA	TCACGGGGCA	GCTTTCCGGC
1351	GGCAACCGCG	GACGTTTGCA	CTTGGCAAAA	ACCTTGTGTG	CGGTTGGCAA
1401	TGTGTTTGCT	CTGGACGAAC	CGTCCAACGA	CCTCGACGTG	GAAACCTTCG
1451	GCGCGTTGGA	AGACGCATTG	CTGGAATTTG	CCGGCAGCGT	GATGGTGATT
1501	TCGCACGACC	GCTGGTTTCT	CGACCGTATT	GCTACGCATA	TCTTGGCTTG
1551	CGAAGGCGAC	TCCAAATGGG	TGTTCTTTGA	CGGCAACTAT	CAGGAATACG
1601	AAGCGCAACA	GAAACGCCGA	CTCGGCGAAG	AAGGCACGAA	ACCGAAACGC
1651	ATCAAATACA	AACCGGTAA	GCGTTAA		

a596.pep

1	MSQQYVYSML	RVSKVPPQK	TIKDISLSF	FPAKIGLLG	LNGAKSTVL
51	RIMAGVDKEF	EGEAVPMGGI	KIGYLPQEPE	LDPEKTVREE	VESGLGEVAA
101	AQKRLEEVYA	EYANPDADFD	ALAEEQGRLE	AIIAAGSSTG	GGAEHELEIA
151	ADALRLPEWD	AKIDNLSGGE	KRRVALCKLL	LSKPDMLLLD	EPTNHLDAES
201	VEWLEQFLVR	FPGTVVAVTH	DRYFLDNAEE	WILELDRGHG	IPWKNGYSWS
251	LEQKEKRLNE	EAKSEAAVRK	AMKQELWEVR	QNAKGRQAKS	KARLARFEEM
301	SNYEYQKRNE	TQEIFIPVAE	RLGNEVIEFV	NVSKSFGDKV	LIDDLSEKVP
351	AGAIVGIIGP	NGAGKSTLFK	MIAGKEQPDS	GEVKIGQTVK	MSLIDQSREG
401	LQNDKTVFDN	IAEGRDILQV	GQFEIPARQY	LGRFNFKGSD	QSKITGQLSG
451	GERGRHLHLK	TLLGGGNVLL	LDEPSNDLDV	ETLRALEDAL	LEFAGSVMVI
501	SHDRWFLDRI	ATHILACEGD	SKWVFFDGNV	QEYEAADKKR	LGEEGTKPKR
551	IKYKPVTR*				

m596/a596 99.3% identity in 558 aa overlap

948

m596.pep	10	20	30	40	50	60
	MSQQYVYSMLRVSKVVPQKTIIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
a596	MSQQYVYSMLRVSKVVPQKTIIKDISLSFFPGAKIGLLGLNGAGKSTVLRIMAGVDKEF					
	10	20	30	40	50	60
m596.pep	70	80	90	100	110	120
	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
a596	EGEAVPMGGIKIGYLPQEPELDPEKTVREEVESGLGEVAAAQKRLEEVYAEYANPDADF					
	70	80	90	100	110	120
m596.pep	130	140	150	160	170	180
	ALAEEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
a596	ALAEEQGRLEAIIAAGSSTGGGAHELEIAADALRLPEWDAKIDNLSGGEKRRVALCKLL					
	130	140	150	160	170	180
m596.pep	190	200	210	220	230	240
	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
a596	LSKPDMLLLDEPTNHLDAESVEWLEQFLVRFPGTVVAVTHDRYFLDNAAEWILELDRGHG					
	190	200	210	220	230	240
m596.pep	250	260	270	280	290	300
	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQLEWVRQNAKGRQAKSKARLARFEEM					
a596	IPWKGNYSWLEQKEKRLNEAKSEAARVKAMKQLEWVRQNAKGRQAKSKARLARFEEM					
	250	260	270	280	290	300
m596.pep	310	320	330	340	350	360
	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
a596	SNYEYQKRNETQEIFIPVAERLGNEVIEFVNVSKSFGDKVLIDDLSEFKVPAGAIVGIIGP					
	310	320	330	340	350	360
m596.pep	370	380	390	400	410	420
	NGAGKSTLFFKMISGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
a596	NGAGKSTLFFKMIAGKEQPDSEVKIGQTVKMSLIDQSREGLQNDKTVFDNIAEGRDILQV					
	370	380	390	400	410	420
m596.pep	430	440	450	460	470	480
	GQFEIPARQYLGRFNFKGSQSKIAGQLSGGERGRHLAKTLLSGGNVLLLDEPSNDLDV					
a596	GQFEIPARQYLGRFNFKGSQSKITGQLSGGERGRHLAKTLLSGGNVLLLDEPSNDLDV					
	430	440	450	460	470	480
m596.pep	490	500	510	520	530	540
	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQYADKKRR					
a596	ETLRALEDALLEFAGSVMVISHDRWFLDRIATHILACEGDSKWVFFDGNVQYQYADKKRR					
	490	500	510	520	530	540
m596.pep	550	559				
	LGEEGAKPKRIKYKPVTRX					
a596	LGEEGAKPKRIKYKPVTRX					
	550					

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1877>

g597.seq

```

1  ATGCTGCTTC ATGTCAGCAA TTCCTCAAA CAGCTTCAGG AAGAGCGTAT
51  CCGCCAAGAA CGTATCCGCC AAGAGCGTAT CCGTCAGGCG CGCGGCAACC
101 TTGCTTCCGT CAACGCAAA CAGCGCGAGG CTTGGGACAA ATTCCAAAAA

```

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151 CTCAATACCG AGCTGAACCG TTTGAAAACG GAAGTCGCCG CTACGAAAGC
201 GCAGATTTCC CGTTTCGTAT CGGGGAAC TA AAAACAGC CGGCCGAATG
251 CGGTTGCCCT GTTCTTGAAA AACGCCGAAC CGGGTCAGAA AAACCGCTTT
301 TTGCGTTATA CGCGTTATGT AAACGCCTCC AATCGGGAAG TTGTCAAGGA
351 TTTGAAAAAA CAGCAGAAGG CTTTGGCGGT ACAAGAGCAG AAAATCAACA
401 ATGAGCTTGC CCGTTTGAAG AAAATTCAGG CAAACGTGCA ATCCCTGCTG
451 AAAAAACAGG GTGTAACCGA TCGCGCGGAA CAGACGGAAA GCCGCAGACA
501 AAATGCCAAA ATCTCCAAAG ATGCCCGAAA ACTGCTGGAA CAGAAAGGGA
551 ACGAGCAGCA GCTGAACAAG CTCTTGAGCA ATTTGgagaa aaAAAAagcc
601 gaacaccgCA TTcaggAtgc ggAagcaaaa agaAAATTGG CTGAagcCaa
651 actGgcggca gccgAAAAAG CCAGAAAAGA AGCGCGCAG CAGAAGGCTG
701 AAGCGCGACG TCGGGAATG TCCAACCTGA CCGCCGAAGA CAGGAACATC
751 CAAGCGCCTT CGGTTATGGG TATCGGCAGT GCCGACGgTT TCAGCCGCAT
801 GCAGGGACGT TTGAAAAAAC CGGTTGACGG TGTGCCGACC GGGCTTTTCG
851 GGCAGAACCG GAGCGGcggc GATGTTTGA AAGCGGTGT CTATTCCACT
901 GCGCTGCAA CGGTTGAAAG CATTGCGCcg gGAACggtaa GCTATGCGGA
951 cgaGTTGGAC GGTACCGCA AAGTGGTCGT GATCGATCAC GGCAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTTCCGCCG CAAGGGTTAT
1051 ACGGTGCGCG CAGGAAGCAA AATCGGCACG AGCGGGTTCG TGCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCGAGGTCAG GTGTTGAACC
1151 CTTCGGGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1878; ORF 597>:

g597.ppep

```

1 MLLHVSNSLK QLQEERIRQE RIRQERIROA RGNLASVNRK QREAWDKFQK
51 LNTLNLRLKT EVAATKAQIS RFVSGNYKNS RPNALVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVOSLL
151 KKQGVTDAAE QTESRRQNAK ISKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEAKLAA AEKARKEAAQ OKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVIDH GENYISIIYAG LSEISAGKGY
351 TVAAGSKIGT SGSLPDGEEG LYLQIRYRQ VLNPSGWIR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1879>:

m597.seq

```

1 ATGCTGCTTC ATGTCAGCAA TTCCCTCAAA CAGCTTCAGG AAGAGCGTAT
51 CCGCCAAGAG CGTATCCGTC AGGCGCGCGG CAACCTTGCT TCCGTCAACC
101 GCAACACAGC CGAGGCTTGG GACAAGTTCC AAAAACTCAA TACCGAGCTG
151 AACCGTTTGA AACCGGAAGT CGCCGCTACG AAAGCGCAGA TTTCCCGTTT
201 CGTATCGGGG AACTATAAAA ACAGCCAGCC GAATGCGGTT GCCCTGTTC
251 TGA AAAACGC CGAACCGGT CAGAAAACC GCTTTTTCG TTATACGCGT
301 TATGTAAACG CCTCCAATCG GGAAGTTGTC AAGGATTGGA AAAAACAGCA
351 GAAGGCTTTG GCGGTACAAG AGCAGAAAAT CAACAATGAG CTTGCCGTT
401 TGAAGAAAAT TCAGGCAAAC GTGCAATCTC TGCTGAAAAA ACAGGGTGTA
451 ACCGATGCGG CGGAACAGAC GGAAGCCGC AGACAGAATG CCAAAATCGC
501 CAAAGATGCC CGAAAAC TGC TGAACAGAA AGGGAACGAG CAGCAGCTGA
551 AAGAGCTCTT GAGCAATTG GAGAAGAAA AGGCCGAACA CCGATTGAG
601 GATGCGGAAG CAAAAGAAA ATTGGCTGAA GCCAGACTGG CGGCAGCCGA
651 AAAAGCCAGA AAAGAAGCGG CGCAGCAGAA GGTGAAGCA CGACGTGCGG
701 AAATGTCCAA CCTGACCGCC GAAGACAGGA ACATCCAAG GCCTTCGGTT
751 ATGGGTATCG GCAGTGCCGA CGGTTTCAGC CGCATGCAAG GACGTTTGAA
801 AAAACCGGTT GACGGTGTGC CGACCGGACT TTTCGGGCGA AACCGGAGCG
851 GCGGCGATAT TTGAAAGGC GTGTTCTATT CCACTGCACC GGCAACGGTT
901 GAAAGCATTTG CGCCGGGAAC GGTAAAGCTAT GCGGACGAGT TGGACGGCTA
951 CGGCAAAGTG GTCGTGGTGC ATCAGGCGCA GAACTACATC AGCATCTATG
1001 CCGGTTTGA GCAAAATTCC GTCGGCAAGG GTTATATGGT CGCGGCAGGA
1051 AGCAAAATCG GCTCGAGCGG GTCGCTGCCG GACGGGGAAG AGGGGCTTTA
1101 CCTGCAAATA CGTTATCAAG GTCAGGTATT GAACCTTCG AGCTGGATAC
1151 GTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1880; ORF 597>:

m597.ppep

```

1 MLLHVSNSLK QLQEERIRQE RIRQARGNLA SVNRKQREAW DKFQKLNTEL
51 NRLKTEVAAT KAQISRFVSG NYKNSQPNV ALFLKNAEPG QKNRFLRYTR
101 YVNASNREV KLEKQKQKAL AVQEQKINNE LARLKKIQAN VQSLLKKQGV
151 TDAAEQTESR RQNAKIAKDA RKLLEQKGNE QQLNKLNSL EKKKAEHRIQ
201 DAEAKRKLAE ARLAAAEKAR KEAAQQAEEA RRAEMSNLTA EDRNIQAPSV
251 MIGSADGFS RMQRLKKPV DGVPTGLFGQ NRSGGDIWKG VFYSTAPATV
301 ESIAPGTVSY ADELGYGKV VVDHGENYI SIYAGLSEIS VGKGYMVAAG
351 SKIGSSGSLP DGEEGLYLQI RYQGQVLNPS SWIR*

```

950

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 597 shows 96.1% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. gonorrhoeae*:

m597/g597 96.1% identity in 389 aa overlap

	10	20	30	40	50	60
g597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNRKLT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNRKLT					
	10	20	30	40	50	
	70	80	90	100	110	120
g597.pep	EVAATKAQISRFVSGNYKNSRPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
g597.pep	QQKALAVQEQQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKISKDARKLLE					
m597	QQKALAVQEQQKINNELARLKKIQANVQSLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
g597.pep	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEAKLAAAEKARKEAAQQKAEARRAEM					
m597	QKGNEQQLNKLKLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
g597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGRLLKPPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
g597.pep	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYAGLSEISAGKGYTVAAGSKIGT					
m597	APATVESIAPGTVSYADELDGYGKVVVIDHGENYISYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
g597.pep	SGSLPDGEEGLYLQIRYRGQVLNPSGWIRX					
m597	SGSLPDGEEGLYLQIRYQGVLPSSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1881>

a597.seq

1	ATGCTGCTTC	ATGTCAGCAA	TTCCTCAAG	CAGCTTCAGG	AAGAGCGTAT
51	CCGCCAAGAA	CGTATCCGCC	AAGAGCGTAT	CCGTCAGGCG	CGCGGCAACC
101	TTGCTTCCGT	CAACCGCAAA	CAGCGCGAGG	CTTGGGACAA	GTTCCAAAAA
151	CTCAATACCG	AGCTGAACCG	TTTGAAAACG	GAAGTCGCGG	CTACGAAAGC
201	GCAGATTTCC	CGTTTCGTAT	CGGGGAACCTA	TAAAAACAGC	CAGCCGAATG
251	CGGTTGCCCT	GTTCTGAAA	AACGCCGAAC	CGGGTCAGAA	AAACCGCTTT
301	TTGCGTTATA	CGCGTTATGT	AAACGCCTCC	AATCGGGAAG	TTGTCAAGGA
351	TTTGGAAGAAA	CAGCAGAAAG	CTTTGGCGGT	ACAAGAGCAG	AAAATCAACA
401	ATGAGCTTGC	CGGTTTGAAG	AAAATTCAGG	CAAACGTGCA	ATCCCTGCTG
451	AAAAACAGAG	GTGTAACCGA	TGCGGCGGAA	CAGACGGAAA	CGCCGAGACA
501	GAATGCCAAA	ATCGCCAAAG	ATGCCCGAAA	ACTGCTGGAA	CAGAAAGGGA
551	ACGAGCAGCA	GCTGAACAAG	CTCTTGAGCA	ATTTGGAGAA	GAAAAAGGCC
601	GAACACCGCA	TTCAGGATGC	GGAAGCAAAA	AGAAAATTGG	CTGAAGCCAG
651	ACTGGCGGCA	GCCGAAAAAG	CCAGAAAAGA	AGCGGCGCAG	CAGAAGGCTG
701	AAGCAACGAC	TGCGGAAATG	TCCAACCTGA	CCGCCGAAGA	CAGGAACATC
751	CAAGCGCCTT	CGGTTATGGG	TATCGGCAGT	GCCGACGGTT	TCAGCCGCAT
801	GCAAGGACGT	TTGAAAAAAC	CGGTTGACGG	TGTGCCGACC	GGACTTTTCG
851	GGCAGAACCG	GAGCGGCGGC	GATGTTTGA	AAGGCGGTGT	CTATTCCACT
901	GCACCGGCAA	CGGTTGAAAG	CATTGCGCCG	GGAACGGTAA	GCTATGCGGA

951

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951  CGAGTTGGAC GGCTACGGCA AAGTGGTCGT GGTGATCAC GCGGAGAACT
1001 ACATCAGCAT CTATGCCGGT TTGAGCGAAA TTCCGTCGG CAAGGGTTAT
1051 ATGGTCGCGG CAGGAAGCAA AATCGGCTCG AGCGGGTCGC TGCCGACGG
1101 GGAAGAGGGG CTTTACCTGC AAATACGTTA TCAAGGTCAG GTATTGAACC
1151 CTTCGAGCTG GATACGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1882; ORF 597.a>:

a597.pep

```

1  MLLHVSNSLK QLQEERIRQE RIRQERIRQA RGNLASVNRK QREAWDKFQK
51  LNTELNR LKT EVAATKAQIS RFVSGNYKNS QPNAVALFLK NAEPGQKNRF
101 LRYTRYVNAS NREVVKDLEK QQKALAVQEQ KINNELARLK KIQANVQSLL
151 KKQGVTDAAE QTESRRQNAK IAKDARKLLE QKGNEQQLNK LLSNLEKKKA
201 EHRIQDAEAK RKLAEARLAA AEKARKEAAQ QKAEARRAEM SNLTAEDRNI
251 QAPSVMGIGS ADGFSRMQGR LKKPVDGVPT GLFGQNRSGG DVWKGVFYST
301 APATVESIAP GTVSYADELD GYGKVVVDH GENYISIIYAG LSEISVGKGY
351 MVAAGSKIGS SGSLPDGEEG LYLQIRYQGG VLNPSWIR*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. meningitidis*

ORF 597 shows 98.5% identity over a 389 aa overlap with a predicted ORF (ORF 597) from *N. meningitidis*

m597/a597 98.5% identity in 389 aa overlap

	10	20	30	40	50	60
a597.pep	MLLHVSNSLKQLQEERIRQERIRQERIRQARGNLASVNRKQREAWDKFQKLNTELNR LKT					
m597	MLLHVSNSLKQLQEERIRQERIRQ-----ARGNLASVNRKQREAWDKFQKLNTELNR LKT					
	10	20	30	40	50	
	70	80	90	100	110	120
a597.pep	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
m597	EVAATKAQISRFVSGNYKNSQPNAVALFLKNAEPGQKNRFLRYTRYVNASNREVVKDLEK					
	60	70	80	90	100	110
	130	140	150	160	170	180
a597.pep	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
m597	QQKALAVQEQKINNELARLKKIQANVQSLLKKQGVTDAAEQTESRRQNAKIAKDARKLLE					
	120	130	140	150	160	170
	190	200	210	220	230	240
a597.pep	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
m597	QKGNEQQLNKLLSNLEKKKAEHRIQDAEAKRKLAEARLAAAEKARKEAAQKAEARRAEM					
	180	190	200	210	220	230
	250	260	270	280	290	300
a597.pep	SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDVWKGVFYST					
m597	SNLTAEDRNIQAPSVMGIGSADGFSRMQGR LKKPVDGVPTGLFGQNRSGGDIWKGVFYST					
	240	250	260	270	280	290
	310	320	330	340	350	360
a597.pep	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
m597	APATVESIAPGTVSYADELDGYGKVVVDHGENYISIIYAGLSEISVGKGYMVAAGSKIGS					
	300	310	320	330	340	350
	370	380	390			
a597.pep	SGSLPDGEEGLYLQIRYQGVVLNPSWIRX					
m597	SGSLPDGEEGLYLQIRYQGVVLNPSWIRX					
	360	370	380			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1883>:

```
g601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTGACGAA ATTGATGTGC CGAATATAGG
 51  TCGTCTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101  ACGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAGGA CGACATCAAC
151  AACGATGCCG CCGCGCTGGA AAAATTTGAA ACCATCCGCG CATATGGCGC
201  GCTGAAAATG GGTTCGATCA GCGACGTATC CGAAGCCGCC GCCCGCGCGC
251  GCACGCCGAA ACCCGCCTTC GTGCGGCCCG CCGCCGATTA CACCGCCTCC
301  AGCGGCAAAA CCGTAAACGC CGCCGACATC GATTTGCCGG TACGCGCCCT
351  GAGCATGGGC AAACCTGCACC ACGCTATGAT GGGCATCGCC TCGGTCGCCA
401  TCGCCGCCGC CGTGCTCGGT ACGCTGGTCA ACCTTGCCGC AGGCGGCGGA
451  ACGCGTAAAG AAGTGCCTT CGGGCATCCG TCAGGTACGC TCGGTGTCGG
501  TGCTGCCGCC GAATGTCAGG ACGGACAATG GACGGCCGCC aaagcgggtca
551  tgaGCCGCAG CGCACgcgtg attatggaaa gttgGGTGCg cgttccccgat
601  gattGTTTTT GA
```

This corresponds to the amino acid sequence <SEQ ID 1884; ORF 601.ng>:

```
g601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE TIRAYGALKM GLISDVSEAA ARARTPKPAF VAPAADYTAS
101  SGKTVNAADI DLPVRALSMG KLHAMMGIA SVAIAAAVLG TLVNLAAGGG
151  TRKEVRFGHP SGTLRVGAAA ECQDQGWTAA KAVMSRSARV IMESWVRVPD
201  DCF*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1885>:

```
m601.seq
  1  ATGTTCCCAA CCGGCAATTT GGTGATGAA ATTGATGTGC CGAATATAGG
 51  CCGTTTGAAA GCCACGCTCA TCAACGCGGG CATTCCGACC GTTTTCCTGA
101  ATGCCGCCGA CTTGGGCTAC ACAGGCAAAG AGTTGCAAGA CGACATCAAC
151  AACGATGCCG CGGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201  GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCTCGCGCGC
251  ACACGCCGAA AGTCGCCTTC GTGCGGCCCG CCGCCGATTA CACCGCCTCC
301  AGTGGCAAAA CCGTGAACGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351  GAGCATGGGC AAACCTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401  TTGCGACCGC CGCCGCCGTA CCCGGTACGC TGGTCAACCT TGCCCGAGGC
451  GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501  CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551  CCGTCATGAG CCGTAGCGCA CGCGTGATGA TGGAAGGTTG GGTGAGGGTG
601  CCTGAGGATT GTTTTAA
```

This corresponds to the amino acid sequence <SEQ ID 1886; ORF 601>:

```
m601.pep
  1  MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
 51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101  SGKTVNAADI DLLVRALSMG KLHAMMGTA SVAIATAAAV PGTLVNLAAG
151  GGTRKEVRFG HPSGTLRVGA AAECQDQWAT ATKAVMSRSA RVMMEGWVRV
201  PEDCF*
```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 601 shows 94.1% identity over a 205 aa overlap with a predicted ORF (ORF 601.ng) from *N. gonorrhoeae*:

m601/g601

```

          10      20      30      40      50      60
m601.pep  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          |||||
g601       MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
          10      20      30      40      50      60

          70      80      90     100     110     120
m601.pep  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLLVRALSMG
```

953

```

      |||
g601  TIRAYGALKMGLISDVSEAAARARTPKPAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT
      |||
g601  KLHHAMMGTA SVAI--AAAVLGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT
      130     140     150     160     170

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |:|||||:|:|:|:|:|
g601  AAKAVMSRSARVIMESWVRVPDDCFX
      180     190     200

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1887>:

```

a601.seq
1   ATGTTCCCAA CCGGCAATTT GGTCGATGAA ATTGATGTGC CGAATATAGG
51  CCGTTTGAAG GCCACGCTCA TCAACGCGGG CATTCGACCG GTTTTCCTGA
101 ATGCCGCCGA CTTGGGCTAC ACGGGCAAAG AGTTGCAAGA CGACATCAAC
151 AACGATGCCG CAGCTTTGGA AAAATTCGAG AAAATCCGCG CTTACGGTGC
201 GCTGAAAATG GGTCTGATCA GCGACGTATC CGAAGCTGCC GCCCGCGCGC
251 ACACGCCGAA AGTCGCCTTC GTCGCGCCCG CCGCCGATTA CACCGCCTCC
301 AGTGGCAAAA CCGTGAATGC CGCCGACATC GATTTGCTGG TACGCGCCCT
351 GAGCATGGGC AAATTGCACC ACGCGATGAT GGGTACCGCC TCTGTTGCCA
401 TTGCGACCGC CGCCGCCGTG CCCGGTACGC TGGTCAACCT TGCCGCAGGC
451 GGCGGAACGC GTAAAGAAGT GCGCTTCGGG CATCCTTCCG GCACATTGCG
501 CGTCGGTGCA GCCGCCGAAT GTCAGGACGG ACAATGGACG GCCACCAAAG
551 CGGTTATGAG CCGCAGCGCA CGCGTGATGA TGGAGAGTTG GGTGAGGGTG
601 CCGGAAGATT GTTTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1888; ORF 601.a>:

```

a601.pep
1   MFPTGNLVDE IDVPNIGRLK ATLINAGIPT VFLNAADLGY TGKELQDDIN
51  NDAAALEKFE KIRAYGALKM GLISDVSEAA ARAHTPKVAF VAPAADYTAS
101 SGKTVNAADI DLLVRALSMG KLHHAMMGTA SVAIATAAAV PGTLVNLAAG
151 GGTKEVRFH HPSGTLRVGA AAECQDGQWT ATKAVMSRSA RVMMEGWVRV
201 PEDCF*

```

m601/a601 100.0% identity in 205 aa overlap

```

      10      20      30      40      50      60
m601.pep MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      |||
a601  MFPTGNLVDEIDVPNIGRLKATLINAGIPTVFLNAADLGYTGKELQDDINNDAAALEKFE
      10      20      30      40      50      60

      70      80      90      100     110     120
m601.pep KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      |||
a601  KIRAYGALKMGLISDVSEAAARAHTPKVAFVAPAADYTASSGKTVNAADIDLVRALSMG
      70      80      90      100     110     120

      130     140     150     160     170     180
m601.pep KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT
      |||
a601  KLHHAMMGTA SVAIATAAAVPGTLVNLAAGGGTRKEVRFHPSGTLRVGAAAECQDGQWT
      130     140     150     160     170     180

      190     200
m601.pep ATKAVMSRSARVMMEGWVRVPEDCFX
      |||
a601  ATKAVMSRSARVMMEGWVRVPEDCFX
      190     200

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1889>:

```
g602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTC CCTTCTGCT
51  CGGCGGGCAG ATAAACCGTC ATCGTCAGGC GAGCAACCGT GGATTGTGTT
101 CCTTCGGCGG TTTTCAGGGT AATCGGGAAG CGCAGGTCTT TAATGCCGAC
151 CTGATTGATC GGCAGGTTGC GCAAATCTCT GCTGGATTGC ACGTCTGCAA
201 TGGCGTTCAT GCGTTGTTTG TCCTTAATAT TCAGATAATT ATTGAGATGT
251 GTGTATTGTA TGGCAGGcag atgccgtctg aAAAAacgct gtcggCCGCC
301 TGCTGCAAAA TgcgagattA TATCACTTGC TTTtggcgGC TGCATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1890; ORF 602.ng>:

```
g602.pep
1  MLLHQCDKAR HMRPFLGGO INRHRQASNR GLCSFGGFQG NREAQVFNAD
51  LIDRQVAQIS AGLHVCNGVH ALFVLNIQII IEMCVLYGRQ MPSEKTLCAA
101 CLQMRDYITC FWRLH*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1891>:

```
m602.seq
1  ATGTTGCTCC ATCAATGCGA CAAACGCGA CATATGCGTC CCCTTCTGCT
51  CAGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAATGGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC GCCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1892; ORF 602>:

```
m602.pep
1  MLLHQCDKTR HMRPLLSRQ VNRHQQTGNG GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS AGEYTVNLQM
101 RDYITRF*QL H*
```

m602/g602 65.2% identity in 115 aa overlap

	10	20	30	40	50	60
m602.pep	MLLHQCDKTRHMRPFLLSRQVNRHGTGNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: : : :: :: :: : : :					
g602	MLLHQCDKARHMRPFLGGINRHRQASNRGLCSFGGFQGNREAQVFNADLIDRQVAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602.pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSAGEYTVN---LQMRDYITRF*QLHX					
	: :: : : : :: :					
g602	AGLHVCNGVHALFVLNIQIIEMCVLYGRMPSEKTLAAQLQMRDYITCFWRLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1893>:

```
a602.seq
1  ATGTTGCTCC ATCAATGCGA CAAAGCGCGA CATATGCGTA CCCTTCTGCT
51  CGGCAGGCAG GTAAACCGTC ATGGTCAGAC GGGCAACTGT GGACTGGATG
101 CCTTCTGCAG TTTGCAGGGT AATCGGAAAG CGCAGGTCTT TGATACCGAC
151 CTGATTGATC GGCAGATTGC GCAAATCTCG GCTGGATTGC ACGTCTGCAA
201 TAGTGTTTAT GAGTTGTTTT TCCTTAATAT TCATGTAATT GTTGAGATGT
251 GTGCATGGTA TGGCGTTTCC ACCGGGGAAT ATACCGTCAA TCTGCAAATG
301 CGAGATTATA TCACTCGCTT TTAGCAGCTG CATTGA
```

This corresponds to the amino acid sequence <SEQ ID 1894; ORF 602.a>:

```
a602.pep
1  MLLHQCDKAR HMRTLLLRQ VNRHQQTGNC GLDAFCSLQG NRKAQVFDTD
51  LIDRQIAQIS AGLHVCNSVH ELFFLNHVI VEMCAWYGVS TGEYTVNLQM
101 RDYITRF*QL H*
```

m602/a602 95.5% identity in 111 aa overlap

955

	10	20	30	40	50	60
m602 . pep	MLLHQCDKTRHMRPLLLSRQVNRHGQTGNNGGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	: :					
a 602	MLLHQCDKARHMRLLLLGRQVNRHGQTGNCGLDAFCSLQGNRKAQVFDTDLIDRQIAQIS					
	10	20	30	40	50	60
	70	80	90	100	110	
m602 . pep	AGLHVCNSVHELFFLNHIVIVEMCAWYGVVSAGEYTVNLQMRDYITREFXQLHX					
a 602	AGLHVCNSVHELFFLNHIVIVEMCAWYGVSTGEYTVNLQMRDYITREFXQLHX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1895>:

g603 . seq

```

1  ATGGATTCCC GCCTGCGTGG GAATGACGCT AGGAAATACG GCATACGCTT
51  TGCCCAAAGA GGCCGTCTGA AACACACTCC GCCCAACGCC CATCCTTTTT
101 CAGACGGCCC CGCACC AAAA AAACAACCAC AAAC TACAAG GAGAAACATC
151 ATGTCCGACC AACTCATTCT TGTCCTGAAC TGCGTCAGTT CATCGCTCAA
201 AGGCGCCGTT ATCGACCGCA AAAGCGGCAG CGTCGTCCTA AGCTGCCTCG
251 GGAACCGCCT GACTACGCCC GAAGCCGTCA TTACCTTCAA CAAAGACGGC
301 AACAAACGCC AAGTTCCCTT GAGCGGCCGC AACTGCCACG CCGGCGCGGT
351 GGGTATGCTG TTGAACGAAC TGGAAAAACA CGGACTGCAC GACCGCATCA
401 AAGCCATCGG CCGCCGCATC GCCCAGCGCG GCGAAAAATA TCACGAGTCC
451 GTCCTCATCG ACCAAGACGT CCTTGACGAA CTGAAAGCCT GCATCCCGTT
501 CGCCCCGCTG CACAACCCCG CCAACATCAG CGGCATCCTC GCCGCGCAGG
551 AACACTTTCC CGGCCTGCCC AACGTCGGCG TGATGGACAC CTCGTTCCAC
601 CAAACCATGC CGGAGCGGGC CTACACTTAT GCCGTGCCGC GCGAATTGCG
651 CAAAAAATAC GCCTTCCGCC GCTACGTTT CCACGGTACC GGTATGCGTT
701 ACGTCGCCCC TGAAGCCGCA CGCATCTTGG GCAAACCTct ggaaGACATC
751 CGCATGATTA TTGCCACTT AGGCAACGGC GCATCTATTA CCGCCGTCAA
801 AAACGGCAAA TCCGTCGATA CCGGTATGGG TTTCACGCCG ATCGAAGGTT
851 TGGTAATGGG TACACGTTGC GCGGACACCG ATCCGGGCGT ATACAGCTAT
901 CCGACTTTCC ACGCAGGGAT GGATGTTGCC CAAGTTGATG AAATGCTGAA
951 CGAAAAATCA GGTTCCTCCG GTATTTCcgA actTCCCAAC GACTGCCGCA
1001 CCCTCGAAAT CGCCGCCGAC GAAGGCCGCG AAGGCGCGCG CCTCGCCCTc
1051 gaAGTCATGA CCTGCGCCT CGCCAAATAC ATCGCTTCGA TGGCTGTGGC
1101 CTGCGGCAGT GTTGACGCAC TCGTGTTTAC CGGCGGTATC GGCAGAAACT
1151 CGCGTAATAT CCGTGCCAAA ACCGTTTCTT ATCTTGATTT CTTGGGTCTG
1201 CACATCGACA CCAAAGCCAA TATGGAAAAA CGTACGGCA ATTCCGGCAT
1251 TATCAGCCCG ACCGATTCTT CTCCGGCTGT TTTGGTCGTC CCGACCAATG
1301 AAGAACTGAT GATTGCCTGC GACACTGCCG AACTTGCCGG CATCTTGTAG

```

This corresponds to the amino acid sequence <SEQ ID 1896; ORF 603.ng>:

g603 . pep

```

1  MDSRLRGNDA RKYGIRFAQR GRLKHTPPNA HPFSDGPAPK KQPQTTRRNI
51  MSDQLILVLN CVSSSLKGAV IDRKSGSVVL SCLGERLTTP EAVITFNKDG
101 NKRQVPLSGR NCHAGAVGML LNELEKHGLH DRIKAIGRRI AHGGEKYHES
151 VLIDQDVLDE LKACIPFAPL HNPANISGIL AAQEHFPGLP NVGVMDTSFH
201 QTMPELAYTY AVPRELRKKY AFRRYGFHGT GMRYVAPEAA RILGKPLEDI
251 RMIIAHLGNG ASITAVKNGK SVDTGMGFTP IEGLVMGTRC GDTDPGVYSY
301 PTFHAGMDVA QVDEMLNEKS GFPGISELPN DCRTLEIAAD EGREGARLAL
351 EVMTCRLAKY IASMAVACGS VDALVFTGGI GENSRNIRAK TVSYLDFLGL
401 HIDTKANMEK RYGNSGIISP TDSSPAVLV PTNEELMIAC DTAELAGIL*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1897>:

m603 . seq

```

1  CTGTCTCGC GTAGCGGGG ACGBAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGGCGGTC TGAAACACCT TGCGCCTGAT GTCTGC.CTT
101 TTTCAGACGA CCCCACTA AAAAAACAAC CACAACTAC AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT CCTCGTTCTG AACTGCGGCA GTTCATCGCT
201 CAAAGGCGCC GTTATCGACC GAmAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG cCtGACCACG CCCGAAGCCG TCATTACGTT CAACAAAGAC

```

301	GGCAACAAAC	GCCAAGTTCC	CCTGAGCGGC	CGAAATTGCC	ACGCCGGCGC
351	GGTGGGTATG	CTTTTGAACG	AACTGGAAAA	ACACGGTCTG	CACGACCGCA
401	TCAAAGCCAT	CGGCCACCGC	ATCGCCACG	GCGGCGAAAA	ATACAGCGAG
451	TCTGTTTTGA	TCGACCAGGC	CGTAATGGAC	GAACTCAATG	CCTGCATTCC
501	GCTTGCGCCG	CTGCACAACC	CCGCCAACAT	CAGCGGCATC	CTTGCCGCAC
551	AGGAACATTT	CCCCGGTCTG	CCCAATGTGC	CGGTGATGGA	TACTTCGTTT
601	CACCAAACCA	TGCCGGAGCG	TGCCTACACT	TATGCCGTGC	CGCGCGAGTT
651	GCGTAAAAAA	TACGCTTTCC	GCCGCTACGG	TTTCCACGGC	ACCAGTATGC
701	GTTACGTTGC	CCCTGAAGCC	GCACGCACTT	TGGGCAAACC	TCTGGAAGAC
751	ATCCGCATGA	TATTATGCCA	CTTAGGCATC	GGCGCATATC	TTACCGCCAT
801	CAAAAACGGC	AAATCCGTCG	ATACCAGTAT	GGGTTTCACG	CCGATCGAAG
851	GTTTGGTAAAT	GGGTACACGT	TGCGGCGACA	TCGATCCGGG	CGTATACAGC
901	TATCTGACTT	CCCACGCCGG	GATGGATGTT	GCCCAAGTGG	ATGAAATGCT
951	GAACAAAAAA	TCAGGTTTGC	TCGGTATTTT	CGAACTTTCC	AACGACTGCC
1001	GCACCCTCGA	AATCGCCGCC	GACGAAGGCC	ACGAAGGCGC	GCGCCTCGCC
1051	CTCGAAGTCA	TGACCTACCG	CCTCGCCAAA	TACATCGCTT	CGATGGCTGT
1101	GGGCTGCGGC	GGCGTTGACG	CACCTCGTGT	CACCGCGCGT	ATCGGCGAAA
1151	ACTCGCGTAA	TATCCGTGCC	AAAACCGTTT	CCTATCTTGA	TTTCTTGGGT
1201	CTGCACATCG	ACACCAAAGC	CAATATGGAA	AAACGCTACG	GCAATTCGGG
1251	CATTATCAGC	CCGACCGATT	CTTCTCCGGC	TGTTTTGGTT	GTCCCGACCA
1301	ATGAAGAACT	GATGATTGCC	TGCGACACTG	CCGAAC TTGC	CGGCATCTTG
1351	TAG				

m603.ppt

1	LSSRRRGRNN	DRKCGIRFAQ	RGLRLKHLAPD	VCXFSDDPTL	KKQPQTTRRN
51	IMSDQLILVL	NCGSSSLKGA	VIDRXSGSVV	LSCLGERLTT	PEAVITFNKD
101	GNKRQVPLSG	RNCHAGAVGM	LLNELEKHGL	HDRIKAIGHR	IAHGGEKYSE
151	SVLIDQAVMD	ELNACIPLAP	LHNPANISGI	LAAQEHFPGL	PNVGVMDSF
201	HQTMPERAYT	YAVPRELRKK	YAFRRYGFHG	TSMRYVAPEA	ARILGKPLED
251	IRMIIAHLGN	GASITAIKNG	KSVDTSMGFT	PIEGLVMGTR	CGDIDPGVYS
301	YLTSHAGMDV	AQVDEMLNKK	SGLLGISELS	NDCRTLEIAA	DEGHEGARLA
351	LEVMTYRLAK	YIASMAVCGC	GVDALVFTGG	IGENSRNIRA	KTVSYDLFLG
401	LHIDTKANME	KRYGNSGIIS	PTDSSPAVLV	VPTNEELMIA	CDTAELAGIL
451	*				

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 603 shows 91.6% identity over a 450 aa overlap with a predicted ORF (ORF 603.ng) from *N. gonorrhoeae*:

m603/q603

		10	20	30	40	50	60
m603.pep		LSSRRRGRNNDRKC	GIRFAQGR	LKHLAPDVC	XFSDDPTL	KKQPQTTRR	NIMSDQLILVL
		: :	: :		: :	: :	
g603		MDSRLRG-NDARKY	GIRFAQGR	LKHTFPNA	HPFSDGPA	PKKQPQTTRR	NIMSDQLILVL
		10	20	30	40	50	
		70	80	90	100	110	120
m603.pep		NCGSSSLKGAVIDR	XSGSVVLS	CLGERLTT	PEAVITFN	KDGNKRQV	PLSGRNCHAGAVGM
g603		NCVSSSLKGAVIDR	KSGSVVLS	CLGERLTT	PEAVITFN	KDGNKRQV	PLSGRNCHAGAVGM
	60	70	80	90	100	110	
		130	140	150	160	170	180
m603.pep		LLNELEKHGLHDRI	KAIGHRIA	HGGEKYS	ESVLIQAV	MDELNACI	PLAPLHN PANISGI
				:		:	:
g603		LLNELEKHGLHDRI	KAIGRRIA	HGGEKYH	ESVLIQD	VDLDELK	ACIPFAPLHN PANISGI
	120	130	140	150	160	170	
		190	200	210	220	230	240
m603.pep		LAAQEHFPGLPNV	GVMDTSF	HQTMPER	AYTYAVP	PRELRKKY	AFRRYGFHGTSMRYVAPEA

957

```

g603      LAAQEHFPLPNVGVMDTSFHQTMPERAYTYAVPRELRKKYAFRRYGFHGTGMRYVAPEA
          180      190      200      210      220      230

          250      260      270      280      290      300
m603.pep  ARILGKPLEDIRMIIAHLGNGASITAIKNGKSVDTSMGFTPIEGLVMGTRCGDIDPGVYS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      ARILGKPLEDIRMIIAHLGNGASITAVKNGKSVDTGMGFTPIEGLVMGTRCGDIDPGVYS
          240      250      260      270      280      290

          310      320      330      340      350      360
m603.pep  YLTSHAGMDVAQVDEMLNKKSGLLGISLSNDCRTLEIAADEGHEGARLALAEVMTYRLAK
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YPTFHAGMDVAQVDEMLNEKSGFPGISLPNDCRTLEIAADEGREGARLALAEVMTCLRAK
          300      310      320      330      340      350

          370      380      390      400      410      420
m603.pep  YIASMAVCGGVVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          |||||:|||||:|||||:|||||:|||||:|||||
g603      YIASMAVACGSVDALVFTGGIGENSRNIRAKTVSYLDFLGLHIDTKANMEKRYGNSGIIS
          360      370      380      390      400      410

          430      440      450
m603.pep  PTDS SPAVLVVPTNEELMIACDTAELAGILX
          |||||:|||||:|||||:|||||:|||||
g603      PTDS SPAVLVVPTNEELMIACDTAELAGILX
          420      430      440      450

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1899>:

```

a603.seq
1   CTGTCCTCGC GTAGGCGGGG ACGGAATAAC GATAGAAAAT GCGGCATACG
51  CTTTGCCCAA AGAGCCGTC  TGAAACACAC TCCGCCAAC  GCCCATCCTT
101 TTTCAGACGA CCCACACC.  AAAAAACAAC CACAACTAC  AAGGAGAAAC
151 ATCATGTCCG ACCAACTCAT TCTTGTCTG  AACTGCGGCA GTTCATCGCT
201 CAAAGGTGCC GTTATCGACC GCAAAAGCGG CAGCGTCGTC CTAAGCTGCC
251 TCGGCGAACG CCTGACCACG CCCGAAGCCG TCATTACGTT CAGCAAAGAC
301 GGCAACAAAC GCCAAGTTCC CCTGAGCGGC CGGAAGTCC  ACGCCGGCGC
351 GGTGGGTATG CTGTTGAACG AACTGGAATA ACACGAACTG CACGACCGCA
401 TTCAAGCCGT CGGCCACCGC ATCGCCACG  GCGGCGAAAA ATACAGCGAG
451 TCTGTTTGA  TCGACCAGGC CGTAATGGAC GAACTCAATG CCTGCATTCC
501 GCTTGCGCCG CTGCACAACC CCGCCAACAT CAGCGGCATC CTCGCCGCAC
551 AGGAACATTT CCCCGTCTG  CCCAATGTCG GCGTGATGGA TACTTCGTTT
601 CACCAAAACA TGCCGAGCG  TGCCTACACT TATGCCGTGC CGCGCGAGTT
651 GCGTAAAAAA TACGCTTTC  GCCGCTACGG TTTCCACGGC ACCAGTATGC
701 GTTACGTTGC CCCTGAAGCC GCATGCATCT TGGGCAAAAC TCTGGAAGAC
751 ATCCGCATGA TTATTGCCCA CTTAGGCAAC GGCGCATCCA TTACCGCCAT
801 CAAAACGGC  AAATCCGTCG ATACCAGTAT GGGTTTCACG CCGATCGAAG
851 GTTTGGTAAT GGGTACGCGC TCGGCGGATA TCGACCCGGG CGTATACAGC
901 TATCTGACTT CACACGCCGG TTTGGATGTT GCACAAGTTG ATGAAATGCT
951 GAATAAAAAA TCAGGCTTGC TCGGTATTTC CGAACTCTCC AACGACTGCC
1001 GCACCCTCGA AATCGCCGCC GACGAAGGCC ACGAAGGCGC GCGCCTCGCC
1051 CTCGAAGTTA TGACCTACCG CCTCGCCAAA TACATCGCTT CGATGGCTGT
1101 GGGCTGCGGC GCGGTTGACG CACTCGTGTT CACCGGCGGT ATCGGCGAAA
1151 ACTCGCGTAA TATCGTGCC  AAAACCGTTT CCTATCTTGA TTTCTGGGT
1201 CTGCACATCG ACACCAAAGC CAATATGGAA AAACGCTACG GCAATTCTGGG
1251 TATTATCAGC CCGACCGATT CTTCTCCGGC TGTTTGGTGT GTCCCGACCA
1301 ATGAAGAACT GATGATTGCC TCGGACACTG CCGAACTTGT CGGCATCTTG
1351 TAG

```

This corresponds to the amino acid sequence <SEQ ID 1900; ORF 603.a>:

```

a603.pep
1   LSSRRRGRNN DRKCGIRFAQ RGRLKHTFPN AHPFSDPTX  KKQPQTRRN
51  IMSDQLILVL NCGSSSLKGA VIDRKSGSVV LSCLGERLTT PEAVITFSKD
101 GNKRQVPLSG  RNCHAGAVGM LLNELEKHEL HDRIQAVGHR IAHGGEKYSE
151 SVLIDQAVMD  ELNACIPLAP LHN PANISGI LAAQEHFPL  PNVGVMDTSF

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958

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201  HQTMPERAYT  YAVPRELRKK  YAFRRYGFHG  TSMRYVAPEA  ACILGKPLED
251  IRMIIAHLGN  GASITAIKNG  KSVDTSMGFT  PIEGLVMGTR  CGDIDPGVYS
301  YLTSHAGLDV  AQVDEMLNKK  SGLLGISELS  NDCRTLEIAA  DEGHEGARLA
351  LEVMTYRLAK  YIASMAVGCG  GVDALVFTGG  IGNSRNIRA  KTVSYLDFLG
401  LHIDTKANME  KRYGNSGIIS  PTDSSPAVLV  VPTNEELMIA  CDTAELVGIL
451  *

```

m603/a603 96.7% identity in 450 aa overlap

	10	20	30	40	50	60
m603.pep	LSSRRRGRNND	RKCGIRFAQR	GRLKHLAPD	VCXFSDDPT	LKKQPQTTR	RNIMSDQLIL
a603	LSSRRRGRNND	RKCGIRFAQR	GRLKHTPPN	AHPFSDDP	TXXKQPQT	TRRNIMSDQL
	10	20	30	40	50	60
	70	80	90	100	110	120
m603.pep	NCGSSSLKGA	IDRXSGSV	VLSC	LGERLTT	PEAVITF	NKDG
a603	NCGSSSLKGA	IDRKSGSV	VLSC	LGERLTT	PEAVITF	SKDGNK
	70	80	90	100	110	120
	130	140	150	160	170	180
m603.pep	LLNELEKHGL	HDRIKAIGH	RIAHGGE	KYSESV	LIDQAVM	DELNACIPL
a603	LLNELEKHGL	HDRIQAVGH	RIAHGGE	KYSESV	LIDQAVM	DELNACIPL
	130	140	150	160	170	180
	190	200	210	220	230	240
m603.pep	LAAQEHFPG	LPNVGVM	DTSFHQT	MPERAYT	YAVPREL	RKKYAFRR
a603	LAAQEHFPG	LPNVGVM	DTSFHQT	MPERAYT	YAVPREL	RKKYAFRR
	190	200	210	220	230	240
	250	260	270	280	290	300
m603.pep	ARILGKPLE	DIRMIIAH	LGNGAS	ITAIKNG	KSVDTSM	GFTPIEGL
a603	ACILGKPLE	DIRMIIAH	LGNGAS	ITAIKNG	KSVDTSM	GFTPIEGL
	250	260	270	280	290	300
	310	320	330	340	350	360
m603.pep	YLTSHAGMD	VQAQVDE	MLNKKSG	LLGISEL	SNDCRT	LEIAADE
a603	YLTSHAGLD	VQAQVDE	MLNKKSG	LLGISEL	SNDCRT	LEIAADE
	310	320	330	340	350	360
	370	380	390	400	410	420
m603.pep	YIASMAVG	CGGVDAL	VFTGGIG	ENSRNIR	AKTVSYL	DFLGLH
a603	YIASMAVG	CGGVDAL	VFTGGIG	ENSRNIR	AKTVSYL	DFLGLH
	370	380	390	400	410	420
	430	440	450			
m603.pep	PTDSSPAVL	VVPTNEE	LMIACTA	ELAGILX		
a603	PTDSSPAVL	VVPTNEE	LMIACTA	ELVGILX		
	430	440	450			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1901>:

g604.seq

```

1  ATGCCCCAAG  CGCACTTCTT  TACGCGTTCC  GCCGCCTGCG  GCAAGGTTGA
51  CCAGCGTACC  GAGCACGGCG  GCGGCGATGG  CGACCGAGGC  GATGCCCCATC
101  ATAGCGTGTT  GCAGTTTGCC  CATGCTCAGG  GCGCGTACCG  GCAAATCGAT
151  GTCGCGGCGG  TTTACGTTT  TGCCGCTGGA  GGCGGTGTAA  TCGCGGCGCG
201  GCGCGACGAA  GGCGGGTTTC  GGCGTGCGCG  CGCGGGCGGC  GGCTTCGGAT

```


251	ACGTCGCTGA	TCAAACCCAT	TTTCAGCGCG	CCATATGCGC	GGATGGTTTC
301	AAATTTTTC	AGCGCGGCGG	CATCGTTGTT	GATGTCGTCC	TGCAACTCTT
351	TGCCCGTGTA	GCCCAAGTCG	GCGGCGTTCA	GGAAACGGT	CGGAATGCCC
401	GCGTTGATGA	GCGTGGCTTT	CAGACGACCT	ATATTGGGCA	CATCAATTTT
451	GTCGACCAA	TTGCCGGTTG	GGAACATACT	GCCTTcgCG	TGGCTGGAT
501	CTAA				

This corresponds to the amino acid sequence <SEQ ID 1902; ORF 604.ng>:

g604 . pep

```

1  MPEAHFFTRS AACGKVDQRT EHGGGDGDRG DAHHSVVFQA HAQGAYRQID
51  VGGVYGFAAG GGVIGGRDE GGFRRARAGG GFGYVADQTH FQRAICADGF
101 KFFQGGIVV DVVLQLFARV AQVGGVQENG RNARVDERGF QTTYIRHINF
151 VDQIAGWEHT AFAVGWI *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1903>:

m604.seq

1	ATGCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCCTGCG	GCAAGGTTGA
51	CCAGCGTACC	GGGTACGGCG	GCGGCGGTCTG	CAATGGCAAC	AGAGGCGGTA
101	CCCATCATCG	CGTGGTGCAG	TTTGCCCATG	CTCAGGGCGC	GTACCAGCAA
151	ATCGATGTCG	GCGCGGTTCA	CGGTTTTGCC	ACTGGAGGCG	GTGTAATCGG
201	CGCGGGGCGC	GACGAAGGCG	ACTTTCGGCG	TGTGCGCGCG	AGCGCCAGCT
251	TCGGATACGT	CGCTGATCAG	ACCCATTTTC	AGCGCACCGT	AAGCGCGGAT
301	TTTCTCGAAT	TTTTCCAAAG	CCGCGGCATC	GTTGTTGATG	TCGTCTTGCA
351	ACTCTTTGCC	TGTGTAGCCC	AAGTCGGCGG	CATTCAAGAA	AACGGTCGGA
401	ATGCCCGCGT	TGATGAGCGT	GGCTTTCAAA	CGGCCTATAT	TCGGCACATC
451	AATTTCAATCG	ACCAAATTGC	CGGTTGGGAA	CATACTGCCT	TCGCCGTCGG
501	CTGGATC				

This corresponds to the amino acid sequence <SEQ ID 1904; ORF 604>:

m604 . pep

1 MPEAHFFTRS AACGKVDQRT GYGGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
51 IDVGGVHGFA TGGGVIGGGR DEGDFRRVRA SGSFGYVADQ THFQRTVSAD
101 FLEFFQSRGI VVDVVLQLFA CVAQVGGIQE NGRNARVDER GFQTAYIRHI
151 NFIDQIAGWE HTAFAVGWI

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

ORF 604 shows 83.4% identity over a 169 aa overlap with a predicted ORF (ORF 604.ng) from *N. gonorrhoeae*:

m604/g604

```

      10      20      30      40      50      60
m604 . pep  MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVQFAHAQGAYQQIDVGGVHGFA
             |||||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g604        MPEAHFFTRSAACGKVDQRTEHGGG--DGDRGDAHHSVVQFAHAQGAYRQIDVGGVYGFA
             10      20      30      40      50

      70      80      90      100     110     120
m604 . pep  TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFFLEFFQSRGIVVDVVLQLFA
             :|||||:||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g604        AGGGVIGGGRDEGGFRRRARAGGGFGYVADQTHFQRAICADGFKFFQRGGIVVDVVLQLFA
             60      70      80      90      100     110

      130     140     150     160     169
m604 . pep  CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
             |||||:|||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
g604        RVAQVGGVQENGRNARVDERGFQTTYIRHINFVDQIAGWEHTAFAVGWIX
             120     130     140     150     160

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1905>:

a604.seq

1	ATGCCCCGAAG	CGCACTTCTT	TACGCGTTCC	GCCGCCTGCG	GCAAGGTTGA
51	CCAGCGTACC	GGGCACGGCG	GCGGCGGTTCG	CAATGGCAAC	AGAGGCGGTA
101	CCCATCATCG	CGTGGTGCAA	TTTGCCCATG	CTCAGGGCGC	GTACCAGCAA
151	ATCGATGTGC	GCGGCATTCA	CGGTTTTGCC	ACTGGAGGCG	GTGTAATCGG

960

```

201  CGGCGGGCGC GACGAAGGCG ACTTTCGGCG TGTGCGCGCG GCGGCGAGCT
251  TCGGATACGT CGCTGATCAG ACCCATTTTC AGCGCACCGT AAGCGCGGAT
301  TTTCTCGAAT TTTTCCAAAG CTGCGGCATC GTTGTGTGATG TCGTCTTGCA
351  ACTCTTTGCC CGTGTAGCCC AAGTCGGCGG CATTTCAGGAA AACGGTCGGA
401  ATGCCCGCGT TGATGAGCGT GGCTTTCAA CGGCCTATAT TCGGCACATC
451  AATTTTCATCG ACCAAATTGC CGGTTGGGAA CATACTGCCT TCGCCGTCGG
501  CTGGATCAAG AAATTCGATT TGTACTTCGG CTGCCGGGAA CGTTACGCCG
551  TCGAGCTCAA AATCGCCTGT TTCCAAAAC GCGCCGTTTT GCATCGGTAC
601  ATGGGCAATA ATGGTTTTGC CGATGTTTTT CTGCCAGATT TTGACTGTGC
651  AGATGCCGTC TGA

```

This corresponds to the amino acid sequence <SEQ ID 1906; ORF 604.a>:

```

a604.pep
  1  MPEAHFFTRS AACGKVDQRT GHGGGGRNGN RGGTHHRVVQ FAHAQGAYQQ
 51  IDVGGIHGFA TGGGVIGGGR DEGDFRRVRA GGSFGYVADQ THFQRTVSAD
101  FLEFFQSCGI VVDVVLQLFA RVAQVGGIQE NGRNARVDER GFQTAYIRHI
151  NFIDQIAGWE HTAFAVGWIK KFDLYFGCRE RYAVELKIAC FQNC AVLHRY
201  MGNNGFADVF LPDFDCADAV *

```

m604/a604 97.0% identity in 169 aa overlap

```

              10      20      30      40      50      60
m604.pep      MPEAHFFTRSAACGKVDQRTGYGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGVHGFA
a604           MPEAHFFTRSAACGKVDQRTGHGGGGRNGNRGGTHHRVVQFAHAQGAYQQIDVGGIHGFA
              10      20      30      40      50      60

              70      80      90      100     110     120
m604.pep      TGGGVIGGGRDEGDFRRVRASGSFGYVADQTHFQRTVSADFLEFFQSRGIVVDVVLQLFA
a604           TGGGVIGGGRDEGDFRRVRAGGSFGYVADQTHFQRTVSADFLEFFQSCGIVVDVVLQLFA
              70      80      90      100     110     120

              130     140     150     160     169
m604.pep      CVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWI
a604           RVAQVGGIQENGRNARVDERGFQTAYIRHINFIDQIAGWEHTAFAVGWIKKFDLYFGCRE
              130     140     150     160     170     180

a604           RYAVELKIACFQNC AVLHRYMGNNGFADVF LPDFDCADAVX
              190     200     210     220

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1907>:

```

g605.seq
  1  ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
 51  AATCGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTAAACAAT
101  ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151  TATATGCAGG CCGGCGACAG CAGCATTGAT TACGCCGCTa tGCCGGACAG
201  CATCATCACG CCCGAAATCA AAGACGATgc cgtcaaagtc aaAGGCTATT
251  TCATCtacc cGCCAGCTT TTTTgcaata ttgccgccga agcCCATCAA
301  AACGAAGAGC TCAACACCAA GCTGAAAGaa atCTTTACCG CGATTGAAAG
351  CTCCGCCTCC GGCTAcccgT CCGAACAAAG CATCAAAGGC TTGTTTGACG
401  ACTTCgACAC CACCAGCAGC CGGCTCGGCA GCACCGTTGC CGACAAAAAC
451  AAACGCCTTG CCGCGTCCTT TAAAGGCGTG GCGGAACTCG ATTTTCGGCAA
501  TTTTGAAGAC CACCGCATCG ACCTTTTCGG TGATGCCTAC GAATACCTGA
551  TTTCCAAC TA CGCgcCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601  CCGCAAAGCG TCTCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGCGAGGA
651  GAAAGTCAAC AAAATCTACG ACCCCGCCTG CGGCTCGGGC AGCCTGCTCT
701  TGCAGGCGAA AAAACAGTTT GACGAACACA TCATCGAAGA AGGCTTCTTC
751  GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCC GCA TGAATATGTT
801  TCTGCACAAC GTCAATTACA ACAAATTCCA CATCGAATTG GGCGACACGC
851  TGACCAACCC CAAACTCAA GACAGCAAAC CCTTTGATGC CGTCGTCTCC
901  AATCCGCCCT ATTCCATCGA CTGGATAGGC AGCGACGACC CCACCTtgaT

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951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTCGCACCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCTA TCGTCTCATT CCCC GGCAATT TTCTATCGCG GCGGCGCAGA
1101 GCAGAAAATc CGCCAATATC TGGTGGAGGG CAACTATGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCTGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ACCGAAGAAC
1301 ACATTGCCGA AATCGTCAAA CTCTTCGCCG ACAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCCGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACCCGCGAG GTCATCGACA
1451 TCAGACAGCT CAACGCCGAA ATCAGCGAAA CCgtcgCcaa AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAA CTTAG

```

This corresponds to the amino acid sequence <SEQ ID 1908; ORF 605.ng>:

g605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ
101 NEELNNTKLKE IFTAIESSAS GYPSEQGIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFED HRIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIEEGFF
251 GQEIHNHTTYN LARMMNMFHN VNYNKFHIEL GDTLTNPCLK DSKPFDVVS
301 NPPYSIDWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYSGRG
351 RAAIVSFPPI FYRGGAEQKI ROYLVEGNYV ETVIALAPNL FYGTCLAVNI
401 LVLSKHKDNT DIQFIDASGF FKKETNNNVL TEEHIAEIVK LFADKADVPH
451 IAQNAAQQT V KONGYNLAVS SYVEAEDTRE VIDIRQLNAE ISETVAKIER
501 LRREIDEVIA EIET*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1909>:

m605.seq

```

1 ATGATGACCG AAATGCAACA ACGCGCCCAA CTGCACCGCC AAATTTGGAA
51 AATTGCCGAC GAAGTACGCG GCGCGGTGGA TGGCTGGGAC TTTAAACAAT
101 ACGTTCTCGG CACACTTTTC TACCGCTTTA TCAGCGAAAA CTTACCGAC
151 TATATGCAGG CAGGCGACAG CAGTATTGAT TACGCCGCTA TGCCGGACAG
201 CATCATCACG CCCGAAATCA AAGACGATGC CGTCAAAGTT AAAGGCTATT
251 TCATCTACCC CGGCCAGCTT TTTTGCAATA TTGCCGCCGA AGCCCATCAA
301 AACGAAGAGC TCAACACCAA GCTGAAAGAA ATTTTACC CGATTGAAAG
351 CTCCGCCTCC GGCTATCCGT CCGAACAGGA CATCAAAGGC CTGTTTGACG
401 ACTTCGACAC CACCAGCAGC CGGCTCGGCA GCACTGTTGC CGACAAGAAC
451 AAACGCCTTG CCGCCGTCCT CAAAGGCGTG GCGGAACTCG ATTTCCGCCA
501 TTTTGAAAC CACCACATCG ACCTTTTCGG CGATGCCTAC GAATACCTGA
551 TTTCCAATA CGCTGCCAAC GCAGGCAAAT CCGGCGGCGA ATTTTTCACC
601 CCGCAAAGCG TATCCAAGCT GATTGCGCGG CTGGCGGTGC ACGGACAGGA
651 GAAAGTCAAC AAAATCTACG ACCCAGCTTG CCGCTCGGGC AGTCTGCTCT
701 TGCAGGCGAA AAAACAGTTT GACGAGCACA TCATCGAAGA AGGCTTCTTC
751 GGGCAGGAAA TCAACCACAC CACCTACAAC CTCGCCCCGA TGAACATGTT
801 CCTGCACAAC GTCAATTACA ACCAATTCCA CATCGAATTG GCGACACAC
851 TGACCAACCC AAAGCTCAAA GACAGCAAAC CCTTTGATGC CATCGTTTCC
901 AATCCGCCTT ATTCCATCAA CTGGATAGGC AGCGACGACC CCACCTTAAT
951 CAACGACGAC CGCTTTGCCC CCGCAGGCGT ACTTGCCCCG AAATCCAAAG
1001 CCGATTTTGC CTTTCATCCTG CACGCACTGA ACTACCTTTC CGGCAGAGGC
1051 CGCGCCGCCA TCGTCTCATT CCCC GGCAATT TTCTATCGCG GCGGCGCAGA
1101 ACAGAAAATC CGCCAATATC TGGTGGAGGG CAACTACGTG GAAACCGTGA
1151 TTGCCCTTGC GCCCAATCTC TTTTACGGCA CCGGCATCGC CGTCAATATC
1201 CTGGTTTTGT CCAAACACAA AGACAATACC GACATCCAAT TCATCGACGC
1251 AAGCGGCTTC TTTAAAAAAG AAACCAACAA CAACGTCTTA ATCGAAGAAC
1301 ACATTGCTGA AATCGTCAAA CTCTTCGCCG ATAAAGCCGA TGTGCCGCAT
1351 ATCGCCCAA ACGCTGCCCA GCAAACCGTC AAAGACAACG GCTACAACCT
1401 CGCCGTCAGC AGCTATGTCG AAGCCGAAGA CACACGCGAA ATTATCGACA
1451 TCAAACAGCT CAACGCCGAA ATCGGCGAAA CCGTCGCCAA AATCGAACGG
1501 CTGCGGCGTG AAATTGACGA AGTGATTGCA GAGATTGAAG CATGA

```

This corresponds to the amino acid sequence <SEQ ID 1910; ORF 605>:

m605.pep

```

1 MMTEMQORAQ LHRQIWKIAD EVRGAVDGWD FKQYVLGTLF YRFISENFTD
51 YMQAGDSSID YAAMPDSIIT PEIKDDAVKV KGYFIYPGQL FCNIAAEAHQ

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962

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101 NEELNTKLKE IFTAIESSAS GYPSEQDIKG LFDDFDTTSS RLGSTVADKN
151 KRLAAVLKGV AELDFGNFEN HHIDLFGDAY EYLISNYAAN AGKSGGEFFT
201 PQSVSKLIAR LAVHGQEKVN KIYDPACGSG SLLLQAKKQF DEHIEEGFF
251 GQEINHTTYN LARMNMF LHN VNYNQFHIEL GDTLTNPCLK DSKPFDAIVS
301 NPPYSINWIG SDDPTLINDD RFAPAGVLAP KSKADFAPIL HALNYLSGRG
351 RAAIVSFPGI FYRGGAEQKI ROYLVEGNYV ETVIALAPNL FYGTGIAVNI
401 LVLKSKHKDNT DIQFIDASGF FKKETNNNVL IEEHIAEIVK LFADKADVP
451 IAQNAAQQTV KDNGYNLAVS SYVEAEDTRE IIDIKQLNAE IGETVAKIER
501 LRREIDEVIA EIEA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 605 shows 97.9% identity over a 513 aa overlap with a predicted ORF (ORF 605.ng) from *N. gonorrhoeae*:

m605/g605

	10	20	30	40	50	60
m605.pep	MMTEMQRAQLHRQIWKIADEVGAVDGFQYVGLGTLFYRFISENFTDYMQAGDSSID					
g605	MMTEMQRAQLHRQIWKIADEVGAVDGFQYVGLGTLFYRFISENFTDYMQAGDSSID					
	10	20	30	40	50	60
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
g605	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSAS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m605.pep	GYPSEQDIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFENHHIDLFGDAY					
g605	GYPSEQGIKGLFDDFDTTSSRLGSTVADKNKRLAAVLKGV AELDFGNFEDHRIDLFGDAY					
	130	140	150	160	170	180
	190	200	210	220	230	240
m605.pep	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
g605	EYLISNYAANAGKSGGEFFT PQSVSKLIARLAVHGQEKVNKIYDPACGSGSLLLQAKKQF					
	190	200	210	220	230	240
	250	260	270	280	290	300
m605.pep	DEHIEEGFFGQEINHTTYNLARMNMF LHN VNYNQFHIELGDTLTNPCLKDSKPFDAIVS					
g605	DEHIEEGFFGQEINHTTYNLARMNMF LHN VNYNKFHIELGDTLTNPCLKDSKPFDAVVS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m605.pep	NPPYSINWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGAAIVSFPGI					
g605	NPPYSIDWIGSDDPTLINDDRFAPAGVLAPKSKADFAPILHALNYLSGRGAAIVSFPGI					
	310	320	330	340	350	360
	370	380	390	400	410	420
m605.pep	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
g605	FYRGGAEQKIRQYLVEGNYVETVIALAPNLFYGTGIAVNILVLSKHKDNTDIQFIDASGF					
	370	380	390	400	410	420
	430	440	450	460	470	480
m605.pep	FKKETNNNVLT EEHIAEIVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEAEDTRE					
g605	FKKETNNNVLT EEHIAEIVKLFADKADVP HIAQNAAQQT VKDNGYNLAVSSYVEAEDTRE					

	430	440	450	460	470	480
	490	500	510			
m605.pep	IIDIKQLNAEIGETVAKIERLRREIDEVIAEIEAX					
	: : : :					
g605	VIDIRQLNAEISETVAKIERLRREIDEVIAEIETX					
	490	500	510			

a605.seq

1	ATGATGACCG	AAATACAACA	ACGCGCCCAA	CTGCACCGCC	AAATTTGGAA
51	AATTGCCGAC	GAAGTACGCG	GCGCGGTGGA	TGGCTGGGAC	TTCAAACAAT
101	ACGTATTCTCGG	CACACTTTTC	TACCGCTTTA	TCAGCGAAAA	CTTTACCGCA
151	TATATGCGAGG	CAGGCGACAG	CAGTATTGAT	TACGCCGATA	TGCCGGACAG
201	CATCATCAGC	CCCGAAATCA	AAGACGATGC	CGTCAAAGTC	AAAGGCTATT
251	TCATCTACCC	CGGCCAGCTT	TTTTGCAATA	TTGCCGCCGA	AGCCCATCAA
301	AACGAAAGCG	TCAACACCAA	GCTGAAAGAA	ATTTTTACCG	CGATTGAAAG
351	CTCCGGCTCC	GGCTATCCGT	CCGAAACAAG	CATTAAGAAGC	CTGTTTGACG
401	ACTTCGACAC	CACGACGAGC	CGGCTCGGCA	GACCGTTGCG	GCACAAGAAC
451	AAACGCCTTG	CCGCCGTCTT	AAAAGGCGTG	GCGGAACTCG	ATTTCTGGCAG
501	TTTTGAAGAC	CACCACATCG	ACCTTTTTCGG	CGATGCCTAC	GAATACCTGA
551	TTTCCAACATA	CGTGCCCAAC	GCAGGCAAAAT	CCGGCGGCGCA	ATTTTTTACC
601	CCGCAAAGCG	TATCCAAGCT	GATTGCGCGG	CTGGCGGTGC	ACGGGCAGGA
651	GAAAGTAAAC	AAAATCTACG	ACCCAGCTTG	CGGCTCGGGC	AGCCTGCTCT
701	TGCAGGCGAA	AAAACAGTTT	GACGAGCACA	TCATCGAAGA	AGGCTTCTTC
751	GGGCGAGAAA	TCAACCACAC	CACCTACAAC	CTCGCCCGCA	TGAATATGTT
801	TCTGCACAAC	GTCAATTACA	ACAAATTTCCA	CATCGAATTG	GGCGACACAT
851	TGACCAATCC	CAAACTCAAA	GACAGCAAAC	CCTTTGATGC	CGTCGTTTCC
901	AATCCGCCCT	ATTCCATCAA	CTGGATAGGC	AGCGGCGACC	CCACCTTAAT
951	CAACGACGAC	CGCTTTTGCC	CTGCAGGCGT	ACTCGCCCCG	AAATCCAAAG
1001	CCGATTTTGC	CTTCATTCTG	CACGCACTGA	ACTACCTTTC	CGGCAGAGGG
1051	CGCGCGGCCA	TCGCTCTAAT	CCCCGGCAAT	TTCTATCGCG	CGGGCGCAGA
1101	GCAGAAAATC	CGCCAATATC	TGGTGGAGGG	CAACTACGTG	GAAACCGTCA
1151	TCGCCCTTGC	GCCCAATCTC	TTTTACGGCA	CCGGCATCGC	CGTCAATATA
1201	CTGGTTTTGT	CCAAACACAA	AGACAATACC	GACATCCAAT	TCATCGAGAT
1251	AGGCGGCTTC	TTTTAAAAAG	AAACCAACAA	CAACGTCTTA	ACCGAAGAAC
1301	ACATTGCCGA	AATCGTCAAA	CTCTTCCGGC	ATAAAGCCGA	TGTGCCGCAT
1351	ATCGCCCAA	ACGCCGCCCA	GCAAACCGTC	AAAGACAACG	GCTACAACCT
1401	CGCCGTGACG	AGCTATGTTG	AACCCGAAGA	CACCCGCGAA	ATTATCGACA
1451	TCAAACAGCT	TAACGCGGAA	ATCAGCGAAA	CCGTTGCCAA	AATCGAACGG
1501	CTGCGGCGTG	AAATTGCAGA	AGTGATTGCA	GAGATTGAAG	CATGA

a605.pcp

1	MMTEIQORAQ	LHRQIWKIAD	EVARGAVDGWD	FKQYVLGTLF	YRFISENFTD
51	YMQAGDSSID	YAAMPDSIIT	PEIKDDAVKV	KGFYIYPGQL	FCNIAAEAHQ
101	NEELNTKLKE	IFTAIESSAS	GYPSEQDIKG	LFDDFDTTSS	RLGSTVADKN
151	KRLAAVLKGV	AELDFGSFED	HHIDFLGDAY	EYLLISNYAAN	ACKSGGEEFFT
201	QQSVSKLIIAR	LAVHGEQEKVN	KIYDPACGSG	SLLLQAKKQF	DEHIEEGFF
251	GQEIHNHTTYN	LARMNMFLEHN	VNYNKFHIEL	GDTLTNPKLK	DSKPFDAVVS
301	NPPYSINWIG	SGDPTLINDD	RFAPAGVLAP	KSKADFAFIL	HALNYLSGRG
351	RAAIVSFPGI	FYRGGAEQKI	RQYLVEGNVY	ETVIALAPNL	FYGTGIAVNI
401	LVLSKHKDNT	DIQFIDAGGF	FKKETNNNVL	TEEHIAEIVK	LFADKADVPH
451	IAQNAAEQTV	KDNNGYNLAVS	SYVEPEDTRE	IIDIKQLNAE	ISETVAKIER
501	LRRAAIDEVIA	EIEA*			

	10	20	30	40	50	60
m605.pep	MMTEMQORQLHRQIWKIADEVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
a605	:					
	10	20	30	40	50	60
	MMTEIQORQLHRQIWKIADEVRGAVDGDWDFKQYVLGTLFYRFISENFTDYMQAGDSSID					
	70	80	90	100	110	120
m605.pep	YAAMPDSIITPEIKDDAVKVKGYFIYPGQLFCNIAAEAHQNEELNTKLKEIFTAIESSA					

a605	Y A A M P D S I I T P E I K D D A V K V K G Y F I Y P G Q L F C N I A A E A H Q N E E L N T K L K E I F T A I E S S A S	70	80	90	100	110	120
m605.pep	GYPSEQDIKGLFDDFDFTTSSRLGSTVADKNKRLAAVLKGVAE LDFGNFENHHIDLFGDAY	130	140	150	160	170	180
a605	GYPSEQDIKGLFDDFDFTTSSRLGSTVADKNKRLAAVLKGVAE LDFGSFEDHHIDLFGDAY	130	140	150	160	170	180
m605.pep	EY L I S N Y A A N A G K S G G E F T P Q S V S K L I A R L A V H G Q E K V N K I Y D P A C G S G S L L L Q A K K Q F	190	200	210	220	230	240
a605	EY L I S N Y A A N A G K S G G E F T P Q S V S K L I A R L A V H G Q E K V N K I Y D P A C G S G S L L L Q A K K Q F	190	200	210	220	230	240
m605.pep	D E H I I E E G F F G Q E I N H T T Y N L A R M N M F L H N V N Y N Q F H I E L G D T L T N P K L K D S K P F D A I V S	250	260	270	280	290	300
a605	D E H I I E E G F F G Q E I N H T T Y N L A R M N M F L H N V N Y N K F H I E L G D T L T N P K L K D S K P F D A V V S	250	260	270	280	290	300
m605.pep	N P P Y S I N W I G S D D P T L I N D D R F A P A G V L A P K S K A D F A F I L H A L N Y L S G R G R A A I V S F P G I	310	320	330	340	350	360
a605	N P P Y S I N W I G S G D P T L I N D D R F A P A G V L A P K S K A D F A F I L H A L N Y L S G R G R A A I V S F P G I	310	320	330	340	350	360
m605.pep	F Y R G G A E Q K I R Q Y L V E G N Y V E T V I A L A P N L F Y G T G I A V N I L V L S K H K D N T D I Q F I D A S G F	370	380	390	400	410	420
a605	F Y R G G A E Q K I R Q Y L V E G N Y V E T V I A L A P N L F Y G T G I A V N I L V L S K H K D N T D I Q F I D A G G F	370	380	390	400	410	420
m605.pep	F K K E T N N N V L I E E H I A E I V K L F A D K A D V P H I A Q N A A Q Q T V K D N G Y N L A V S S Y V E A E D T R E	430	440	450	460	470	480
a605	F K K E T N N N V L T E E H I A E I V K L F A D K A D V P H I A Q N A A Q Q T V K D N G Y N L A V S S Y V E P E D T R E	430	440	450	460	470	480
m605.pep	I I D I K Q L N A E I G E T V A K I E R L R R E I D E V I A E I E A X	490	500	510			
a605	I I D I K Q L N A E I S E T V A K I E R L R R E I D E V I A E I E A X	490	500	510			

q606.seq

This corresponds to the amino acid sequence <SEQ ID 1914; ORF606.ng>:

g606.pep
 1 MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNATFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTLL
 101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSLL STHPSLDNRI ARLKSL*

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1915>:

m606.seq
 1 ATGTCCAAAT TTATCGCCAA ACAATCGGTC GCGCGGAAG TTATCGACAC
 51 GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
 101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
 151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
 201 CGTCAGCACC GGTTTGCTCG ACCATATGAC GCGTGACGAA GTGAAGCCG
 251 TATTGGCGCA CGAAATGGCA CACGTCGCA ACGGCGATAT GGTACGCTG
 301 ACGCTGATTC AAGGCGTGGT CAATACCTT GTCGTGTTCC TGTCGCGCAT
 351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
 401 CTTATTTCTT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
 451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGCGAATACC GCGCCGATGC
 501 GGGCGCGGCA AAACCTGGTC GCGCGCCGAA AATGATTTC GCCCTGCAAA
 551 GGCTCAAAG CAACCCGGTC GATTTGCCCC AAGAAATGAA CGCAATGGGC
 601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCACC CTTGCTGGA
 651 CAACCGTATC GCGCGCCTCA AATCGCTTAA A

This corresponds to the amino acid sequence <SEQ ID 1916; ORF 606>:

m606.pep
 1 MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
 51 EPNATFATGAS RNSSLIAVST GLLDHMTRE VEAFLAHEMA HVGNGDMVTLL
 101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
 151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
 201 IAGDTRDSLL STHPSLDNRI ARLKSL*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 606 shows 100.0% identity over a 225 aa overlap with a predicted ORF (ORF 606.ng) from *N. gonorrhoeae*:

m606/g606

	10	20	30	40	50	60
m606.pep	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNATFATGAS					
g606	MSKFIKQSVGAEVIDTPRTEEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNATFATGAS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m606.pep	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNMGDMVTLLTLIQGVVNTFVVFLSRIIAN					
g606	RNSSLIAVSTGLLDHMTREDEVEAVLAHEMAHVGNMGDMVTLLTLIQGVVNTFVVFLSRIIAN					
	70	80	90	100	110	120
	130	140	150	160	170	180
m606.pep	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
g606	LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS					
	130	140	150	160	170	180
	190	200	210	220		
m606.pep	ALQRLKGNPVDLPPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
g606	ALQRLKGNPVDLPPEEMNAMGIAGDTRDSLLSTHPSLDNRIARLKSLX					
	190	200	210	220		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1917>:

a606.seq

966

```

1  ATGTCCAAAT TCATCGCCAA ACAATCGGTC GGC GCGGAAG TTATCGACAC
51  GCCGCGCACC GAAGAAGAAG CCTGGCTTTT GAACACTGTC GAAGCCCAAG
101 CGCGGCAATG GAACCTGAAA ACGCCCGAAG TCGCCATCTA CCACTCCCCC
151 GAACCCAATG CCTTTGCCAC GGGCGCATCG AGAAACAGCT CCCTGATCGC
201 CGTCAGCACC GGTTCGCTCG ACCATATGAC GCGTGACGAA GTGGAAGCCG
251 TATTGGCGCA CGAAATGGCA CACGTCGGCA ACGGCGATAT GGTTACGCTG
301 ACGCTGATTC AAGGCGTGGT CAATACCTTT GTCGTGTTCC TGTCGCGCAT
351 TATTGCCAAC CTGATTGCCC GAAACAACGA CGGCAGCCAG TCCCAGGGAA
401 CTTATTTTCT GGTGAGCATG GTATTCCAAA TCCTGTTCGG CTTCTTGCC
451 AGCTTAATTG TCATGTGGTT CAGCCGACAA CGGAATACC GCGCCGACGC
501 GGGCGCGGCA AAATGGTTCG GCGCGCCGAA AATGATTTCG GCCCTGCAAA
551 GGCTTAAAGG CAACCCGGTC GATTGCCCCG AAGAAATGAA CGCAATGGGC
601 ATCGCCGGAG ATACGCGCGA CTCCCTGCTC AGCACCCACC CTTGCTGGA
651 CAACCGAATC GCCCGCTCA AATCGCTTTA A

```

This corresponds to the amino acid sequence <SEQ ID 1918; ORF 606.a>:

```

a606.pep
1  MSKFIKQSV GAEVIDTPRT EEEAWLLNTV EAQARQWNLK TPEVAIYHSP
51  EPNAFATGAS RNSSLIAVST GLLDHMTRE VEAVLAHEMA HVGNGDMVTL
101 TLIQGVVNTF VVFLSRIIAN LIARNNDGSQ SQGTYFLVSM VFQILFGFLA
151 SLIVMWFSRQ REYRADAGAA KLVGAPKMIS ALQRLKGNPV DLPEEMNAMG
201 IAGDTRDSSL STHPSLDNRI ARLKS*

```

m606/a606 100.0% identity in 226 aa overlap

```

m606.pep      10      20      30      40      50      60
MSKFIKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
|||||
a606          10      20      30      40      50      60
MSKFIKQSVGAEVIDTPRT EEEAWLLNTVEAQARQWNLKTPEVAIYHSPEPNAFATGAS
|||||

m606.pep      70      80      90      100     110     120
RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
|||||
a606          70      80      90      100     110     120
RNSSLIAVSTGLLDHMTREVEAVLAHEMAHVGNGDMVTLTLIQGVVNTFVVFLSRIIAN
|||||

m606.pep      130     140     150     160     170     180
LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
|||||
a606          130     140     150     160     170     180
LIARNNDGSQSQGTYFLVSMVFQILFGFLASLIVMWFSRQREYRADAGAAKLVGAPKMIS
|||||

m606.pep      190     200     210     220
ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSIX
|||||
a606          190     200     210     220
ALQRLKGNPVDLPEEMNAMGIAGDTRDSSLSTHPSLDNRIARLKSIX
|||||

```

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1919>:

```

g607.seq
1  ATGCTGCTCG accTcgaCCG CTTTTCTTt tccGTCTTCC TGAAAGAAAT
51  CCGCTGCTG ACCGCCCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTCGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGATTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGGCGC GGTAAAACC GgtgAAGCAG GCGAAACGGG GCGGCAGGGG
301 ATTTGGTTTC GGCTGATTTT GGGGATTTTC GGCATGATT TGTGTGGGC
351 GGCGATTACG CCGTTCGCA ACTGGCTGAC TTTGAGCGAT TATGTGGAAG
401 gcacAatggc gcAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGTACACC GCGACTGCA CGCCTACGCT TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCGCTGA
551 ACTATATTTT CGTTACGGC AAATTCGGTA TGCCCGCTT GGGTGGCGCA

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601  GGTTCGGCGC  TGGCGACAAT  GGCGGTGTTC  TGGTTCAGCG  CGCTGGCATT
651  GTGGATTTAT  ATCGCCAAGG  AAAAATTCTT  CCGCCCGTTC  GGACTGACAG
701  CGAAATTCGg  caaACCGGat  tGGgcGGTGT  TCAAACAGAT  TtGGAAAAATC
751  gGcgcgCCCA  TCGGGCTGTC  TTATTTTTTG  GAAGccaGcg  cGTTTTCGTT
801  TATCGTGTTC  TTGATTGCGC  CTtccggCGA  GGATTATGTG  GCGGCGCAGC
851  AGGTCGGCAT  CAGTTGTGTC  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901  GGCTCGGCAG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951  TTCGCGGGCG  CGTTATATTT  CAGGAGTGTC  GCTGGTGTG  GGCTGGGTGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCCGTTC  GCCGCTGGCA
1051 AGCATGTACA  ACGATGaTCC  GGCAGTTTTA  AGCATCGCCT  CCACCGTCCT
1101 GCTGTTCGCC  GGCCTGTtcc  aACCGGCAGA  CTTACCCAA  TGTATCGCGT
1151 CCTATGCCCT  GCGCGGCTAC  AAAGTCACCA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCT  TCTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCGAT  ATGGGCATTT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  AGCCGTCGCC  TTGGTGTGGT  GCTTGGAATA  ATACAGTATG
1351 GAGTTGGTCA  AATCACACAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1920; ORF 607.ng>:

g607.pep

```

1  MLLDLDRFSF  SVFLKEIRLL  TALALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  GEAGETGRQG
101 IWFGLLIGIF  GMILMWAAIT  PFRNWLTLSD  YVEGTMAYQM  LFTSLAMPAA
151 MVHRAHAYAY  SSLNRRLIM  LVSFAAFVLN  VPLNYIFVYG  KFGMPALGGA
201 GCGVATMAVF  WFSALALWIY  IAKEKFFRPF  GLTAKFGKPD  WAVFKQIWKI
251 GAPIGLSYFL  EASAFSFIWF  LIAPFGEDYV  AAQQVGISLS  GILYMIPQSV
301 GSAGTVRIGF  SLGRREFSRA  RYISGVSLVS  GWVLAVITVL  SLVLFRSPLA
351 SMYNDPAVL  SIASTVLLFA  GLFQPADFTQ  CIASYALRGY  KVTKVPFMFIH
401 AAAFWCGLL  PGYLLAYRFD  MGIYGFWTAL  IASLTIAAVA  LVWCLEKYSM
451 ELVKSHKAV*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1921>:

m607.seq

```

1  ATGCTGCTCG  ACCTCAACCG  CTTTTCCTTT  CCCGCTCTCC  TGAAAGAAGT
51  CCGCCTGCTG  ACCACTCTTG  CCCTGCCCAT  GCTGTTGGCG  CAGGTCGCGC
101 AGGTGGGCAT  CGGTTTTGTC  GATACTGTGA  TGGCGGGCGG  TGCGGGCAAG
151 GAAGACTTGG  CGGCGGTGGC  TTTGGGCAGC  AGCGCGTTTG  CCACGGTTTA
201 TATTACCTTT  ATGGGCATTA  TGGCGGCGCT  GAACCCGATG  ATTGCCCAGC
251 TTTACGGCGC  GGGTAAAACC  GACGAAGTGG  GCGAAACGGG  GCGGCAGGGG
301 ATTTGGTTCG  GGCTGT'TTT  GGGCGTGTTC  GGCATGGTCT  TGATGTGGGC
351 GGCGATTACG  CCGTTCGCCA  ACTGGCTGAC  CTTGAGCGAT  TATGTGGAAG
401 GCACGATGCG  GCAGTATATG  TTGTTACCA  GCTTGGCGAT  GCCGGCGGCA
451 ATGGTACACC  GCGCGCTGCA  CGCCTACACT  TCCAGCCTGA  ACCGCCCGCG
501 CCTGATTATG  TTGGTCAGCT  TTGCGGCGTT  TGTGTTGAAC  GTGCCGCTGA
551 ACTATATTTT  CGTTTACGGC  AAATTCGGTA  TGCCCGCTTT  GGGCGGCGCA
601 GGCTGCGGAC  TGGCGACGAT  GGCGGTGTTT  TGGTTCAGCG  CGCTGGCATT
651 GTGGATTTAT  ATCGCCAAGG  AAAATTTCTT  CCGCCATTTC  GGACTGACGG
701 CGAAATTCGG  CAAACCGGAT  TGGGCGGTGT  TCAAACAGAT  TTGGAAAAATC
751 GCGCACCCCA  TCGGGCTGTC  TTATTTTTTG  GAAGCCAGCG  CGTTTTCGTT
801 TATCGTGTTC  TTGATTGCGC  CTTTTCGGCGA  GGATTATGTG  GCGGCGCAGC
851 AGGTGCGCAT  CAGTTTGTGTC  GGGATTCTCT  ATATGATTCC  GCAAAGCGTC
901 GGCTCGGCGG  GGACGGTGCG  CATCGGCTTT  TCGCTTGGGC  GGCGCGAATT
951 TTCGCGGGCG  CGTTATATTT  CGGGCGTGTC  ACTGGTGTTA  GGATGGATGC
1001 TCGCCGTGAT  TACCGTGCTT  TCCTTGGTAT  TATTCCGTTC  GCCGCTGGTA
1051 AGTATGTACA  ACAATGATCC  GGCGGTTTTA  AGCATCGCCG  CCACCGTCTT
1101 ACTGTTTCGCC  GGCTTGT'TCC  AACCGGCAGA  CTTACCCAA  TGTATCGCCT
1151 CCTACGCCTT  GCGCGGCTAC  AAAGTTACAA  AGGTGCCGAT  GTTCATCCAC
1201 GCCGCCGCT  TTTGGGGCTG  CGGCCTGCTG  CCGGGCTATC  TGCTCGCCTA
1251 CCGTTTCAAT  ATGGGCATTT  ACGGCTTCTG  GACGGCATTG  ATTGCCTCGC
1301 TCACCATCGC  CGCCATCGCC  TTGGTGTGGT  GCTTGGAATT  GTGCAGTAGG
1351 GAGATGGTCA  GATCGCATAA  GGCCGTCTGA

```

This corresponds to the amino acid sequence <SEQ ID 1922; ORF 607>:

m607.pep

```

1  MLLDLNRFSS  PVFLKEVRLL  TTLALPMLLA  QVAQVGIGFV  DTVMAGGAGK
51  EDLAAVALGS  SAFATVYITF  MGIMAALNPM  IAQLYGAGKT  DEVGETGRQG

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968

101 IWFGFLFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
 151 MVHRALHAYT SSLNRPR LIM LVSF AAFVLN VPLNYIFVYG KFGMPALGGA
 201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
 251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYMIPQSV
 301 GSAGTVRIGF SLGRREFSRA RYISGVSLVL GWMLAVITVL SLVLFERSPLV
 351 SMYNNDDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPMFIH
 401 AAAPWGCGLL PGYLLAYRFN MGIYGFWTAL IASLTIAAIA LVWCLELCSR
 451 EMVRSHKAV*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 607 shows 94.8% identity over a 459 aa overlap with a predicted ORF (ORF 607.ng) from *N. gonorrhoeae*:

m607/g607

m607.pep	10	20	30	40	50	60
	MLLDLNRFSFPVFLKEVRLTTLALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
g607	MLLDLDRFSFSVFLKEIRLLTALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
m607.pep	70	80	90	100	110	120
	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
g607	SAFATVYITFMGIMAALNPMIAQLYGAGKTGEAGETGRQGIWFGFLILGIFGMILMWAAIT					
	70	80	90	100	110	120
m607.pep	130	140	150	160	170	180
	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYTSSLNRPR LIMLVSF AAFVLN					
g607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAA MVHRALHAYASSLNRPR LIMLVSF AAFVLN					
	130	140	150	160	170	180
m607.pep	190	200	210	220	230	240
	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD					
g607	VPLNYIFVYGKFGMPALGGAGCGVATMAVFWFSALALWIYIAKEKFFRPFGLTAKFGKPD					
	190	200	210	220	230	240
m607.pep	250	260	270	280	290	300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV					
g607	WAVFKQIWKIGAPIGLSYFLEASAFSFIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV					
	250	260	270	280	290	300
m607.pep	310	320	330	340	350	360
	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWMLAVITVLSLVLFERSPLVSMYNNDDPAVL					
g607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWVLAVITVLSLVLFERSPLASMYNDDPAVL					
	310	320	330	340	350	360
m607.pep	370	380	390	400	410	420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFN					
g607	SIASVLLFAGLFQPADFTQCIASYALRGYKVTKVPMFIHAAAFWGCGLLPGYLLAYRFD					
	370	380	390	400	410	420
m607.pep	430	440	450	460		
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX					
g607	MGIYGFWTALIASLTIAAVALVWCLEKYSMELVKSHKAVX					
	430	440	450	460		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1923>:

```
a607.seq
1  ATGCTGCTCG ACCTCAACCG CTTTTCCTTT TCCGTCTTCC TGAAAGAAGT
51  CCGCCTGCTG ACCGCTCTTG CCCTGCCCAT GCTGTTGGCG CAGGTCGCGC
101 AGGTGGGCAT CGGTTTTGTC GATACCGTGA TGGCGGGCGG TGCGGGCAAG
151 GAAGACTTGG CGGCGGTGGC TTTGGGCAGC AGCGCGTTTG CCACGGTTTA
201 TATTACCTTT ATGGGCATTA TGGCGGCGCT GAACCCGATG ATTGCCCAGC
251 TTTACGCGCG GGTAAAACG GACGAAGTGG CCGAAACGGG ACGGCAGGGG
301 ATTTGGTTCG GGCTGTTTTT GGGCGTGTTT GGCATGGTCT TGATGTGGGC
351 GGCATTACG CCGTCCGCA ACTGGCTGAC CTTGAGCGAT TATGTGGAAG
401 GCACAATGGC GCAGTATATG CTGTTACCA GCTTGGCGAT GCCGGCGGCA
451 ATGGTACACC GCGCACTGCA CGCCTACGCC TCCAGCCTGA ACCGCCCGCG
501 CCTGATTATG TTGTCAGCT TTGCGGCGTT TGTGTTGAAC GTGCCCGTGA
551 ACTATATTTT CGTTACGGC AAATTCGGTA TGCCCGCTTT GGGCGGCGCA
601 GGCTGCGGAC TGGCGACGAT GGCGGTGTTT TGGTTCAGCG CGCTGGCATT
651 GTGGATTAT ATCGCCAAGG AAAATTTCTT CCGCCCATTC GGAATGACGG
701 CGAAATTCGG CAAACCGGAT TGGGCGGTGT TCAAACAGAT TTGGAAAATC
751 GGGCGACCCA TCGGGCTGTC TTATTTTTTG GAAGCCAGCG CGTTTTCGTT
801 TATCGTGTTT TTGATTGCGC CTTTCGGCGA GGATTATGTG GCGGCGCAGC
851 AGGTGCGCAT CAGTTGTGCG GGGATTCTCT ATATGATTCC GCAAAGCGTC
901 GGCTCGGCGG GGACGGTGCG CATCGGCTTT TCGCTTGGGC GCGCGGAATT
951 TTCGCGGGCG CGTTATATTT CGGGCGGTGT ACTGGTGTCA GGATGGATGC
1001 TCGCCGTGAT TACCGTGCTT TCCTTGGTAT TATTCCGTTT GCCGCTGGTA
1051 AGTATGTACA ACAATGATCC GCGGTTTTTA AGCATCGCCG CCACCGTCTT
1101 ACTGTTGCGC GGCTTGTTCC AACCGGCAGA CTTACCCCAA TGTATCGCCT
1151 CCTACGCCCT GCGCGGCTAC AAAGTTACAA AGGTGCCGAT GTTCATCCAC
1201 GCCGCCGCTT TTTGGGGCTG CCGTCTGCTG CCGGGCTACC TGCTCGCCTA
1251 CCGTTTCGAT ATGGGCATTT ACGGCTTCTG GACGGCATTG ATTGCCTCGC
1301 TCACCATCGC CGCCATCGCC TTGGTGTGGT GCTTGAATT GTGCAGTAGG
1351 GAGATGGTCA GATCGCATAA GGCTGTCTGA
```

This corresponds to the amino acid sequence <SEQ ID 1924; ORF 607.a>:

```
a607.pep
1  MLLDLNRFSF SVFLKEVRLL TALALPMLLA QVAQVGIGFV DTMVAGGAGK
51  EDLAAVALGS SAFATVYITF MGIMAALNPM IAQLYGAGKT DEVGETGRQG
101 IWFGFLGVF GMVLMWAAIT PFRNWLTLSD YVEGTMAQYM LFTSLAMPAA
151 MVHRALHAYA SSLNRPRILM LVSFAAFVLN VPLNYIFVYG KFGMPALGGA
201 GCGLATMAVF WFSALALWIY IAKENFFRPF GLTAKFGKPD WAVFKQIWKI
251 GAPIGLSYFL EASAFSFIVF LIAPFGEDYV AAQQVGISLS GILYIMIPQSV
301 GSAGTVRIGF SLGRREFSRA RYISGVSLVS GWMLAVITVL SLVLFPSPLV
351 SMYNDPAVL SIAATVLLFA GLFQPADFTQ CIASYALRGY KVTKVPFPIH
401 AAFAWGCGLL PGYLLAYRFD MGIYGFWTAL IASLTIAAIA LVWCLELCRS
451 EMVRSHKAV*
```

m607/a607 98.9% identity in 459 aa overlap

	10	20	30	40	50	60
m607.pep	MLLDLNRFSFPVFLKEVRLLTTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
a607	MLLDLNRFSFSVFLKEVRLLTALALPMLLAQVAQVGIGFVDTVMAGGAGKEDLAAVALGS					
	10	20	30	40	50	60
	70	80	90	100	110	120
m607.pep	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
a607	SAFATVYITFMGIMAALNPMIAQLYGAGKTDEVGETGRQGIWFGFLGVFGMVLMWAAIT					
	70	80	90	100	110	120
	130	140	150	160	170	180
m607.pep	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYTSSLNRPRILMLVSFAAFVLN					
a607	PFRNWLTLSDYVEGTMAQYMLFTSLAMPAAMVHRALHAYASSLNRPRILMLVSFAAFVLN					
	130	140	150	160	170	180
	190	200	210	220	230	240

970

m607.pep	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
a 607	VPLNYIFVYGKFGMPALGGAGCGLATMAVFWFSALALWIYIAKENFFRPFGLTAKFGKPD
	190 200 210 220 230 240
m607.pep	250 260 270 280 290 300
	WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
a 607	WAVFKQIWKIGAPIGLSYFLEASAFSFIIVFLIAPFGEDYVAAQQVGISLSGILYMIPQSV
	250 260 270 280 290 300
m607.pep	310 320 330 340 350 360
	GSAGTVRIGFSLGRREFSRARYISGVSLVLGWLAVITVLSLVLFRSPLVSMYNNDPAVL
a 607	GSAGTVRIGFSLGRREFSRARYISGVSLVSGWLAVITVLSLVLFRSPLVSMYNNDPAVL
	310 320 330 340 350 360
m607.pep	370 380 390 400 410 420
	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFMIHAAAFWGCGLLPGYLLAYRFN
a 607	SIAATVLLFAGLFQPADFTQCIASYALRGYKVTKVPFMIHAAAFWGCGLLPGYLLAYRFD
	370 380 390 400 410 420
m607.pep	430 440 450 460
	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
a 607	MGIYGFWTALIASLTIAAIALVWCLELCSREMVRSHKAVX
	430 440 450 460

The following partial DNA sequence was identified in *N.gonorrhoeae* <SEQ ID 1925>:

g608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTACCT CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CAGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTCCGCA ACAGCGCGAT
201 ACGGAAAATC CTCCAAGGCG GCGAACCCGG GGCTGGCGAC ATCAGGCTCG
251 AAGGCGACCT CATCCTCGGC ATcGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGacgA ATTGGCACGG ATTTTCGGCA CGCAGGCAGg
351 catcggcagc CGTGCCACCG ACATCGGACA CGGCaTCaaa cAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAACC CGAGTCcgCa
451 aacaccggca acgaagccct tgccgactgc ctCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACAGG CTCGAACGCG
551 ACATTGGAT AGACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1926; ORF 608.ng>:

g608.pep

```

1  MSALLPIINR LILQSPDSRS ELTSFAGKTL TLNIAGLKLA GRITEDGLLS
51  AGNGFADTEI TFRNSAIRKI LQGGEPGAGD IRLEGDLILG IAVLSLLGSL
101 RSRASDELAR IFGTQAGIGS RATDIGHGIK QIGRNIAEQI GGFSREPESA
151 NTGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

```

The following partial DNA sequence was identified in *N.meningitidis* <SEQ ID 1927>:

m608.seq

```

1  ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51  CAGCCGCTCG GAACTTGGCG CCTTTGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGCT GAAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATT ACCTCCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGAG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCGG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAATC GGCGGATTTT CCCGCGAATC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT

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971

501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1928; ORF 608>:

m608.pep
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLLIG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GGFSRESESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N.gonorrhoeae*

ORF 608 shows 95.2% identity over a 188 aa overlap with a predicted ORF (ORF 608.ng)

from *N. gonorrhoeae*:

m608/g608

	10	20	30	40	50	60
m608.pep	MSALLPIINRLILQSPDSRS ELAAFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	:					
g608	MSALLPIINRLILQSPDSRSELT SFAGKTL TLNIAGLKLAGRITEDGLLSAGNGFADTEI					
	10	20	30	40	50	60
	70	80	90	100	110	120
m608.pep	TFRNSAVQKILQGGEPEGAGDIGLEGLLIGIAVLSLLGSLRSRASDELARIFGTQADIGS					
	:					
g608	TFRNSAIRKILQGGEPEGAGDIRLEGLDILIGIAVLSLLGSLRSRASDELARIFGTQAGIGS					
	70	80	90	100	110	120
	130	140	150	160	170	180
m608.pep	RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR					
	:					
g608	RATDIGHGIKQIGRNIAEQIGGFSREPESANTGNEALADCLDEISRLRDGVERLNERLDR					
	130	140	150	160	170	180
	189					
m608.pep	LERDIWIDX					
g608	LERDIWIDX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1929>:

a608.seq
1 ATGTCCGCCC TCCTCCCCAT CATCAACCGC CTGATTCTGC AAAGCCCGGA
51 CAGCCGCTCG GAACTTGCCG CCTTCGCAGG CAAAACACTG ACCCTGAACA
101 TTGCCGGGTT GAACTGGCG GGACGCATCA CGGAAGACGG TTTGCTCTCG
151 GCGGGAAACG GCTTTGCAGA CACCGAAATC ACCTTCGCA ACAGCGCGGT
201 ACAGAAAATC CTCCAAGGCG GCGAACCCGG GGCGGGCGAC ATCGGGCTCG
251 AAGGCGACCT CATCCTCGGC ATCGCGGTAC TGTCCCTGCT CGGCAGCCTG
301 CGTTCCCGCG CATCGGACGA ATTGGCACGG ATTTTCGGCA CGCAGGCAGA
351 CATCGGCAGC CGTGCCGCCG ACATCGGACA CGGCATCAAA CAAATCGGCA
401 GGAACATCGC CGAACAAATC GGCAGATTTT CCCGCGAACC CGAGTCCGCA
451 AACATCGGCA ACGAAGCCCT TGCCGACTGC CTCGACGAAA TAAGCAGACT
501 GCGCGACGGC GTGGAACGCC TCAACGAACG CCTCGACCGG CTCGAACGCG
551 ACATTGGAT AGACTAA

This corresponds to the amino acid sequence <SEQ ID 1930; ORF 608.a>:

a608.pep
1 MSALLPIINR LILQSPDSRS ELAAFAGKTL TLNIAGLKLA GRITEDGLLS
51 AGNGFADTEI TFRNSAVQKI LQGGEPEGAGD IGLEGLLIG IAVLSLLGSL
101 RSRASDELAR IFGTQADIGS RAADIGHGIK QIGRNIAEQI GRFSREPESA
151 NIGNEALADC LDEISRLRDG VERLNERLDR LERDIWID*

m608/a608 98.9% identity in 188 aa overlap

10 20 30 40 50 60

972

```

m608.pep      MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
a608           MSALLPIINRLILQSPDSRSELAAFAGKTLTLNIAGLKLAGRITEDGLLSAGNGFADTEI
                10      20      30      40      50      60

                70      80      90      100     110     120
m608.pep      TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
a608           TFRNSAVQKILQGGEPGAGDIGLEGDLILGIAVLSLLGSLRSRASDELARIFGTQADIGS
                70      80      90      100     110     120

                130     140     150     160     170     180
m608.pep      RAADIGHGIKQIGRNIAEQIGGFSRESESANIGNEALADCLDEISRLRDGVERLNERLDR
a608           RAADIGHGIKQIGRNIAEQIGRFSREPESANIGNEALADCLDEISRLRDGVERLNERLDR
                130     140     150     160     170     180

                189
m608.pep      LERDIWIDX
a608           LERDIWIDX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1931>:

```

g609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACTCTTGA
51 TGCCTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGTT TCCACATAAT
201 CGATAACTTC CTCGATACCG ACTTCGGCAT CGGAAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGATTATG CGCGCCATAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTAGT TGGCCGTATG
351 CCCCGTCTTT CATTTCACCC GTGAGGCTGA CATCATAATC CAGtaa

```

This corresponds to the amino acid sequence <SEQ ID 1932; ORF 609.ng>:

```

g609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRFHIIDNF LDTDFGIGSQ ADGNVRTLM RAILGNFFGT
101 RAKRGYGNHD LHTVAVCPVF HFTREADIII Q*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1933>:

```

m609.seq
1  ATGGTTGTGG ATAGACTCGA AATTCTCGCT CTCGACGACG AAACTCTTGA
51 TGCCTTTGTC GGCAATCAGC GAAGTAGCGA CATCGCGCAC CATATCTTCC
101 ACGAATTTTCG GGTTCGTA GGCCTTTTCG GTAACGTATT TTTCATCGGG
151 GCGTTTGAGC AGGCCGTAGA GTTGGCAGCT CGCCTGCGCC TCCACATAAT
201 CGATGACTTC CTCGATACCG ACTTCGGCAT CGGCAGTCAG GCTGACGGTA
251 ACGTGCGAAC GCTGTTGTG CGCGCCGTAT TGGGAAATTT CTTTGAACA
301 CGGGCAAAGC GAGGTTACGG GAATCATGAC CTTCACTAGT TGGCCGTATG
351 CCCCGTCTTT GATTTCGCCC GTGAGACAGA CATCATAATC CAGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1934; ORF 609>:

```

m609.pep
1  MVVDRLEILA LDETLDFAV GNQRSSDIAH HIFHEFRV FVGLFGNVFFIG
51 AFEQAVELAA RLRLHIIDDF LDTDFGIGSQ ADGNVRTLVV RAVLGNFFGT
101 RAKRGYGNHD LHTVAVCPVF DFARETDIII Q*

```

m609/g609 93.1% identity in 131 aa overlap

```

                10      20      30      40      50      60
m609.pep      MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
g609           MVVDRLEILALDDETLDFAVGNQRSSDIAHHIFHEFRV FVGLFGNVFFIGAFEQAVELAA
                10      20      30      40      50      60

                70      80      90      100     110     120
m609.pep      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF

```

```
a609.seq
1  ATG GTT GTG G  ATAG ACT C G A  AAT T C T C G C T  C T C G A C G A C G  A A A C T C T T G A
51  T G C G T T T G T C  G G C A A T C A G C  G A A G T A G C G A  C A T C G C G C A C  C A T A T C T T C C
101 A C G A A T T T C G  G G T T T T C G T A  G G C T T T T C G  G T A A C G T A T T  T T T C A T C G G G
151 G C G T T T G A G C  A G G C C G T A G A  G T T G G C A G C T  C G C T G C G C C  T C C A C A T A A T
201 C G A T G A C T T C  C T C G A T A C C G  A C T T C G G C A T  C G G C A G T C A G  G C T G A C G G T A
251 A C G T G C G A A C  G C T G G T T G T G  C G C G C C A T A T  T G G G A A A T T T  C T T T G G A A C A
301 C G G G C A A A G C  G A G G T T A C G G  G A A T C A T G A C  C T T C A T A C T G  T G G C G G T A T G
351 C A C C G T C T T T  C A T T T C G C C C  G T G A G G C T G A  C A T C A T A A T C  C A G T A A
```

a609.pep

1	MVVDRLLEILA	LDDETLDAFV	GNQRSSDIAH	HIFHEFRVFV	GFFGNVFFIG
51	AFEQAVELAA	RLRLHIIDDF	LDTDFGIGSQ	ADGNVRTLVV	RAILGNFFGT
101	RAKRGYGNHD	LHTVAVCTVF	HFAREADIII	Q*	

```

                                10      20      30      40      50      60
m609.pep  MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEQAVELAA
          |||||:|||||
a609      MVVDRLEILALDDETLDAFVGNQRSSDIAHHIFHEFRVFVGFFGNVFFIGAFEQAVELAA
                                10      20      30      40      50      60

                                70      80      90      100     110     120
m609.pep  RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAVLGNFFGTRAKRGYGNHDLHTVAVCPVF
          |||||:|||||
a609      RLRLHIIDDFLDTDFGIGSQADGNVRTLVVRAILGNFFGTRAKRGYGNHDLHTVAVCTVF
                                70      80      90      100     110     120

                                130
m609.pep  DFARETDIIIX
          ||||:|||||
a609      HFAREADIIIX
                                130

```

```

g610.seq
1  ATGATTGGAG  GGCTTATGCA  ATTTCCTTAC  CGCAATGTTT  CGGCTTCGCG
51  TATGCGCCGT  ATGCGCAGGG  ATGATTTTTC  ACGCCGCCTG  ATGCGCGAGC
101 ATATGCTGAC  GCGCGATGAT  TTGATTTATC  CGGTGTTCTG  ATTGGAGGGG
151 GCGGCGCGCG  AGGAGGATGT  GCCTTCTATG  CCGGGCGTGA  AGCGTCAGAG
201 TTTGGACAGG  CTGCTGTTTA  CGGCGGAAGA  GCGGGTGAA  CTCGGTATTC
251 CGATGTTGCG  ATCTTTCCCG  TGTGTTACGG  CAAACAAAAC  CCGGCGTCGG
301 CAGGAGGCGT  ACAATCCCGA  AGGACTCGTG  CCGTCAACTG  tccgagccTT
351 GCGCGAGAGG  TttcCgcaac  tggggattat  gacggaatgc  gcgctcgATc
401 cttacccggt  gaacGGTCAG  GACGACATGA  CGGACgaaaa  cgttcaCGTG
451 ATGAatgATg  aaacCGTAGA  AGTCTTGGTG  AAACAGGCTT  TGTGTCATGC
501 AGAGCGCGGC  ACGCAGGTCG  TTGCTCCTTC  CGATATGATG  GACGGCGGCG
551 TCGGCGCCAT  CCGCGAGGCT  TTGAGGAGTG  CCGGACATAT  CCATACGCGG
601 ATTATGGCAT  ATTCCGCCAA  ATATGCTTCT  GCATTCTACG  GCCCTTTCCG
651 TGATGCGGTA  GGCAGTTCGG  GCAATTGGGG  AAAGGCAGAT  AAAAAGAGCT
701 ATCAGATGGA  TCCTGCAAA  ACCGATGAGG  CGCTGCATGA  AGTTGGCGCT
751 GATATTcAGG  AAGGTGCGGA  TATGGTGATG  GTGAAGCCCG  GTTTGCCGTA

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974

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801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTA CCGACTTATG
851 CCTATCAGGT TTCGGGCGAA TATGCGATGT TGCAGGCGGC GGTGCGCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1938; ORF 610.ng>:

```

g610.pep
1  MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHMLTADD LIYPVFVLEG
51  AAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTGRA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG TQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSSE YAMLQAAVAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1939>:

```

m610.seq
1  ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CCGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCTG ATGCGCGAAC
101 ACACGCTGAC CGCCGATGAT TTGATTATC CGGTGTTCTG ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGTGTGA AGCGTCAAAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT TCACGGTCAG GACGGGCTGA CGGACGAAA CGGTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGCCACGC
501 TGAAGCGGGC GCGCAGGTGG TTGCCCTTTC CGATATGATG GACGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGCGCT ATTCCGCCAA ATATGCTTCT GCATTTTACG GCCCTTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTCAGG AAGGTGCGGA TATGGTAATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TAAAGGACGA GTTCGGTGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGT TGCAGGCAGC GATTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGACGGGA TTTTGACCTA TTACGCTATT GAGGCGGCAA
1001 AGATGTTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1940; ORF 610>:

```

m610.pep
1  MIGGLMQFPY RNPASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENGYV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIRES LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFGV PTYAYQVSSE YAMLQAAIAN
301 GWLDGGKVVL ESLLAFKRAG ADGILTYAI EAAKMLKR*

```

m610/g610 98.5% identity in 338 aa overlap

	10	20	30	40	50	60
m610.pep	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM					
g610	MIGGLMQFPYRNPASRMRRMRRDDFSRRLMREHMLTADDLIYPVFVLEGAAREEDVPSM					
	10	20	30	40	50	60
	70	80	90	100	110	120
m610.pep	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER					
g610	PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTGRAQEAYNPEGLVPSTVRALRER					
	70	80	90	100	110	120
	130	140	150	160	170	180
m610.pep	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVVAPSDMM					
g610	FPELGIMTDVALDPYTVHGQDGLTDENGYVMNDETVEVLVKQALCHAEAGTQVVAPSDMM					
	130	140	150	160	170	180
	190	200	210	220	230	240
m610.pep	DGRIGAIRESLEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN					

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g610      DGRIGAIREALDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
           190      200      210      220      230      240

           250      260      270      280      290      300
m610.pep  TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTAYQVSGEYAMLQAAIAN
|||||
g610      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFVPTAYQVSGEYAMLQAAVAN
           250      260      270      280      290      300

           310      320      330      339
m610.pep  GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
|||||
g610      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
           310      320      330

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1941>:

```

a610.seq
1   ATGATTGGAG GGCTTATGCA GTTTCCTTAC CGCAATGTTT CGGCTTCGCG
51  TATGCGCCGT ATGCGCAGGG ACGATTTTTC ACGCCGCCGT ATGCGCGAGC
101 ATACGCTGAC TGCCGATGAT TTGATTATC  CGGTGTTCGT ATTGGAGGGG
151 TCGGCGCGCG AGGAGGATGT GCCTTCTATG CCGGGCGTGA AGCGTCAGAG
201 TTTGGACAGG CTGCTGTTTA CGGCGGAAGA GGCGGTAAAG CTCGGTATTC
251 CGATGTTGGC ACTGTTCCCC GTGGTTACGG CAAACAAAAC CGAGCGTGCG
301 CAGGAGGCGT ACAATCCCGA AGGACTCGTG CCGTCAACTG TCCGCGCCTT
351 GCGCGAGAGG TTTCCCGAAC TGGGCATTAT GACGGATGTC GCGCTCGATC
401 CTTATACGGT GCACGGTCAG GACGGGCTGA CGGACGAAAA CGGTTATGTG
451 ATGAACGATG AAACCGTAGA GGTTTTGGTC AAGCAGGCTT TGTGTCATGC
501 AGAGGCAGGC GCACAGGTCG TTGCTCCTTC CGATATGATG GATGGGCGTA
551 TCGGTGCGAT TCGCGAGGCG TTGGAGGATG CCGGGCATAT CCATACGCGG
601 ATTATGGCGT ATTCGCCCAA ATATGCTTCT GCATTTTACG GCCCTTCCG
651 TGATGCGGTA GGCAGTTCGG GCAATTTGGG CAAGGCAGAT AAAAAGACCT
701 ACCAGATGGA TCCGGCAAAT ACCGATGAGG CGTTGCACGA AGTGGCGTTG
751 GACATTACAG AAGGTGCGGA TATGGTGATG GTCAAGCCCG GTTTGCCGTA
801 TTTGGACGTT GTCCGCCGCG TGAAGGACGA GTTCGGCGTG CCGACTTATG
851 CCTATCAGGT TTCGGGAGAA TACGCGATGC TGCAGGCGGC GGTTGCCAAC
901 GGCTGGCTGG ACGGCGGCAA AGTGGTTTTG GAAAGCCTGC TGGCATTCAA
951 ACGTGCGGGT GCGGATGGGA TTTTGACCTA TTACGCCATT GAGGCGGCAA
1001 AGATGCTGAA GCGTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1942; ORF 610.a>:

```

a610.pep
1   MIGGLMQFPY RNVASRMRR MRRDDFSRRL MREHTLTADD LIYPVFVLEG
51  SAREEDVPSM PGVKRQSLDR LLFTAEEAVK LGIPMLALFP VVTANKTERA
101 QEAYNPEGLV PSTVRALRER FPELGIMTDV ALDPYTVHGQ DGLTDENG YV
151 MNDETVEVLV KQALCHAEAG AQVVAPSDMM DGRIGAIREA LEDAGHIHTR
201 IMAYSAKYAS AFYGPFRDAV GSSGNLGKAD KKTYYQMDPAN TDEALHEVAL
251 DIQEGADMVM VKPGLPYLDV VRRVKDEFV PTAYQVSGE YAMLQAAVAN
301 GWLDGGKVV L ESLLAFKRAG ADGILTYAI EAAKMLKR*

m610/a610  99.4% identity in 338 aa overlap

           10      20      30      40      50      60
m610.pep  MIGGLMQFPYRNPASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
|||||
a610      MIGGLMQFPYRNVASRMRRMRDDFSRRLMREHTLTADDLIYPVFVLEGSAREEDVPSM
           10      20      30      40      50      60

           70      80      90      100     110     120
m610.pep  PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
|||||
a610      PGVKRQSLDRLLFTAEEAVKLGIPMLALFPVVTANKTERAQEAYNPEGLVPSTVRALRER
           70      80      90      100     110     120

           130     140     150     160     170     180

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976

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m610.pep      FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a610          FPELGIMTDVALDPYTVHGDGLTDENGYVMNDETVEVLVKQALCHAEAGAQQVAPSDMM
                130      140      150      160      170      180

                190      200      210      220      230      240
m610.pep      DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
                |||||||||||||||||||||||||||||||||||||||||||||||||||
a610          DGRIGAIREALEDAGHIHTRIMAYSAKYASAFYGPFRDAVGSSGNLGKADKKTYQMDPAN
                190      200      210      220      230      240

                250      260      270      280      290      300
m610.pep      TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAIAN
                ||||||||||||||||||||||||||||||||||||||||||||||||:|
a610          TDEALHEVALDIQEGADMVMVKPGLPYLDVVRVKDEFGVPTYAYQVSGEYAMLQAAVAN
                250      260      270      280      290      300

                310      320      330      339
m610.pep      GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
                |||||||||||||||||||||||||||||||||||||||||||||
a610          GWLDGGKVVLESLLAFKRAGADGILTYAIEAAKMLKRX
                310      320      330

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1943>:

```

g611.seq
1   ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCCCGGA CTCTGTCGAG
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TTTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT Ctcgcgcagg ttgtGGCtgt
201 tatectTGGG CGGGCTGggt tgtttgcccc ccataaTtTc cagtacctgA
251 TcgcgGTCTa tggtttCCa ttCcatcagg gctttgcaca TCGTTTCCAT
301 cttgTCGCGG TTTTcatcga ggaTTTGTa ggcaacCTGA TACTgctcgt
351 ccaaaaAtccg Gcggatttcc gcgtcgAtgt cctgctgggt tTTCTCGGAA
401 ATGTTTTGCG AACGGgttac gctGCGCCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc gTCAtgcCG TAGCGCGTTA
501 CCATTTCCGC TGCCATTG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1944; ORF 611.ng>:

```

g611.pep
1   MPSENGMKR QLAGCRLFGK LSLVFRLLPG LCRGGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVILG RAGLFARHNF QYLIAVYGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AAPQEDFAFV
151 FRINHHAFHV AHAVARYHFA CHLGCAFKVV *

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1945>:

```

m611.seq
1   ATGCCGCTCTG AAAACGGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51  GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCCGCCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTG TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTGTa GGCAACCTGA TATTGCTCGT
351 CCAAAATCCG GCGGATTTC GCGTCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTGTc GTCATGCCG TAGCGCGTTA
501 CCATTTCCGC CGCCATTG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1946; ORF 611>:

```

m611.pep
1   MPSENGMKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51  RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIAVDGFP FHQGFARHFH
101 LVAVFIEDFV GNLILLVQNP ADFRVDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAFHV AHAVARYHFA RHLGCAFKVV *

```

m611/g611 96.1% identity in 180 aa overlap

10 20 30 40 50 60

977

```

m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
g611           MPSENGMGKRQLAGCRLFGKLSLVFRLLLPGLCRGGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
g611           LAQVVAVILGRAGLFARHNFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               |||||
g611           ADFRVDVLLGFLGNVLRGTGYAAPQEDFAFVFRINHHAHFVAHAVARYHFACHLGCAFKVV
               130     140     150     160     170     180

m611.pep      X
               |
g611           X

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1947>:

```

a611.seq
1  ATGCCGTCTG AAAACAGGAT GGGAAAACGG CAGCTTGCGG GCTGCCGTTT
51 GTTCGGGAAG TTAAGCCTTG TTTTCAGGCT GCTGCTCGGA CTCTGTTCGAA
101 GCGGTGTCTG CCGGGGCAGG TGCTTCGGTT TCTTCCCGAG TCGGAGCGTG
151 CGGCGCGTTA TCTTCGCGCG CGTCCGCATT CTCGCGCAGG TTGTGGCTGT
201 AATCTTTGGG CGGGCTGGGT TGTTCGCCG CCATGATTTC CAGTACCTGA
251 TCGCGGTCTG TGGTTTCCCA TTCCATCAGG GCTTTGCACA TCGTTTCCAT
301 CTTGTGCGCG TTTTCATCGA GGATTTTGTA GGCAACCTGA TACTGCTCGT
351 CCAAAATCCG GCGGATTTC GCATCGATGT CCTGCTGGGT TTTCTCGGAA
401 ATGTTTTGCG AACGGGTAC GCTGCGTCCC AAGAAGACTT CGCCTTCGTT
451 TTCCGCATAA ACCATCACGC CCATTTTGTC GTCATGCCG TAGCGCGTTA
501 CCATTTCGCG CGCCATTGG GTTGCGCGTT CAAAGTCGTT TGA

```

This corresponds to the amino acid sequence <SEQ ID 1948; ORF 611.a>:

```

a611.pep
1  MPSENRMGKR QLAGCRLFGK LSLVFRLLLG LCRSGVCRGR CFGFFPSRSV
51 RRVIFRRVRI LAQVVAVIFG RAGLFARHDF QYLIADVGF FHQGFARHFL
101 LVAVFIEDFV GNLILLVQNP ADFRIDVLLG FLGNVLRGTG AASQEDFAFV
151 FRINHHAHFV AHAVARYHFA RHLGCAFKVV *

```

m611/a611 98.9% identity in 180 aa overlap

```

               10      20      30      40      50      60
m611.pep      MPSENGMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               |||||
a611           MPSENRMGKRQLAGCRLFGKLSLVFRLLLGLCRSGVCRGRCFGFFPSRSVRRVIFRRVRI
               10      20      30      40      50      60

               70      80      90      100     110     120
m611.pep      LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
               |||||
a611           LAQVVAVIFGRAGLFARHDFQYLIADVGFPPFHQGFARHFLVAVFIEDFVGNLILLVQNP
               70      80      90      100     110     120

               130     140     150     160     170     180
m611.pep      ADFRVDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               |||||
a611           ADFRIDVLLGFLGNVLRGTGYAASQEDFAFVFRINHHAHFVAHAVARYHFAHRLGCAFKVV
               130     140     150     160     170     180

m611.pep      X

```

a611 I
 X

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1949>:

g612.seq
1 ATGGGcttcg gcggaatat tgcAAAAAAG CTGGCcgGg taGATGAAAT
51 AGCCTttgac tttgacggcA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCataG CCGCGTAATC AATGCTGCTG TCGCCGGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCGATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA TAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttTAC GGGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1950; ORF 612.ng>:

g612.pep
1 MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NAAVAGLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GDFPNLAVQL GALLHFGHHR
101 NPYIKLNKSK SPDIFRRFFY GHSN*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1951>:

m612.seq
1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTAAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTAAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGCATTTCGG TCATCATCGA
301 AATCCATATA .AAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTttTAC GGGCATTCAA ATTAA

This corresponds to the amino acid sequence <SEQ ID 1952; ORF 612>:

m612.pep
1 MGFGGNIAKK LAGVDEIAFN FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
51 GEVFADKAVE KCAENVLFKV PAIHRAAYFV GNFPNLAVQL GALLHFGHHR
101 NPYXKLKSK SPDIFRRFFY GHSN*

m612/g612 96.0% identity in 124 aa overlap

	10	20	30	40	50	60
m612.pep	MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE					
g612	MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINAAVAGLHIVGEVFADKAVE					
	10	20	30	40	50	60
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLKSKSPDIFRRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLKSKSPDIFRRFFY					
g612	KCAENVLFKVP AIHRAAYFVGDFPNLAVQLGALLHFGHHRNPYIKLNKSKSPDIFRRFFY					
	70	80	90	100	110	120
m612.pep	GHSNX					
g612	GHSNX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1953>:

a612.seq
1 ATGGGCTTCG GCGGCAATAT TGCAAAAAAG CTGGCCGGGG TAGATGAAAT
51 AGCCTTTGAC TTTGACGGCA TCGTCTTTGA TTTCGGGCGT GATGATGCTG
101 TCCGGCATAG CCGCGTAATC AATACTGCTG TCGCCTGCCT GCATATAGTC
151 GGTGAAGTTT TCGCTGATAA AGCGGTAGAA AAGTGTGCCG AGAACGTATT
201 GTTTGAAGTC CCAGCCATCC ACCGCGCCGC GTACTTCGTC GGCAATTTTC
251 CAAATTTGGC GGTGCAGTTG GCGCGTTGT TGTATTTCGG TCATCATCGA
301 AATCCATAT. AAAAGTTAAA CAAATCAAAA TCGCCTGATA TTTTCAGACG
351 ATTTTtt.AC GGGCATTCAA ATTAA

979

This corresponds to the amino acid sequence <SEQ ID 1954; ORF 612.a>:

```

a612.pep
  1  MGFGGNIAKK LAGVDEIAFD FDGIVDFDGR DDAVRHSGVI NTAVACLHIV
 51  GKVFADKAVE KCAENVLFEV PAIHRAAYFV GNFPNLAVQL GALLYFGHHR
101  NPYXKLNKSK SPDIFRRFFX GHSN*

m612/a612    96.0% identity in 124 aa overlap

              10      20      30      40      50      60
m612.pep     MGFGGNIAKKLAGVDEIAFNFDGIVDFDGRDDAVRHSGVINTAVACLHIVGEVFADKAVE
              |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          MGFGGNIAKKLAGVDEIAFDGIVDFDGRDDAVRHSGVINTAVACLHIVGKVFADKAVE
              10      20      30      40      50      60

              70      80      90     100     110     120
m612.pep     KCAENVLFKVP AIHRAAYFVGNFPNLAVQLGALLHFGHHRNPYXKLNKSKSPDIFRRFFY
              |||||:|||||:|||||:|||||:|||||:|||||:|||||
a612          KCAENVLFEVPAIHRAAYFVGNFPNLAVQLGALLYFGHHRNPYXKLNKSKSPDIFRRFFX
              70      80      90     100     110     120

m612.pep     GHSNX
              ||||
a612          GHSNX

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1955>:

```

g613.seq
  1  ATGTCGCGTT CGAGCCTGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC ggcaagggct tcgttgccgg
101  tgtttGcgGA CTCGGGTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTgtttGAt GCCGTGTCCG ATGTCGGTGG CACGgctgcc
201  gatgcCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CgATGCCGAG GATGAGGTCG
301  CCTTCGAGCC TGATGTCGCC AGCCCCGGGT TCGCCGCCCTT GGAGGATTTT
351  CCGTATCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCTGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGAGGTAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATTGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT
601  ATTTTACAGG CTAA

```

This corresponds to the amino acid sequence <SEQ ID 1956; ORF 613.ng>:

```

g613.pep
  1  MSRSSLSRRS LRRSTPSRSL LISSRQSARA SLPVFADSGS RENPPICSAM
 51  FLPICLMPCP MSVARLPMPA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSLMSPAPG SPPWRIFRIA LLRKVISVSA KPFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KEVSSERLSG LCRIRRLMMG RRADIFSDWG GECLLLLLPL
201  ILQA*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1957>:

```

m613.seq
  1  ATGTCGCGTT CGAGCCGGTC GAGGCGTTTCG TTGAGGCGTT CCACGCCGTC
 51  GCGCAGTCTG CTTATTTCGT CGAGGCAGTC GGCAAGGGCT TCgtTGCCGA
101  TGTTTGCGGA CTCGGATTTCG CGGGAAAATC CGCCGATTG TTCGGCGATG
151  TTCCTGCCGA TTTGTTTGAT GCCGTGTCCG ATGTCGGCGG CACGGCTGCC
201  GATGTCTGCC TGCGTGCCGA AAATCCGTGC CAATTcgtCC GATGCGCGGG
251  AACGCAGGCT GCCGAGCAGG GACAGTACCG CGATGCCGAG GATGAGGTCG
301  CCTTCGAGCC CGATGTCGCC CGCCCCGGGT TCGCCTCCTT GGAGGATTTT
351  CTGTACCGCG CTGTTGCGGA AGGTAATTTT GGTGTCTGCA AAGCCGTTTC
401  CCGCCGAGAG CAAACCGTCT TCCGTGATGC GTCCCGCCAG TTTCAGCCCG
451  GCAATGTTCA GGGTCAGTGT TTTGCCTGCA AAGGCGGCAA GTTCCGAGCG
501  GCTGTCCGGG CTTTGCAGAA TCAGGCGGTT GATGATGGGG AGGAGGGCGG
551  ACATATTTTC TGATCGGGGC GGAGAATGCC TGTTGTTGCT GTTGCCGCTT

```

980

601 ATTTTACAGG CTTAA

This corresponds to the amino acid sequence <SEQ ID 1958; ORF 613>:

```

m613.pep
  1  MSRSSRSRRS LRRSTPSRSL LISSRQSARA SLPMFADSDS RENPPICSAM
 51  FLPICLMPCP MSAARLPMSA CVPKIRANSS DARERRLPSR DSTAMPRMRS
101  PSSPMSPAPG SPPWRIFCTA LLRKVISVSA KFFPAESKPS SVMRPASFSP
151  AMFRVSVLPA KAASSERLSG LCRIRRLMMG RRADIFSDRG GECLLLLLPL
201  ILQA*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m613/g613 94.6% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
g613	MSRSSLRRSLRRSTPSRSLLISSRQSARASLPVFADSGSRENPPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPMSACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSPMSPAPGSPPWRIFCTA					
	:					
g613	MSVARLPMPACVPKIRANSSDARERRLPSRDSTAMPRMRSPSSLMSAPAGSPPWRIFRIA					
	70	80	90	100	110	120

981

	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
	:					
g613	LLRKVISVSAKPFPAESKPSSVMRPASFSPPAMFRVSVLPAAKEVSSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
g613	RRADIFSDWGGECLLLLLPLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1959>:

```

a613.seq
1   ATGTCGCGTT  CGAGCCGGTC  GAGGCGTTCG  TTGAGGCGTT  CCACGCCGTC
51  GCGCAGTCTG  CTTATTTCGT  CGAGGCAGTC  GGCAAGGGCT  TCGTTGCCGA
101 TGTTCGCGGA  CTCGGGTTTCG  CGGGAATATC  TGCCGATTTG  TTCGGCGATG
151 TTCCTGCCGA  TTTGTTTGAT  GCCGTGTCCG  ATGTCGGCGG  CACGGCTGCC
201 GATGTCTGCC  TGCGTGCCGA  AAATCCGTGC  CAATTCGTCC  GATGCGCGGG
251 AACGCAGGCT  GCCGAGCAGG  GACAGTACCG  CGATGCCGAG  GATGAGGTCG
301 CCTTCGAGCC  CGATGTGCCG  CGCCCCGGGT  TCGCCGCCTT  GGAGGATTTT
351 CTGTACCGCG  CTGTTGCGGA  AGGTGATTTT  GGTGTCTGCA  AAGCCGTTTC
401 CCGCCGAGAG  CAAACCGTCT  TCCGTGATGC  GTCCCGCCAG  TTTCAACCCG
451 GCAATGTTCA  GGGTCAGTGT  TTTGCCTGCG  AAGGCGGCAA  GTTCCGAGCG
501 GCTGTCCGGG  CTTTGCAGAA  TCAGGCGGTT  GATGATGGGG  AGGAGGGCGG
551 ACATATTTTC  TGATCGGGGC  GGAGAATGCC  TGTGTGTGCT  GTTGACGCTT
601 ATTTTACAGG  CTTAA

```

This corresponds to the amino acid sequence <SEQ ID 1960; ORF 613.a>:

```

a613.pep
1   MSRSSRSRRS  LRRSTPSRSL  LISSRQSARA  SLEPMFADSGS  RENLPICSAM
51  FLPICLMPCP  MSAARLPSA  CVPKIRANSS  DARERRLPSR  DSTAMPRMRS
101 PSSPMSPAPG  SPPWRIFCTA  LLRKVISVSA  KPFPAESKPS  SVMRPASFPN
151 AMFRVSVLPA  KAASSERLSG  LCRIRRLMMG  RRADIFSDRG  GECLLLLLTL
201 ILQA*

```

m613/a613 98.0% identity in 204 aa overlap

	10	20	30	40	50	60
m613.pep	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENPPICSAMFLPICLMPCP					
a613	MSRSSRSRRSLRRSTPSRSLISSRQSARASLPMFADSDSRENLPICSAMFLPICLMPCP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m613.pep	MSAARLPSACVVPKIRANSSDARERRLPSRDSTAMPMRSPSSPMSPAPGSPPWRIFCTA					
a613	MSAARLPSACVVPKIRANSSDARERRLPSRDSTAMPMRSPSSPMSPAPGSPPWRIFCTA					
	70	80	90	100	110	120
	130	140	150	160	170	180
m613.pep	LLRKVISVSAKPFPAESKPSSVMRPASFSPPAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
	:					
a613	LLRKVISVSAKPFPAESKPSSVMRPASFPNPFAMFRVSVLPAAKASSERLSGLCRIRRLMMG					
	130	140	150	160	170	180
	190	200				
m613.pep	RRADIFSDRGGECLLLLLPLILQAX					
a613	RRADIFSDRGGECLLLLLTLILQAX					
	190	200				

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1961>:

982

g614.seq

```

1   AtggcTgcgt  tcAacgcttt  ggacggcaaa  aaagaagaca  acggggcaaat
51  cgaaTATTCT  CAGTTCATCC  GACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGTT  ACCTGATTAA  AGGCGAGCGC
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCCTTGGATG  ACAACCTGAT
201 TCAAACCTTT  TTGAACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCAGAGCG  GCTGACTGCC  CTGTTTACA  GCCTGCTGCC  CGTCCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGGCGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCCT  TCGGCAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTTACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TGCAGGAAAT  CGTCGATTAC  CTCAAAGCAC  CGAACCGCTa
501 tcaAAGcctc  ggcggccgtg  ttcCGCGCGG  CATCctgCtg  gcgGgcagcc
551 CGGGAaccgg  taaAACACTC  TTGGCGAAAG  CCATTGCAGG  CGAGGCCGGC
601 GTGCCGTTCT  TCAGCATTTC  CGGTTCGGAT  TTTGTCGAAA  TGTTTCGTCG
651 TGTCGGTGCA  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCA  AAGAAAAACG
701 CCCCATGCAT  TATCTTTATC  GACGAGATTG  ACGCGGTAGG  CCGCCAACGC
751 GGCGCAGgTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTATTGGTT  GAAATGGACG  GTTTTGAGAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTACTCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGCTTCG  ACCGCCAAGT  CGTCGTCCCC  CTGCCGGACA  TCCGGGGGCG
951 CGAACAGatn  ttGAACGTCC  ATTctaaAAA  AGTGCcttTG  gacgaATCTg
1001 tggatTTATT  GTCCCTCGCG  CGCGGCACGC  cgggtttTt  cggcgcggat
1051 tTggcgaaac  tggTcaacga  agccccctg  tttgccggcc  gccgcaacaa
1101 agtgaaagtc  gatcaaacgc  atttGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1962; ORF 614.ng>:

g614.pep

```

1   MAAFNALDGK  KEDNGQIEYS  QFIRQVNNGE  VSGVNIIEGSV  VSGYLIKGER
51  TDKSTFFFTNA  PLDDNLIQTL  LKNKVRVKVT  PEEKPSALTA  LFYSLLPVLL
101 LIGAWFYFMR  MQAGGGGKGG  AFSFGKSRAR  LLDKDANKVT  FADVAGCDEA
151 KEEVQEIVDY  LKAPNRYQSL  GGRVPRGILL  AGSPGTGKTL  LAKAIIAGEAG
201 VPFFSISGSD  FVEMFVGUGA  SRVRDMFEQA  KKNAPCIIFI  DEIDAVGRQR
251 GAGLGGGNDE  REQTLNQLLV  EMDGFESNQT  VIVIAATNRP  DVLDPALQRP
301 GRFDRQVVVP  LPDIRGREQX  LNVHSKKVPL  DESVDLLSLA  RGTPGFSGAD
351 LAKLVNEAPL  FAGRRNKVKV  DQSDLKTPKT  KSIWVRNAAV  W*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1963>:

m614.seq

```

1   ATGGCTGCGT  TCAACGCTTT  AGACGGTAAA  AAAGAAGACA  ACGGGCAAAAT
51  CGAATACTCT  CAGTTCATCC  AACAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCAGCGGCT  ACCTGATTAA  GGGCGAGCGC
151 ACCGACAAAA  GCACTTTCTT  CACCAACGCG  CCTTGGACG  ACAACCTAAT
201 TAAACACTG  CTCGACAAAA  ACGTCCGCGT  AAAAGTAACG  CCGGAAGAAA
251 AACCAGAGCG  GCTGGCTGCC  CTGTTTACA  GCCTGCTGCC  CGTCCTGCTG
301 CTGATTGGCG  CATGGTTCTA  CTTTATGCGT  ATGCAGACGG  GCGGCGGCGG
351 AAAAGGCGGC  GCATTCTCAT  TCGGTAAAAG  CCGCGCCCGC  CTGCTGGACA
401 AAGATGCCAA  CAAAGTGACC  TTTGCCGATG  TCGCCGGCTG  CGACGAAGCC
451 AAAGAAGAAG  TACAGGAAAT  CGTCGATTAC  CTCAAAGCGC  CGAACCGCTa
501 TCAAAGCCTG  GGCGGGCGCG  TGCCGCGCGG  CATCCTGCTG  GCGGGCAGCC
551 CGGGTACGGG  TAAGACGCTT  TTGGCGAAAG  CGATTGCAGG  CGAAGCCGGC
601 GTGCCGTTCT  TCAGCATTTC  AGGTTCGGAC  TTTGTCGAAA  TGTTTCGTCG
651 TGTCGGTGCG  AGCCGCGTCC  GCGATATGTT  CGAGCAGGCG  AAGAAAAACG
701 CCCCCTGCAT  CATCTTTATC  GACGAGATTG  ACGCACTCGG  CCGCCAACGC
751 GGCGCAGGTT  TGGGCGGCGG  CAATGATGAG  CGCGAGCAAA  CATTAAACCA
801 ATTGTTGGTT  GAAATGGACG  GTTTTGAGAG  CAATCAGACT  GTAATTGTGA
851 TTGCGGCAAC  CAACCGCCCC  GACGTACTCG  ATCCTGCGCT  GCAACGCCCC
901 GGCCGTTTCG  ACCGCCAAGT  GGTGTCCCC  CTGCCGGACA  TCCGAGGGCG
951 CGAACAGATT  TTGAACGTCC  ATTCTAAAAA  AGTGCCTTTG  GACGAATCTG
1001 TGGATTTATT  GTCCCTCGCG  CGCGGCACGC  CGGGTTTTTC  CGGCGCGGAT
1051 TTGCGCAACT  TGGTCAACGA  AGCCGCCCTG  TTTGCCGGCC  GCCGCAATAA
1101 AGTCAAAGTC  GATCAGAGCG  ATTTGAAGAC  GCCAAAGACA  AAATCTATAT
1151 GGGTCCGGAA  CGCCGCAGTA  TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1964; ORF 614>:

Homology with a predicted ORF from *N. gonorrhoeae*

	10	20	30	40	50	60
m614.pep	MAAFNALDGKKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVSVSGYLIKERTDKSTFFFTNA					
g614	MAAFNALDGKKKEDNGQIEYSQFIQQVNNGEVSGVNIEGSVSVSGYLIKERTDKSTFFFTNA					
	10	20	30	40	50	60
m614.pep	PLDDNLIKTLDDKNVRVKVTPPEEKPSALAAFYSLLPVLLLIGAWFYFMRMQTGGGGKGG					
g614	PLDDNLIQTLLNKNVRVKVTPPEEKPSALTALFYSLLPVLLLIGAWFYFMRMQAGGGGGKGG					
	70	80	90	100	110	120
m614.pep	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
g614	AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDYLKAPNRYQSLGGRVPRGILL					
	130	140	150	160	170	180
m614.pep	AGSPGTGKTL LAKAIAIEAGVPFFFSISGSDFVEMFVGASRVRDMFEQAKKNAPCIIFI					
g614	AGSPGTGKTL LAKAIAIEAGVPFFFSISGSDFVEMFVGASRVRDMFEQAKKNAPCIIFI					
	190	200	210	220	230	240
m614.pep	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTVIVIAATNRDPVLDPALQRP					
g614	DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQTVIVIAATNRDPVLDPALQRP					
	250	260	270	280	290	300
m614.pep	GRFDRQVVVPLPDIRGREQILNVHSKKVPLDESVDLLSLARGTPGFSGADLANLVNEAAL					
g614	GRFDRQVVVPLPDIRGREQILNVHSKKVPLDESVDLLSLARGTPGFSGADLAKLVNEAPL					
	310	320	330	340	350	360
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
g614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

```
a614.seq
1  ATGGCTGCGT  TCAACGCTTT  AGACGGTAAA  AAAGAAGACA  ACGGGCAAAT
51  CGAATATTCT  CAGTTTCATCC  ATCAGGTCAA  CAACGGCGAA  GTATCCGGCG
101 TCAACATCGA  AGGATCCGTC  GTCACGGCT  ACGTATGATA  GGATCGAGCG
151 ACCGACAAAA  GCACCTTCTT  CACCAACGCG  CCTTTGGACG  ACAACCTGAT
201 TAAACACACTG  CTCGACAAAA  ACGTCCGTGT  AAAAGTAACG  CCGGAAGATA
251 AACCAGAGCG  GCTGGCTGCC  CTGTTTTACA  GCGTGTGCC  CGTCTGTCTG
```

984

```

301 CTGATTGGCG CGTGGTTCTA CTTTATGCGT ATGCAGACGG GCGGCGGCGG
351 AAAAGGCGGC GCATTCTCAT TCGGCAAAAG CCGCGCCCGC CTACTGGACA
401 AAGATGCCAA CAAAGTTACC TTTGCCGATG TCGCCGGCTG CGACGAAGCC
451 AAAGAAGAAG TGCAGGAAAT CGTCGATTAC CTCAAAGCGC CGAACCGCTA
501 TCAAAGCCTG GCGGGGCGCG TGCCGCGCGG CATCCTGCTG GCGGGCAGCC
551 CGGGTACGGG TAAGACGCTT TTGGCGAAAG CGATTGCAGG CGAAGCCGGC
601 GTGCCGTTCT TCAGCATTTT AGGTTCCGAC TTTGTCGAAA TGTTGCTCGG
651 TGTCCGTGCA AGCCGCGTCC GCGATATGTT CGAGCAGGCG AAGAAAAACG
701 CCCCCTGCAT CATCTTTATC GACGAGATTG ACGCAGTCGG CCGCCAACGC
751 GGCGCAGGTT TGGGCGGCGG TAATGATGAG CGCGAGCAAA CATTAACCA
801 ATTGTTGGTT GAAATGGACG GTTTTGAGAG CAATCAGACT GTAATTGTGA
851 TTGCGGCAAC CAACCGCCCC GACGTACTCG ATCCTGCGCT GCAACGCCCC
901 GGCGGTTTCG ACCGCCAAGT GGTTGTCCCC CTGCCGGACA TCCGGGGGCG
951 CGAACAGATT TTGAACGTCC ACTCTAAAAA AGTGCCTTTG GACAAATCTG
1001 TGGATTTATT GTCCCTCGCG CGCGGCACGC CGGGTTTTTC CGGCGCGGAT
1051 TTGGCGAACT TGGTCAACGA AGCCGCCCTG TTTGCCGGCC GCCGCAATAA
1101 AGTCAAAGTC GATCAGAGCG ATTTGAAGAC GCCAAAGACA AAATCTATAT
1151 GGGTCCGGAA CGCCGCAGTA TGGTGA

```

This corresponds to the amino acid sequence <SEQ ID 1966; ORF 614.a>:

```

a614.pep
1  MAAFNALDGK KEDNGQIEYS QFIQQVNNGE VSGVNIIEGSV VSGYLIKGER
51  TDKSTFFFTNA PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL
101 LIGAWFYFMR MQTGGGGKGG AFSFGKSRAR LLDKDANKVT FADVAGCDEA
151 KEEVQEIVDY LKAPNRYQSL GGRVPRGILL AGSPGTGKTL LAKAIIAGEAG
201 VPFFSISGSD FVEMFVGVA SRVRDMFEQA KKNAPCIIFI DEIDAVGRQR
251 GAGLGGGND ERLQTLNQLLV EMDGFESNQT VIVIAATNRP DVLDPALQRP
301 GRFDRQVVVP LPDIRGREQI LNVHSHKKVPL DKSVDLLSLA RGTGPGFSGAD
351 LANLVNEAAL FAGRRNKVKV DQSDLKTPKT KSIWVRNAAV W*

```

m614/a614 99.7% identity in 391 aa overlap

```

              10      20      30      40      50      60
m614.pep      MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
              |||||||
a614           MAAFNALDGKKEDNGQIEYSQFIQQVNNGEVSGVNIIEGSVVSGYLIKERTDKSTFFFTNA
              10      20      30      40      50      60

              70      80      90      100     110     120
m614.pep      PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG
              |||||||
a614           PLDDNLIKTL LDKNVRVKVT PEEKPSALAA LFYSLLPVLL LIGAWFYFMR MQTGGGGKGG
              70      80      90      100     110     120

              130     140     150     160     170     180
m614.pep      AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
              |||||||
a614           AFSFGKSRARLLDKDANKVTFADVAGCDEAKEEVQEIVDY LKAPNRYQSLGGRVPRGILL
              130     140     150     160     170     180

              190     200     210     220     230     240
m614.pep      AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGASRV RDMFEQAKKNAPCIIFI
              |||||||
a614           AGSPGTGKTL LAKAIIAGEAGVPFFSISGSD FVEMFVGASRV RDMFEQAKKNAPCIIFI
              190     200     210     220     230     240

              250     260     270     280     290     300
m614.pep      DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRP DVLDPALQRP
              |||||||
a614           DEIDAVGRQRGAGLGGGNDEREQTLNQLLVEMDGFESNQT VIVIAATNRP DVLDPALQRP
              250     260     270     280     290     300

              310     320     330     340     350     360
m614.pep      GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDESVDLLSLARGT PGFSGADLANLVNEAAL
              |||||||
a614           GRFDRQVVVPLPDIRGREQILNVHSHKKVPLDKSVDLLSLARGT PGFSGADLANLVNEAAL

```

985

	310	320	330	340	350	360
	370	380	390			
m614.pep	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
a614	FAGRRNKVKVDQSDLKTPKTKSIWVRNAAVWX					
	370	380	390			

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1967>:

```

g615.seq
1  ATGTGGAAC  GCGGCGGCG  CGGTGtcggC  AGCTTtgaag  agcagcGaAT
51  agatgCCGCC  GGCAAACCAC  AATGCGGAaA  gcaggCtgaa  gcGGTTgcgC
101  GGCagcTTca  tGCCGCCTCC  TcGTCCaGCC  ACGtttGgca  gattttggac
151  aggcgcAGGa  ATTTGCcgCc  gcgtgcggCA  agtatgtcgc  gcCAttgtgc
201  cacttcttcg  gcggacggTG  cttcgtcgaT  gctgCATTCG  TACagcagga
251  aatcgagggt  ttcttcgatg  acggGgatgg  AttccgTTTG  GataAgCTgc
301  ttgagttcgt  tcatgactGt  TCgGATAcgg  aaatcgggaa  aatgcggtct
351  gAaagggcct  CAGACGGCat  tggATTATTT  GCTGTGCAGG  AAgcgcgttg
401  cctcttccca  tttgcCGGAA  AtgATGTCGg  gtacggcctg  cAGGGATttg
451  gCGACGGcat  cgtcgatttg  ccgGcggtgc  ttCcgcgctc  ggtttGTTca
501  agacgtagcc  gaCGACGagg  ttgcggtcGC  CGGGGtggcC  GATGCCGAGG
551  CGCAGGCGGt  aatagtctgC  CGTGCCGAGT  TTTGCctgAA  TGTCTTTCAA
601  GCCGTTGTGT  CcgcCGttgc  cgcCGCCGAG  TTTGAATTTg  ATCCGTCCGC
651  AAGGGATGTC  GAGTTCGTCG  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACCGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCCGGT  TTGAGCAGCC  AAACATCGCC  GTCGGGCAGG  GCGGCGCGGG
801  CAACTTCGCC  GAAGAATTTT  TTTTCTTCTT  TAAACGAAGC  CTTCCATTTT
851  CACGCCAGTT  CGTCGAGGAA  CCAAAAGCCC  GCATTGTGGC  GGGTCTGTTC
901  GTATTCTTTG  CCCGGGTTGC  CCAAGCCGAC  AACCATTTTG  ATTGTGttcg
951  acatgataTT  TtccgtgTTT  CTgTCGaatg  cggtCtgaAG  GCTTCAGacg
1001  gcatggTtaT  TCTTCTTgaT  TTtgaACcg  tgtgcggCGC  GCTTCTTTGG
1051  GGTTCGATCA  CAGCGGCGGG  TACACTTCGA  TCGGTCGCC  GTCGCGCAGC
1101  GCGGTGTCGT  CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1968; ORF 615.ng>:

```

g615.pep
1  MWKRRRRGVG  SFEEQRIDAA  GKPQCGKQAE  AVARQLHAAS  SSSHVWQILD
51  RRRNLPPRAA  SMSRHCAATSS  ADGASSMLHS  YSRKSRVSSM  TGMDSVWISC
101  LSSFMTVRIR  KSGKCRLLGL  QTALDYLLCR  KRVASSHLPE  MMSGTACRDL
151  ATASSICRRC  FRARFVQDVA  DDEVAVAGVA  DAEAQAVIVC  RAEFCLNVFO
201  AVVSAVAAAE  FEFDPsARDV  EFVVDDEDF  GFDFVELCKR  GNRLSGTVHE
251  RGRFEQPNIA  VGQGGAGNFA  EEEFFFFKRS  LPFPRQFVEE  PKARIVAGLF
301  VFFARVAQAD  NHFDCVRHDI  FRVSVCEGLK  ASDGMVILLD  FERVCGALLW
351  GRSTAGGTLR  CGRRRAAACH  L*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1969>:

```

m615.seq  Length: 1116
1  ATGCGGAAAA  GCGGTTGGCG  CGGTTTCGGC  AGCTTTGAAA  AGCAGTGAGT
51  AAATGCTGCC  TGCAAACCAC  AATGCCGAGA  GCAGGATAAA  GCGGTTGCGT
101  GGCAGATTCA  TGCTTGTTC  TCTTCAAGCC  ATGTCTGGCA  TAGTTTGAT
151  AGGCGCAGGA  ATTTTCCGCC  GCGTGC GGCC  AGCATATCGC  GCCAAACGGC
201  AATTTCTTCG  GCGGAGGGGG  CATCGTCTAT  GCTGCATTCG  TAGAGCAGGA
251  AATCGAGGGT  TTCTTCGATG  ACGGGGATGG  ATTTCGTTTG  GATAAGCTGC
301  TTGAGTTCGG  TCATGACTGT  TCGGATATGG  AAATCGGGAA  CATGCCGTCT
351  GAAAGGGCTT  CAGACGGCAT  CGGGTCATTT  GCTGTGCAGG  AAGCGGGTTG
401  CTTCTTCCCA  TTTGCCGGCA  AGGATGTCGG  GTATGGCTTG  CAGGGATTTG
451  GCGACGGCAT  CGTCAATCTG  TCGGCGGTGT  .TCCGTA CTG  GGTGTTGTTCA
501  GGACATAGCC  GACGACGAGG  TTGCGGTTCG  CCGGGTGGCC  GATGCCGAGG
551  CGCAGGCGGT  AATAGTCTGC  CGTGCCGAGT  TTTGCCTGAA  TGTCTTTCAA
601  GCCGTTGTGT  CCGCCGTTGC  CGCCGCCGAG  TTTGAATTTG  ATCCGTCCGC
651  AGGGAATGTC  GAGTTCGTCG  TGGACGACGA  GGATTCTTTC  GGGTTTGATT
701  TTGTAGAACT  GTGCAAGCGC  GGCAACTGCC  TGTCCGGAAC  GGTTCATGAA
751  CGTGGCAGGT  TTGAGCAGCC  AAACGTTCGC  GTCGGGCAGG  GCGGCACGGG

```

986

```

801 CGACTTCGCC GAAGAATTTT TTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGTCGAATG CTGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTGCGGCGC GCTTCTTTTG
1051 GGTGCATCAA CAGCGGGCGG TACACTTCGA TCGGGTCGCC GTCGCGCAGC
1101 GCGGTGTCGT CTTTGA

```

This corresponds to the amino acid sequence <SEQ ID 1970; ORF 615>:

```

m615.pep Length: 372
1 MRKRRWRGFG SFKQXVNA CKPQCREQDK AVAQIHACS SSSHVWHS LD
51 RRRNFPPRAA SISQTAISS AEGASSMLHS XSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRC XRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFQ
201 AVVSAVAAAE FEFDPSAGNV EFVVDDEDFE GFDFVELCKR GNCLSGTVGE
251 RGRFEQPNVA VGQGGTGDFE EEEEEFFKXS LPFPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCVXHDI FRVSVECCCLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAAACR L*

```

Computer analysis of this amino acid sequence gave the following results:

Homology with a predicted ORF from *N. gonorrhoeae*

m615/g615 86.8% identity in 371 aa overlap

m615.pep	10	20	30	40	50	60
	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAQIHACSSSSHVWHS LDRRRNFPPRAA					
g615	10	20	30	40	50	60
	MWKRRRRGVGSFEEQRIDAAGKPGQCGKQAEAVARQLHAASSSSHVWQILDRRRNLPPRAA					
m615.pep	70	80	90	100	110	120
	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
g615	70	80	90	100	110	120
	SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSFMVTRIRKSGKCR LKGL					
m615.pep	130	140	150	160	170	180
	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRCXRTGFVQDIADDEVAVARVA					
g615	130	140	150	160	170	180
	QTALDYLLCRKRVASSHLPENMSGTACRDLATASSICRRCFRARFVQDVADDEVAVAGVA					
m615.pep	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPSAGNV EFVVDDEDFE GFDFVELCKR					
g615	190	200	210	220	230	240
	DAEAQAVIVCRAEFCLNVFQAVVSAVAAAEFEFDPSARDVEFVVDDEDFE GFDFVELCKR					
m615.pep	250	260	270	280	290	300
	GNCLSGTVHERGRFEQPNVAVGQGGTGDFAE EEEEEFFKXSLPFPRQFVEE PKTRIVACLF					
g615	250	260	270	280	290	300
	GNRLSGTVHERGRFEQPNIAVGQGGAGNFA EEEEEFFKXSLPFPRQFVEE PKARIVAGLF					
m615.pep	310	320	330	340	350	360
	VFFARVAQADNHFDCVXHDI FRVSVECCCLKASDGMVILLDFERVCGALLWGRSTAGGTLR					
g615	310	320	330	340	350	360
	VFFARVAQADNHFDCVRHDI FRVSVECCGLKASDGMVILLDFERVCGALLWGRSTAGGTLR					
m615.pep	370					
	CGRRRAAACRLX					
g615	370					
	CGRRRAAACRLX					

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1971>:

```
a615.seq
1   ATGCGGAAAC GGC GGCGGCGG CCGGTGTCGGC AGCTTTGAAG AGCAGCGAAT
51  AGATGCCGCC GGCAAACCAC AATGCGGAAA GCAGGCTGAA GCGGTTGCGC
101 GGCAGCTTCA TGCCGCCTCC TCGTCCAGCC ACGTTTGGA GATTTTGGAC
151 AGGCGCAGGA ATTTGCCGCC GCGTGCGGCA AGTATGTCGC GCCATTGTGC
201 CACTTCTTCG GCGGATGGTG CGTCGTCGAT GCTGCATTCG TACAGCAGGA
251 AATCGAGGGT TTCTTCGATG ACGGGGATGG ATTCGGTTTG GATAAGCTGC
301 TTGAGTTCGG TCATGACTGT TCGGATATGG AAATCGGGAA CATGCCGTCT
351 GAAAGGGCTT CAGACGGCAT CGGGTCATTT GCTGTGCAGG AAGCGGGTTG
401 CCTCTTCACA TTTGCCGGCA AGGATGTCGG GTATGGCTTG CAGGGATTTG
451 GCGACGGCAT CGTCAATCTG TCGGCGGTG TTCCGTA CTG GGTGTGTTCA
501 GGACATAGCC GACGACGAGG TTGCGGTCGC CCGGTGCGC GATGCCGAGG
551 CGCAGGCGGT AATAGTCTGC CGTGCCGAGT TTTGCCTGAA TGTCTTTCAA
601 GCGGTTGTGT CCACCGTTGC CGCCGCCGAG TTTGAATTTG ATCCGTCGCG
651 AGGGAATGTC GAGTTCGTCG TGGACGACGA GGATTCTTC GGGTTTGATT
701 TTATAAAACT GCGCAAGGGC GGCAACTGCC TGTCCGGAAC GGTTCATGAA
751 CGTGGTCGGC TTGAGCAGCC AGACATCGCC GTCGGGCAGG GTAGCACGGG
801 CGACTTCGCC GAAGAATTTT TTTTCTTCTT TAAATGAAGC CTTCCATTTT
851 CACGCCAGTT CGTCGAGGAA CCAAAAACCC GCATTGTGGC GTGTCTGTTT
901 GTATTCTTTG CCCGGGTTGC CCAAGCCGAC AACCATTTTG ATTGTGTTTG
951 ACATGATATT TTCCGTGTTT CTGCCGAATG CCGTCTGAAG GCTTCAGACG
1001 GCATGGTTAT TCTTCTTGAT TTTGAACGCG TTTGCGGCGC GCTTCTTTTG
1051 GGTGATCAA CAGCGGCGG TACACTCGA TCGGTCGCC GTCGCGCAGC
1101 GCGTGTCTGT CTTTGA
```

This corresponds to the amino acid sequence <SEQ ID 1972; ORF 615.a>:

```
a615.pep
1   MRKRRRRGVG SFEEQRIDAA GKPCGKQAE AVARQLHAAS SSSHWQILD
51  RRRNLPPRAA SMSRHCATSS ADGASSMLHS YSRKSRVSSM TGMDSVWISC
101 LSSVMTVRIW KSGTCRLKGL QTASGHLLCR KRVASSHLPA RMSGMACRDL
151 ATASSICRRX FRTGFVQDIA DDEVAVARVA DAEAQAVIVC RAEFCLNVFO
201 AVVSTVAAAE FEFDPSAGNV EFVVDDEDF GFDFIKLRKG GNCLSGTVHE
251 RGRLEQPDIA VGQGSTGDEA EEEEEFFK*S LPPPRQFVEE PKTRIVACLF
301 VFFARVAQAD NHFDCV*HDI FRVSAECRLK ASDGMVILLD FERVCGALLW
351 GRSTAGGTLR CGRRRAACR L*
```

m615/a615 90.3% identity in 371 aa overlap

	10	20	30	40	50	60
m615.pep	MRKRRWRGFGSFEKQXVNAACKPQCREQDKAVAWQIHACSSSSHWVHSLDRRRNFP	PRAA				
a615	MRKRRRRGVGSFEEQRIDAAAGKPCGKQAEAVARQLHAASSSSHVWQILDRRRNLPPRAA					
	10	20	30	40	50	60
m615.pep	SISRQTAISSAEGASSMLHSXSRKSRVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
a615	SMSRHCATSSADGASSMLHSYSRKSRSVSSMTGMDSVWISCLSSVMTVRIWKSGTCRLKGL					
	70	80	90	100	110	120
m615.pep	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
a615	QTASGHLLCRKRVASSHLPARMSGMACRDLATASSICRRXRTGFVQDIADDEVAVARVA					
	130	140	150	160	170	180
m615.pep	DAEAQAVIVCRAEFCLNVFQAVVS	AVAAAEFEFDPSAGNVEFVVDDEDF	GFDFIKLRKG			
a615	DAEAQAVIVCRAEFCLNVFQAVVSTVAAAEFEFDPSAGNVEFVVDDEDF	GFDFIKLRKG				
	190	200	210	220	230	240
m615.pep						
a615						
	250	260	270	280	290	300

988

```

m615.pep      GNCLSGTVHERGRFEQPNVAVGQGGTGDFAEFFFFFFFKXSLPFPQFVEEPKTRIVACLF
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615          GNCLSGTVHERGRLEQPDIAVGQGSTGDFAEFFFFFFFKXSLPFPQFVEEPKTRIVACLF
                250      260      270      280      290      300

                310      320      330      340      350      360
m615.pep      VFFARVAQADNHFDVCXHDIFRVSVCECLKASDGMVILDFERVCGALLWGRSTAGGTLR
|||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
a615          VFFARVAQADNHFDVCXHDIFRVSAECLKASDGMVILDFERVCGALLWGRSTAGGTLR
                310      320      330      340      350      360

                370
m615.pep      CGRRRAAACRLX
|||||:||||:
a615          CGRRRAAACRLX
                370

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1973>:

```

g616.seq
1  atgtcgaaCA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACCGCCACA ATGCGGGCTT TTGGTTCCTC GACGAAC TGG
101 CGTGGAAATG GAAGGCTTCG TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTTGCCCGCG CCGCCCTGCC CGACGGCGAT GTTTGGCTGC TCAAACCGGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATC
301 CCTTGC GGAC GGATCAAATT CAAACTCGGC GgcggcaacG gcgGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGcagac tattaCCGCC
401 TGCGCCTCGG CATCGgccaC CCCGGCgacc gcaacctCGT CGTcggttac
451 gtcttgAaCa aaccgagcgc gGaagcaccg Ccggcaaatc gacgatgCCG
501 TCGccaaATC CCTGcagggc gtaccCGACA TcaTTCCGg caaatgggaa
551 gaggcaacgc gcTTCCTGCA CAGCAATAA TccaatGCCG TCTGaagccc
601 ttTcagacgg cattttcccg atttccgTAT CcGAaCagtc atgaacgaac
651 tcaagcAGcT tatCCAAACg gaaTccateC ccgtcatcga agaaaccctc
701 gatttcctgc tGTACGAATG cagcAtcgcac gaagCAccgt ccgccgaaga
751 agtggcacaa TGcgcgcaca tactTGccgc acgcgGcgGC AAATtcCTgc
801 gcctgtccaa aatctgcCaa aCGTGGcTGG ACgAGGAGGC GGCatgAAgc
851 tGCCGgcgAA CCgtttcaGc ctgctTTCCG CATTGTGGTT TGCCGGCGGc
901 atctATtCgc tgctcttcaa AGCTGccgaC ACCGCGCCGC CGCCGTTTCC
951 ACATTtcgaC AAAGCAGCAC ACCTTGCCCT GTTTTTCGCA CAaatCTTgt
1001 tTctGGCCAA AGCATTCAAA ACCGGAAGAC TTCCCATCCC CTACCGCAGC
1051 CTGATTGCGT TCGCCTTCTG TTTTGCCGTC GGCAGCGAAT GCGCGCAGGC
1101 ATGGTTTACC GCAACGCGAA CCGGCAGTTT GGGCGATGTC CTTGCCgACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTGCCG CGCGTTCTGC CTGCCGcccg
1201 gactaa

```

This corresponds to the amino acid sequence <SEQ ID 1974; ORF 616.ng>:

```

g616.pep
1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSQAVAAAL AQFYKIKPEE ILVVHDELDI
101 CGRIKFKLKG GNGGHNGLK DIQAKLGTAD YYRLRLGIGH PGDRNLVVG Y
151 VLNKPSAEAP PANRRRRIQI PAGRTRHFR QMGRGNALPA QQIIQCRLKP
201 FQAFSRFPY PNSHERTOAA YPNGIHPRHR RNPFRPAVRM QHRRSTVRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRG GGMKLPNRFS LLSALWFAGG
301 IYSLLFKAAD TAPPPFPFHD KAHLALFFA QILFLAKAFK TGKLPIPYRS
351 LIAFAFCAV GSECAQAWFT ATRTGSLGDV LADLTGAALA LFAARSACRP
401 D*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1975>:

```

m616.seq
1  ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAC TGG
101 CGTGGAAATG GAAGGCTTCA TTAAAGAAG AAAAAAATT CTTCGGCGAA
151 GTCGCCCCTG CCGCCCTGCC CGACGGCGAC GTTTGGCTGC TCAAACCTGC
201 CACGTTTCATG AACCGTTCCG GACAGGCGGT TGCCGCGCTT GCACAGTTCT
251 ACAAATCAAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GCGGCAACG GCGGACACAA
351 CGGCTTGAAA GACATTcagG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCAGTAC GGAACA.CCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CTTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGGGAA

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989

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551 GAAGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTCAGACGG CATGTTCCCG ATTTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCTC
701 GATTTCCTGC TCTACGAATG CAGCATAGAC GATGCCCCCT CCGCCGAAGA
751 AATTGCCGCT TGGCGCGATA TGCTGGCCGC ACGCCGCGGA AAATTCCTGC
801 GCCTATCCAA ACTATGCCAG ACATGGCTTG AAGAGGAACA AGCATGAATC
851 TGCCACGCAA CCGCTTTATC CTGCTCTCGG CATTGTGGTT TGCAGGCAGC
901 ATTTACTCAC TGCTTTTCAA AGCTGCCGAA ACCGCCAC CGCCTTTTCC
951 GCATTTTGAC AAAGTGGCGC ACCTCGCCCT GTTTTTCGCA CAAATCTGGC
1001 TTCTGACCAA AGCATTGAGA ACCGACAACC GCCCATCCC CTATCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGTTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTC CTTGCCGACC
1151 TGACGGGCGC AGCCCTTGCC CTCTTTACCG CGCGAGCTGC CTGCCGCCCG
1201 GACTAA

```

This corresponds to the amino acid sequence <SEQ ID 1976; ORF 616>:

m616.pep

```

1  MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKKAS FKEEKKFFGE
51  VARAALPDGD VWLLKPATFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGGHNLK DIQAKLGTA YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTDXRRCRQI PASHTRHPCR QMGRSNPLPA QMTRCRLKP
201 FQTACSRFPY PSHDRTOAA YPNRIHPRHR RNPFPALRM QHRRCP LRR
251 NCRLARYAGR TRRKIPAPIQ TMPDAXRGT SMNLPRNRFI LLSALWFAGS
301 IYSLLFKAAE TAPPPFPFHD KVAHLALFFA QIWLTLKAFR TDNRPIPYRS
351 LMVFALCFAL FSECAQAWFT ATRTGLGDV LADLTGAALA LFTARAACRP
401 D*

```

m616/g616 86.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
g616	MSNTIKMVVGLGNGPGKEYEQTRHNAGFWFLDELAWKKASFKEEKKFFGEVARAALPDGD					
	10	20	30	40	50	60
	70	80	90	100	110	120
m616.pep	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNLK					
g616	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGGNGGHNLK					
	70	80	90	100	110	120
	130	140	150	160	170	180
m616.pep	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
g616	DIQAKLGTADYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
	190	200	210	220	230	240
m616.pep	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
g616	QMGRSNPLPAQMTRCRLKPFQTACSRFPYPNSHRTQAAAYPNRIHPRHRNPRFPALRM					
	190	200	210	220	230	240
	250	260	270	280	290	300
m616.pep	QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPDAXRGTSMNLPRNRFILLSALWFAGS					
g616	QHRRCP LRRRNCRLARYAGRTRRKIPAPIQTMPDAXRGTSMNLPRNRFILLSALWFAGS					
	250	260	270	280	290	300
	310	320	330	340	350	360
m616.pep	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTLKAFRTDNRPIPYRSLMVFALCFAL					
g616	IYSLLFKAAETAPPPFPFHDKVAHLALFFAQIWLTLKAFRTDNRPIPYRSLMVFALCFAL					
	310	320	330	340	350	360
	370	380	390	400		
m616.pep	FSECAQAWFTATRTGLGDVLADLTGAALALFTARAACRPDX					
g616	FSECAQAWFTATRTGLGDVLADLTGAALALFAARSACRPDX					
	370	380	390	400		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1977>:

990

a616.seq

```

1   ATGTCAAACA CAATCAAAAT GGTGTGCGGC TTGGGCAACC CGGGCAAAGA
51  ATACGAACAG ACACGCCACA ATGCGGGTTT TTGGTTCCTC GACGAAGTGG
101 CGTGGAATG GAAGGCTTCA TTAAAGAAG AAAAAAAT CTTCGGCGAA
151 GTCGCCCCGTG CTACCGTGCC CGACGGCGAT GTCTGGCTGC TCAAGCCGAC
201 CACGTTTCATG AACCGTTCGG GACAGGCGAGT TGCCGCCCTT GCGCAGTTTT
251 ATAAATCAA ACCCGAAGAA ATCCTCGTCG TCCACGACGA ACTCGACATT
301 CCCTGCGGAC GGATCAAATT CAAACTCGGC GGCGGCAACG GTGGACACAA
351 CGGCTTGAAA GACATTCAGG CAAACTCGG CACGGCAGAC TATTACCGCC
401 TGCGCCTCGG CATCGCCAC CCGGGCGACC GCAACCTCGT CGTCGGCTAT
451 GTCCTGAACA AACCCAGTAC GGAA.CACCG CCGACAGATT GACGATGCCG
501 TCGCCAAATC CCTGCAAGCC ATACCCGACA TCCTTGCCGG CAAATGTGAA
551 GAGGCAACCC GCTTCCTGCA CAGCAAATGA CCCGATGCCG TCTGAAGCCC
601 TTTTCAGACGG CATGTTCCCG ATTCCATAT CCGAACAGTC ATGACCGAAC
651 TCAAGCAGCT TATCCAAACC GAATCCATCC CCGTCATCGA AGAAACCCCTC
701 GATTTTCCTGC TGTACGAATG CAGCATCGAC GACGCACCAT CCGCCGAAGA
751 AGTGGCACAA TGGCGCGACA TACTTGCCGC ACGCGCGGCG AAATTCCTGC
801 GCCTGTCCAA AATCTGCCAA ACGTGGCTGG ACGAGGAGGC GGCATGAAGC
851 TGCCGCGCAA CCGCTTCAGC CTGCTTCCG CATTGTGGTT TGCCGCGCGC
901 ATCTATTTCGC TGCTCTTCAA AGCTGCCGAC ACCGCGCCGC CGCCGTTTCC
951 GCATTTTCGAC AAAGCAGCAC ACCTTGCCCT GTTTTTTCGCA CAAATCTGGC
1001 TTTTGACCAA AGCATTCAAA ACCGGAAGAC TTCCCATCCC CTACCGCAGC
1051 CTGATGGTCT TTGCCCTCTG TTTCGCCCTC TTCAGCGAAT GCGCGCAGGC
1101 ATGATTTACC GCAACGAGAA CCGGCAGTTT GGGCGATGTT CTTGCCGATA
1151 TGGCAGGTAC GGTTCCTCGA CTCTTGCCG CCCGCGCCGC CGACCGCCCG
1201 GACTGA

```

This corresponds to the amino acid sequence <SEQ ID 1978; ORF 616.a>:

a616.pep

```

1   MSNTIKMVVG LGNPGKEYEQ TRHNAGFWFL DELAWKWKAS FKEEKKFFGE
51  VARATLPDGD VWLLKPTTFM NRSGQAVAAL AQFYKIKPEE ILVVHDELDI
101 PCGRIKFKLG GNGGHNGLK DIQAKLGTD YRLRLGIGH PGDRNLVVG
151 VLNKPSTEXP PTD*RCRRQI PASHTRHPCR QM*RGNPLPA QOMTRCRLKP
201 FQTACSRFPY PNSHRTQAA YPNRIHPRHR RNPRFPARM QHRRRTIRRR
251 SGTMARHTCR TRRQIPAPVQ NLPNVAGRGG GMKLPNRNFS LLSALWFAGG
301 IYSLLFKAAD TAPPPPHFD KAAHLALFFA QIWLTLKAFK TGKLPPIYRS
351 LMVFALCFAL FSECAQA*FT ATRTGSIGDV LADMAGTVLA LFAARAADRP
401 D*

```

m616/a616 90.0% identity in 401 aa overlap

	10	20	30	40	50	60
m616.pep	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARAALPDGD					
a616	MSNTIKMVVGLGPNPGKEYEQTRHNAGFWFLDELAWKWKASFKEEKKFFGEVARATLPDGD					
	10	20	30	40	50	60
m616.pep	VWLLKPATFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
a616	VWLLKPTTFMNRSGQAVAALAQFYKIKPEEILVVHDELDIPCGRIKFKLGGNGGHNGLK					
	70	80	90	100	110	120
m616.pep	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
a616	DIQAKLGTDYYRLRLGIGHPGDRNLVVGYYLNKPSTEXPPTDXRCRRQIPASHTRHPCR					
	130	140	150	160	170	180
m616.pep	QMGSRNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPALRM					
a616	QMXRGNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPARM					
	190	200	210	220	230	240
m616.pep	QMGSRNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPALRM					
a616	QMXRGNPLPAQOMTRCRLKPFQTACSRFPYPNSHRTQAAYPNRIHPRHRNPRFPARM					
	250	260	270	280	290	300

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m616.pep    QHRRCP LRRRNCR LARYAGR TRRKIPAPIQTMPD MAXRGTS MNLPNRNFILLSALWFAGS
            ||||  :|||:  ||::  |||:||||:|::|:|  ||  :|:||||  |||||:|:|
a616        QHRRRTIRRRSGT MARHTC RTTRQIPAPVQNL PNVAGRGGGMKLPNRNFSLLSALWFAGG
            250      260      270      280      290      300

            310      320      330      340      350      360
m616.pep    IYSLLFKAAETAPPPFP HFDKVAHLALFFAQI WLLTKAFRTDNRPIPYRSLMVFALCFAL
            |||||:|||||:|||||:|||||:|||||:|||||:|  :  |||||:|:|
a616        IYSLLFKAADTAPPPFP HFDKAAHLALFFAQI WLLTKAFKTGKLPPIPYRSLMVFALCFAL
            310      320      330      340      350      360

            370      380      390      400
m616.pep    FSECAQAWFTATRTGSLGDV LADLTGAALALFTARAACRPDX
            |||||  |||||:|||||:|:|:|:|:|  ||||  ||||
a616        FSECAQAXFTATRTGSLGDV LADMAGTVLALFAARAADRPDX
            370      380      390      400

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1979>:

```

g619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGTCGGTT
51  GCGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
101 TCAACGTCAA AGGAGATTGG GACTTTGTCT TGCACCTGCG CCTGACCAAG
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACTCAACT
201 CTTCCAAACG CTGACCAACA ACCCGATTCT GACCCCTTCG ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGgtGTT TACGttcgGC
301 GCGGTGGGCT ATAcatccct gccgttgacg gGCAAATTCG GCTTTGAAct
351 GGTtGTtATG ATGGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCCGTC
401 AGGGCGGGCG CGATTtGCCG CACATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTtCC GCAGCCTTTC CTCGCTGCTT TCGCGCATGA TAGACCCCGA
501 AGAATTtACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 GCAGCGAGCT TTTAGGCATA GGCGCGCTGG TCCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC ACGAACGCTA CCGCTCGGAC GTACACCTTT TGGGGCGCGA
651 CCAAGCCGTC AATTtGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT TGTCGGCCCG
751 GTGAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 gtCCGTGCGC CATTCCGTCC GCCTGCcgat gacggtttGC gtcgGcggCA
851 TCCTCTTGGt cggCggacaA ACCGTATTTC AACACTTCTT GGCATGAag
901 gCggTATTAA GCGTGGTGGt cgAATTTCG ggcggactcG TTTTCCTCTA
951 TCTCGTTTtA AAACACAAA AATGA

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This corresponds to the amino acid sequence <SEQ ID 1980; ORF 619.a>:

```

g619.pep
1  MPSEKNIGFM AGSSRPLRVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSL YVF LQTL LVFTFG
101 GVGYTSPLT GKFGFELVVM MGSLLLFYT LIRQGGRLD LHMILIGVIFG
151 ILFRSLSSL SRMIDPEEFT AAQANMFAGF NTVRSELLGI GALVLLVSA
201 VVWHERYRSD VHLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
251 VSFGLLAAS LANHFSPSVR HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVL SVVVEFA GGLVFLYLVL KHKK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1981>:

```

m619.seq
1  ATGCCGCTCTG AAAAAAATAT CGGTTTTATG GCAGGAAGCA GCCGCCCCGT
51  GTGGGTCGCC TTTGCGCTGT TGCTGGTTTC CTGCCTCCTG TTTATGACGC
101 TCAACGTCAA AGGCGATTGG GATTTTGTtT TGCAACTGCG GCTGACCAAA
151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTGT CCACGCAACT
201 CTTCCAAACG CTGACCAATA ATCCGATTCT GACCCCTTCA ATTTTGGGTT
251 TCGATTGCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTt TACGTTCCGC
301 GCGGTGGGCT ATGCTTCCCT GCCGTTGACG GGCAAATTCG GCTTTGAAct
351 GGTGTCATG ATGGGCGGCT CGCTGCTGCT GTTCTACACG CTCATCAAC
401 AGGGCGGACG CGATTtGTTCG CGCATGATTT TAATCGGCGT GATTTTCGGG
451 ATTTTGTtCC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGATCCCGA
501 AGAATTtACC GCCGCGCAGG CGAATATGTT TGCCGGATTC AATACCGTCC
551 ACAGCGAGCT TTTGGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
601 GTCGTTTGGC GCGAACGCTA CCGCTTGGAC GTTTACCTTT TGGGGCGTGA
651 CCAAGCCGTC AATTtGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
701 TGCTTTGGAT TGCCGCATTG GTGGCGACGG CGACCGCCGT GGTTCGGCCC
751 TGAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAA CATTCCGTCC GCCTGCCGAT GACGTTTGT ATCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTGTTTC AACACCTGCT CGGTATGCAG

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901 GCAGTGTGA GCGTAGTAGT AGAATTTGCC GCGGACTCG TTTTCCTCTA
 951 TCTCGTTTTA AACACAAAA AATGA

This corresponds to the amino acid sequence <SEQ ID 1982; ORF 619>:

m619.pep
 1 MPSEKNIGFM AGSSRPLWVA FALLLVSCVL FMTLNVKGDW DFVLQRLTK
 51 LAALLMVAYA VGVSTQLFQT LTNNPILTPS ILGFDSLTVF LQTLNVFTFG
 101 GVGYASLPLT GKFGFELVVM MGSLLLFYT LIKQGRDLS RMILIGVIFG
 151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
 201 VVWRERYRLD VYLLGRDQAV NLGISYTRNT LWILLWIAAL VATATAVVG
 251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC IGGILLVGGQ TVFEHLLGMQ
 301 AVLSVVVEFA GGLVFLYLVL KHKH*

m619/g619 95.1% identity in 324 aa overlap

m619.pep	10	20	30	40	50	60
	MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLTKLAALLMVAYA					
g619	MPSEKNIGFMAGSSRPLRVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA					
	10	20	30	40	50	60
m619.pep	70	80	90	100	110	120
	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLNVFTFGGVGYASLPLTGKFGFELVVM					
g619	VGVSTQLFQTLTNNPILTPSILGFDSLTVFLQTLNVFTFGGVGYTSLPLTGKFGFELVVM					
	70	80	90	100	110	120
m619.pep	130	140	150	160	170	180
	MGSLLLFYTLIKQGRDLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
g619	MGSLLLFYTLIRQGRDLPHMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF					
	130	140	150	160	170	180
m619.pep	190	200	210	220	230	240
	NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL					
g619	NTVRSELLGIGALVLLVSAAVVWHERYRSDVHLLGRDQAVNLGISYTRNTLWILLWIAAL					
	190	200	210	220	230	240
m619.pep	250	260	270	280	290	300
	VATATAVVGVPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ					
g619	VATATAVVGVPVSFFGLLAASLANHFSPSVRHSVRLPMTVCVGGILLVGGQTVFEHFLGMK					
	250	260	270	280	290	300
m619.pep	310	320				
	AVLSVVVEFAGGLVFLYLVLKHKHXX					
g619	AVLSVVVEFAGGLVFLYLVLKHKHXX					
	310	320				

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1983>:

a619.seq
 1 ATGCCGCTCTG AAAAAAATAT CGGTTTATG GCAGGAAGCA GCCGTCCGTT
 51 GTGGGTTGCC TTTGCGCTGT TGCTGGTTTC CTGCATCCTG TTTATGACGC
 101 TCAACGTCAA AGGCGATTGG GATTTTGTTT TGCACCTGCG CCTGACCAAG
 151 CTTGCCGCGC TGCTGATGGT CGCCTATGCG GTCGGCGTTT CGACCCAGCT
 201 TTTTCAAACG CTGACCAACA ATCCGATTCT GACCCCTTCG ATTTTGGGTT
 251 TCGATTTCGT GTATGTGTTT TTGCAGACCT TGCTGGTGTT TACGTTGGGC
 301 GGCCTGGGCT ATGCTTCCCT GCCGTGACG GGCAAATTCG GCTTTGAACT
 351 GGTGCTTATG ATGGCGGCT CGCTGCTGCT GTTTTACACG CTCATCAAAC
 401 AGGCGGGGCG CGATTTGCCG CGTATGATT TAATCGGCGT GATTTTCGGG
 451 ATTTTGTTC GCAGCCTGTC GTCGCTGCTT TCGCGCATGA TCGACCCGA
 501 AGAATTTACG GCGGCGCAGG CGAATATGTT TGCCGATTTC AATACCGTCC
 551 ACAGCGAGCT TTTAGGCATA GGCGCGCTGA TTCTGCTCGT CAGCGCGGCG
 601 GTCGTTTGGC GCGAACGCTA CCGCTTGAC GTACACCTTT TGGGGCGCGA
 651 CCAAGCCATA AATTTGGGCA TCAGCTACAC GCGCAACACC TTATGGATAC
 701 TGCTTTGGAT TGCCGCGCTG GTGGCGACGG CGACCGCCGT TGTGCGCCCG

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751 GTAAGCTTTT TCGGGCTTCT CGCCGCCTCG CTTGCCAACC ACTTTTCCCC
801 GTCGGTCAAA CATTCCGTCC GCCTGCCGAT GACGGTTTGT GTCGGCGGCA
851 TCCTCTTGGT CGGCGGACAG ACCGTATTCG AACACTTCTT GGGCATGAAG
901 GCGGTATTAA GCGTGGTGGT CGAATTGCG GCGGACTCG TTTTCCTCTA
951 TCTCGTTTTA AGACACAAAA AATGA

```

This corresponds to the amino acid sequence <SEQ ID 1984; ORF 619.a>:

```

a619.pep
1  MPSEKNIGFM AGSSRPLWVA FALLLVSCIL FMTLNVKGDW DFVLHLRLTK
51  LAALLMVAYA VGVSTQLFOT LTNNPILTPS ILGFDSLYVF LQTLVFTFG
101 GVGYASLPLT GKFGFELVVM MGGSLLLFYT LIKQGGRLDP RMILIGVIFG
151 ILFRSLSSLL SRMIDPEEFT AAQANMFAGF NTVHSELLGI GALILLVSAA
201 VVWRERYRLD VHLLGRDQAI NLGISYTRNT LWILLWIAAL VATATAVVGPF
251 VSFFGLLAAS LANHFSPSVK HSVRLPMTVC VGGILLVGGQ TVFEHFLGMK
301 AVLSVVVEFA GGLVFLYLVL RHKK*

m619/a619 97.2% identity in 324 aa overlap

10      20      30      40      50      60
m619.pep MPSEKNIGFMAGSSRPLWVAFALLLVSCVLFMTLNVKGDWDFVLQRLRLTKLAALLMVAYA
a619      MPSEKNIGFMAGSSRPLWVAFALLLVSCILFMTLNVKGDWDFVLHLRLTKLAALLMVAYA
10      20      30      40      50      60

70      80      90      100     110     120
m619.pep VGVSTQLFOTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
a619      VGVSTQLFOTLTNNPILTPSILGFDSLYVFLQTLVFTFGGVGYASLPLTGKFGFELVVM
70      80      90      100     110     120

130     140     150     160     170     180
m619.pep MGGSLLLFYTLIKQGGRLSRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
a619      MGGSLLLFYTLIKQGGRLPRMILIGVIFGILFRSLSSLLSRMIDPEEFTAAQANMFAGF
130     140     150     160     170     180

190     200     210     220     230     240
m619.pep NTVHSELLGIGALILLVSAAVVWRERYRLDVYLLGRDQAVNLGISYTRNTLWILLWIAAL
a619      NTVHSELLGIGALILLVSAAVVWRERYRLDVHLLGRDQAINLGISYTRNTLWILLWIAAL
190     200     210     220     230     240

250     260     270     280     290     300
m619.pep VATATAVVGPPVSFFGLLAASLANHFSPSVKHSVRLPMTVCIGGILLVGGQTVFEHLLGMQ
a619      VATATAVVGPPVSFFGLLAASLANHFSPSVKHSVRLPMTVCVGGILLVGGQTVFEHFLGMK
250     260     270     280     290     300

310     320
m619.pep AVLSVVVEFAGGLVFLYLVLKHKKX
a619      AVLSVVVEFAGGLVFLYLVLKHKKX
310     320

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1985>:

```

g620.seq
1  ATGAAGAAAA CCCTGTTGGc AATTGTTGCC gtTTTCGCCT TAAGTGCCTG
51  CCGGCaggcg gaAGaggcac cgcgcCCTTT ACCCCGGCAG AtTAGCGacc
101 gttcggtcgg aCACTAttgC Agtatgaacc tgaccgaaca caacggcccc
151 aaagcccaga tttttttgaa cGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCGTcaag cagatgttcg GCTATACCAA GCTGCCCGAA GAGCCCAAAG
251 GCATCCGCGT GATTACGTT ACCGATATGG GCAATGTAC CGATTGGACG
301 AATCCTAATG CCGACACGGA GTGGATAGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG CGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA GGAGCAGGCT GAAAAATTG CAAAGGATAA AGCGCGCAAG
451 GTCGTCGGTT TTGACGATAT GCCCGATGCT TACATTTTCA AGTAA

```

This corresponds to the amino acid sequence <SEQ ID 1986; ORF 620.ng>:

```
g620.pep
1  MKKTLLAIVA VFALSACRQA EEAPPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTVK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWID AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDA YIFK*
```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1987>:

```
m620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTC CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1988; ORF 620>:

```
m620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

m620/g620 97.0% identity in 164 aa overlap

	10	20	30	40	50	60
m620.pep	MKKTLLAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
g620	MKKTLLAIVAVFALSACRQAEEAPPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP					
	10	20	30	40	50	60
	70	80	90	100	110	120
m620.pep	DQPVWFSTIKQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWMDAKKAFYVIDS					
g620	DQPVWFSTVKQMFGYTKLPEEPKGIRVIYVTDMGNTDWTNPNADTEWIDAKKAFYVIDS					
	70	80	90	100	110	120
	130	140	150	160		
m620.pep	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDTYIFKX					
g620	GFIGGMAEDALPFGNKEQAEKFAKDKGGKVVGFDMPDAYIFKX					
	130	140	150	160		

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1989>:

```
a620.seq
1  ATGAAAAAAA CCCTGTTGGC AATTGTTGCC GTTTCGCCT TAAGTGCCTG
51  CCGGCAGGCG GAAGAGGGAC CGCCGCCTTT ACCCGGCAG ATTAGCGACC
101 GTTCGGTCGG ACACTATTGC AGTATGAACC TGACCGAACA CAACGGCCCC
151 AAAGCCCAGA TTTTCTTGAA CGGCAAACCC GATCAGCCCG TTTGGTTCTC
201 CACCATCAAG CAGATGTTTCG GCTATACCAA GCTGCCCGAA GAGCCTAAAG
251 GCATCCGCGT GATTTACGTT ACCGATATGG GCAATGTTAC CGATTGGACG
301 AATCCCAATG CCGACACGGA GTGGATGGAT GCGAAAAAAG CCTTTTACGT
351 CATCGACAGC GGCTTTATCG GCGGTATGGG TGCGGAAGAC GCGCTGCCGT
401 TCGGCAACAA AGAGCAGGCT GAGAAATTTC CAAAGGATAA AGGCGGTAAG
451 GTTGTCGGTT TCGACGATAT GCCTGATACC TATATTTTCA AATAA
```

This corresponds to the amino acid sequence <SEQ ID 1990; ORF 620.a>:

```
a620.pep
1  MKKTLLAIVA VSALSACRQA EEGPPPLPRQ ISDRSVGHYC SMNLTEHNGP
51  KAQIFLNGKP DQPVWFSTIK QMFGYTKLPE EPKGIRVIYV TDMGNVTDWT
101 NPNADTEWMD AKKAFYVIDS GFIGGMAED ALPFGNKEQA EKFAKDKGGK
151 VVGFDMPDT YIFK*
```

995

m620/a620 100.0% identity in 164 aa overlap

```

              10      20      30      40      50      60
m620.pep      MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
              |||||
a620           MKKTLIAIVAVSALSACRQAEEGPPPLPRQISDRSVGHYCSMNLTEHNGPKAQIFLNGKP
              10      20      30      40      50      60

              70      80      90      100     110     120
m620.pep      DQPVWFSTIKQMFQYTKLPEEPKGIRVIYVTDMGNVTDWTNPADTEWMDAKKAFYVIDS
              |||||
a620           DQPVWFSTIKQMFQYTKLPEEPKGIRVIYVTDMGNVTDWTNPADTEWMDAKKAFYVIDS
              70      80      90      100     110     120

              130     140     150     160
m620.pep      GFIGGMGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDITYIFKX
              |||||
a620           GFIGGMGAEDALPFGNKEQA EKFAKDKGGKVVGFDMPDITYIFKX
              130     140     150     160

```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1991>:

```

g622.seq
1   ATGCAactta ccgctgtcgg ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAag ctggCGTTTG CCGCCGCCGC CCTGCCAGAA gccgTccgCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGCGAT TCGGAAGaaa TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACACGCTGGA TATGCAGGAA ACCGTGCGCC ACGCCTTCCG CGTTGCCTGC
301 GGCTTGGAAT CGATGGTTT GGGCGAGCCG CAGATTTTGG GGCAGATTAA
351 AGATGCGGTG CGTGCGGCTC AAGAACAGGA AAGTATGGGG GCAAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAAGAAAGT CCGTACCGAT
451 ACCGCTGTGC GCGAAAATTC GGTTCGATG GCTTCCGCGT CCGTCAAGTT
501 GCGCGAACAG ATTTTCCCG ACATCGGCGA TTGAACGTA TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAAT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTTA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTGGTGG TTTCTCAAC GCGAGCCAG
751 CTTCCGATAG TCGGCAAAGG CATGGTCGAA CGCGCATTGA AACAGCGTCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGC GATATTGAAG
851 CGGAAGTCGG CGATTTGAAC GATGCGTATC TTTATACGGT GGACGATATG
901 GTCACATCG TCCAAAGCGg caaggaggca aggcagaaag ccgccgcCgc
951 cgccgaaacy ctggTGTCGG AAAAGGTTGC CGAATTGTGC AGGCAGCAGC
1001 AGGCAGGCA GagcgttcCG CTGATTAAGG CTTGCGGGA CGAGGCGAG
1051 AAAGCGCGCA AGCAGGTGTT GGAAAATGCG ATGAAACAGC TTGCCAAAGG
1101 CGcaaCGGCG GAAGaggttt TGgaacggct gtccgtcCAA CTGACCAACA
1151 AGCTGCTGCA TTCGCCAACT CAAACCTTGA ATAAGCGGG GGAAGAAGAT
1201 AAAGatttGG TTCATGCCgt cGCGCAGATt tatcatttGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1992; ORF 622.ng>:

```

g622.pep
1   MQLTAVGLNH QTAPLSIREK LAFAAAALPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYTLDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGOIKDAV RAAQEQUESMG AKLNALFQKT FSVAKEVRTD
151 TAVGENSVMT ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKN
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMP LFMLDLAVPR DIEAEVGD LN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSV P LIKALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAVAQI YHLDK*

```

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1993>:

```

m622.seq
1   ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCCGCCGC CCTGCCATAA GCCGTCCGCA
101 ATCTTGCCCC AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGCACCG AGCTTTACTG CGTCGGTGAT TCGGAAGAAA TCATCCGATG
201 GCTTGCCGAT TACCACAGTT TGCCGATTGA AGAAATCCGT CCGTATCTGT
251 ACGCGCTGGA TATGCAGGAG ACTGTGCGCC ATGCTTTCGG CGTCGCGCTGC

```

```

301 GGGCTGGATT CGATGGTGT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCCGTT AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCCGTTG CTAAGAGGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCCTATG GCTCCGCTT CCGTCAAATT
501 GCGGGAACAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GCGCAGGCGA AATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCCAGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTC ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTCT GCACGATTAC GACGTAGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCATTG TCGGCAAAGG CATGGTGGAG CGTGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTCATG TTGATTGGC AGTGCCCGCT GACATTGAAG
851 CGGAAGTCGG CGATTGTAAT GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCCG
951 CGCCGAAACG CTGGTGTCCG AGAAAGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTGATTAAGG CGTTGCGGGA CGAGGCGCAG
1051 AAAGCGCGCA AACAGGTGTT GGAAATGCC ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGAACGGCT GTCCGTCCAA CTGACCAACA
1151 AGCTGTGCGA TTCGCCGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGG TTCATGCCGT CGCGCAGATT TATCATTGG ACAAATAA

```

This corresponds to the amino acid sequence <SEQ ID 1994; ORF 622>:

m622.pep

```

1  MQLTAVGLNH QTAPLSIREK LAFAAAAALPK AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIR PYLYALDMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEQUESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHDY DVVVSSTASQ
251 LPIVGKGMVE RALKQROSMPL FMLDLAVPR DIEAEVGLND DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVPLI KALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSVQ LTNKLLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*

```

m622/g622 98.8% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
g622	MQLTAVGLNHQTAPLSIREKLAFAAAAALPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
g622	SEEIIRWLADYHSLPIEEIRPYLYTLDQMOTVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	RVAQEQUESMGKKLNALFQKTFFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
g622	RAAQEQUESMGAKLNALFQKTFFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
g622	LFIGAGEMIELVATYFAAKNPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
	190	200	210	220	230	240
m622.pep	DVVVSSTASQLPIVGKGMVERALKQROSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
g622	DVVVSSTASQLPIVGKGMVERALKQROSMPLFMLDLAVPRDIEAEVGLNDAYLYTVDDM					
	250	260	270	280	290	300
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
g622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQQGRQSVPLIKALRDEGEKARKQVLENA					
	310	320	330	340	350	360
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAQAQIYHLDKX					
g622	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAQAQIYHLDKX					

370 380 390 400 410

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1995>:

```
a622.seq
1   ATGCAACTTA CCGCTGTCGG ACTCAATCAT CAAACCGCAC CTTTAAGCAT
51  ACGGGAAAAG CTGGCGTTTG CCGCGGCCTG CCTGCCCGAA GCCGTCCGCA
101 ATCTTGCCCG AAGCAATGCG GCAACGGAGG CGGTAATCCT TTCTACCTGC
151 AACCGTACCG AGCTTTACTG TGTAGGTGAT TCGGAAGAAA TCATCCGTTG
201 GCTCGCAGAC TATCACAGCC TTCCCATAGA AGAAATCAGC CCCTACCTTT
251 ATACTTTGGG GATGCAGGAG ACTGTGCGCC ATGCTTTCCG CGTCGCCTGC
301 GGCTTGGAAT CGATGGTGTT GGGCGAGCCG CAGATTTTAG GACAGATTAA
351 GGATGCGGTC AGGGTTGCTC AAGAGCAGGA AAGTATGGGT AAGAAACTCA
401 ATGCCCTGTT CCAAAAAACC TTTTCTGTTG CTAAGAGAGT CCGTACCGAT
451 ACTGCCGTCG GCGAAAACTC GGTTCATG GCTTCCGCTT CCGTCAAGTT
501 GGCAGAGCAG ATTTTCCCG ACATCGGCGA TTTGAATGTC TTGTTTATCG
551 GTGCGGGTGA GATGATTGAG CTGGTTGCCA CTTATTTTGC CGCCAAAAGT
601 CCCC GGCTGA TGACGGTTGC CAACCGGACG CTGGCGCGTG CACAGGAGTT
651 GTGCGACAAG CTCGGTGTCA ACGCCGAACC GTGCCTGCTG TCCGATCTGC
701 CTGCCATTTT GCATGAGTAC GACGTGGTGG TTTCTTCAAC GGCAAGCCAG
751 TTGCCCATTG TCGGCAAAGG TATGGTGGAG CGCGCATTGA AACAAAGGCA
801 GAGTATGCCG TTGTTTATGC TTGACTTGGC CGTGCCGCGA GACATTGAGG
851 CGGAAGTCGG AGATTTGAAC GATGCCTATC TTTATACGGT GGACGATATG
901 GTCAATATCG TCCAAGCGG CAAGGAGGCA AGGCAGAAGG CCGCCGCCGC
951 CGCCGAAACG CTGGTGTCG AGAAGGTTGC CGAATTTGTC AGGCAGCAGC
1001 AGGGCAGGCA GAGTGTCCCG TTAATCAGGG CATTGAGGGA TGAGGGAGAG
1051 AAAGCGCGCA AACAGGTCTT GGAATATGCG ATGAAACAGC TTGCCAAAGG
1101 CGCAACGGCA GAAGAGGTTT TGGAAAGGCT GTCGATCCAA CTGACCAACA
1151 AGTGCTGCA TTCGCGGACC CAAACCTTGA ATAAGGCGGG GGAAGAAGAT
1201 AAAGATTGTTG TTCACGCCGT CGCGCAGATT TATCATTTGG ACAAATAA
```

This corresponds to the amino acid sequence <SEQ ID 1996; ORF 622.a>:

```
a622.pep
1   MQLTAVGLNH QTAPLSIREK LAFAAACLPE AVRNLARSNA ATEAVILSTC
51  NRTELYCVGD SEEIIRWLAD YHSLPIEEIS PYLYTLGMQE TVRHAFRVAC
101 GLDSMVLGEP QILGQIKDAV RVAQEESMG KKLNALFQKT FSVAKEVRTD
151 TAVGENSVSM ASASVKLAEQ IFPDIGDLNV LFIGAGEMIE LVATYFAAKS
201 PRLMTVANRT LARAQELCDK LGVNAEPCLL SDLPAILHEY DVVVSSTASQ
251 LPIVGKGMVE RALKQRQSMF LFMLDLAVPR DIEAEVGLDN DAYLYTVDDM
301 VNIVQSGKEA RQKAAAAAET LVSEKVAEFV RQQQGRQSVF LIRALRDEGE
351 KARKQVLENA MKQLAKGATA EEVLERLSIQ LTNKLHSPT QTLNKAGEED
401 KDLVHAQAQI YHLDK*
```

m622/a622 98.1% identity in 415 aa overlap

	10	20	30	40	50	60
m622.pep	MQLTAVGLNHQTAPLSIREKLAFAAAALPKAVRNLARSNAATEAVILSTCNRTELYCVGD					
a622	MQLTAVGLNHQTAPLSIREKLAFAAAACLPEAVRNLARSNAATEAVILSTCNRTELYCVGD					
	10	20	30	40	50	60
m622.pep	SEEIIRWLADYHSLPIEEIRPYLYALDMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
a622	SEEIIRWLADYHSLPIEEISPYLYTLGMQETVRHAFRVACGLDSMVLGEPQILGQIKDAV					
	70	80	90	100	110	120
m622.pep	RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
a622	RVAQEESMGKKLNALFQKTFSVAKEVRTDTAVGENSVSMASASVKLAEQIFPDIGDLNV					
	130	140	150	160	170	180

998

	190	200	210	220	230	240
m622.pep	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHDY					
a622	LFIGAGEMIELVATYFAAKSPRLMTVANRTLARAQELCDKLGVNAEPCLLSDLPAILHEY					
	190	200	210	220	230	240
	250	260	270	280	290	300
m622.pep	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
a622	DVVVSSTASQLPIVGKGMVERALKQRQSMPLFMLDLAVPRDIEAEVGDLDNDAYLYTVDDM					
	250	260	270	280	290	300
	310	320	330	340	350	360
m622.pep	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQGRQSVPLIKALRDEGEKARKQVLENA					
a622	VNIVQSGKEARQKAAAAAETLVSEKVAEFVRQQGRQSVPLIRALRDEGEKARKQVLENA					
	310	320	330	340	350	360
	370	380	390	400	410	
m622.pep	MKQLAKGATAEEVLERLSVQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
a622	MKQLAKGATAEEVLERLSIQLTNKLLHSPTQTLNKAGEEDKDLVHAVAQIYHLDKX					
	370	380	390	400	410	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 1997>:

g624.seq
 1 ATGATCCGTT ATCTTTTAAT TGCCTGCGGC GGCATCTCCC TGCTGTTGGG
 51 GATAATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTAC
 101 TCTCCGCCGC CTGCTGGGCA AAGGCAtccc cgcgcTTTca ccgCTGGCTG
 151 CACcgGCacc gCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AGATTTTCGC CATCAGCATG AtaaccgcAt
 251 cctgcctcat gatcctTTtgg CattTTCccc aacnctggtg ggtcGGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGcacc ATacggatgt gGcacAGacC
 351 cgaatCTTGA

This corresponds to the amino acid sequence <SEQ ID 1998; ORF 624.ng>:

g624.pep
 1 MIRYLLIACG GISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFHRWL
 51 HRRHYFGPMV HNWEQNGAVP RKAKIFAISM ITASCLMIFW HFPQXWWVGA
 101 VSSVFCSLVT IRMWHRPES*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 1999>:

m624.seq
 1 ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCT TACTGTTGGG
 51 TATCATCGGC ATTTTTTTCG CGCTGTTGCC GACCACGCCG TTCGTACTGC
 101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTTA CCGCTGGCTG
 151 CACCGGCACC GCTATTTTCGG CCCGATGGTT CATAACTGGG AACAAAACGG
 201 CGCAGTGCCG CGCAAAGCCA AAATATTCGC CATCAGTATG ATGACCGCAT
 251 CCTGCCTGAT AATGTTTTCG CAGTTTCCCC AACGCTGGTG GGTGCGGGCG
 301 GTTTCATCGG TTTTGTGTC CCTGTGCGCC ATATGGATGT GCGCAGGCC
 351 CGAATCTTGA

This corresponds to the amino acid sequence <SEQ ID 2000; ORF 624>:

m624.pep
 1 MIRYLLIACG CISLLLGIIG IFPLPLPTTP FVLLSAACWA KASPRFYRWL
 51 HRRHYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLMIFW QFPQRWWVGA
 101 VSSVFCSLVA IWMWRPES*

m624/g624 91.6% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLPTTPFVLLSAACWAKASPRFYRWLHRRHYFGPMV					
g624	MIRYLLIACGGISLLLGIIGIFLPLPTTPFVLLSAACWAKASPRFHRWLHRRHYFGPMV					
	10	20	30	40	50	60

999

	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	: : : : :					
g624	HNWEQNGAVPRKAKIFAISMITASCLMIFWHFPQXWWVGAVSSVFCSLVTIRMWHRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2001>:

```
a624.seq
1  ATGATACGTT ATCTTTTAAT TGCCTGCGGC TGCATTTCCC TGCTGTTGGG
51  TATCATCGGC ATTTTTTTTC CGCTGTTGCC GACCACGCCG TTCGTA CTGC
101 TCTCCGCCGC CTGCTGGGCA AAGGCATCCC CGCGCTTTCA CCGCTGGCTG
151 CACCGGCACC GCTATTTCGG TCCGATGGTT CATAACTGGG AACAAAACGG
201 CGCAGTGCCG CGCAAAGCCA AAATATTTCG CATCAGTATG ATGACCGCAT
251 CCTGCCTGAT AATGTTTGG CAGTTTCCCC AACGCTGGTG GGTCGGGGCG
301 GTTTCATCGG TTTTGTGTC CCTGTGCGC ATATGGATGT GGCGCAGGCC
351 CGAATCTTGA
```

This corresponds to the amino acid sequence <SEQ ID 2002; ORF 624.a>:

```
a624.pep
1  MIRYLLIACG CISLLLGIIG IFLPLLPTTP FVLLSAACWA KASPRFHRWL
51  HRHRYFGPMV HNWEQNGAVP RKAKIFAISM MTASCLIMFW QFPQRWWVGA
101 VSSVFCSLVA IWMWRRPES*
```

m624/a624 99.2% identity in 119 aa overlap

	10	20	30	40	50	60
m624.pep	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFYRWLHRHRYFGPMV					
	: : : : :					
a624	MIRYLLIACGCISLLLGIIGIFLPLLPTTPFVLLSAACWAKASPRFHRWLHRHRYFGPMV					
	10	20	30	40	50	60
	70	80	90	100	110	120
m624.pep	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	: : : : :					
a624	HNWEQNGAVPRKAKIFAISMMTASCLIMFWQFPQRWWVGAVSSVFCSLVAIWMWRRPESX					
	70	80	90	100	110	120

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2003>:

```
a625.seq
1  ATGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
101 CGGTGCTTCC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
351 GTAA
```

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2004>:

```
g625.seq
1  atGTTTGCAA CCAGGAAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
51  ACGGtCTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC AttgCCGCGC
101 CGGtCGttcC CATGATAGAG GCAAGTGCCG TACCGACGGC AAGCAGGGCG
151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAGGGG ATATATTCTT
251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
301 AAACGAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TGATTTTGCC
351 gTAA
```

This corresponds to the amino acid sequence <SEQ ID 2005; ORF 625.ng>:

```
g625.pep
1  MFATRKMKKM TMCTRRVRSW LAFSSGRIIS IAAPVVPMIE ASAVPTASRA
```

1000

51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG IYSSTSACAT VWIPADAPKT
 101 KLNGMRKSNV QKAVILP*

The following partial DNA sequence was identified in *N. meningitidis* <SEQ ID 2006>:

m625.seq
 1 ATGTTTGCAA CCAGGAAAT GAAGAAGATG ACGATGTGCA CGCGGCGGGT
 51 ACGGTTTTGG TTGGCTTTCA GCAGCGGACG AATCATCAGC ATTGCTGCGC
 101 CGGTCGTTCC CATGATAGAG GCAAGTGCCG TACCGACGCG AAGCAGGGCG
 151 GTGTTGAGCT TGGGTGTGCC GTTCAAGTCG CCCCAAACCA AAATGCCGCC
 201 TGAAATGGTG TACAGGGCAA GCAGCAGCAG GATGAAAGGG ATGTATTCTT
 251 CAACGAGTGC GTGTGCGACG GTATGGATAC CGGCGGACGC GCCAAAACCC
 301 AAACGTAACG GGATGAGGAA GAGCAATGTC CAAAAGGCGG TAATTTTGCC
 351 GTAA

This corresponds to the amino acid sequence <SEQ ID 2007; ORF 625>:

m625.pep
 1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
 51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
 101 KLNGMRKSNV QKAVILP*

m625/g625 98.3% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
g625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKGmYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	:					
g625	PQTkmppEMVYRASSSRMKGiYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

This corresponds to the amino acid sequence <SEQ ID 2008; ORF 625.a>:

a625.pep
 1 MFATRKMKKM TMCTRRVRFW LAFSSGRIIS IAAPVVPmie ASAVPTASRA
 51 VLSLGVPFKS PQTkmppEMV YRASSSRMKG MYSSTSACAT VWIPADAPKT
 101 KLNGMRKSNV QKAVILP*

m625/a625 100.0% identity in 117 aa overlap

	10	20	30	40	50	60
m625.pep	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
a625	MFATRKMKKMTMCTRRVRFWLAFSSGRIISIAAPVVPmieASAVPTASRAVLSLGVPFKS					
	10	20	30	40	50	60
	70	80	90	100	110	
m625.pep	PQTkmppEMVYRASSSRMKGmYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
a625	PQTkmppEMVYRASSSRMKGmYSSTSACATVWIPADAPKTKLNGMRKSNVQKAVILPX					
	70	80	90	100	110	

The following partial DNA sequence was identified in *N. gonorrhoeae* <SEQ ID 2009>:

g627.seq
 1 ATGTCCGGCC TTTGGAAACC CGAACACCCG GGATTTGAAA TCCTCGGCAG
 51 CCGTTACGCC CTGCAAAACC TTGTCCGCGA TGTCATCCTG ATTACATTGA
 101 CCGCCGTATC TATGGCAATC ACGCCCAAAC AAGTCCGCGC AGGCAACGAA
 151 TTCAACTTTG AACCCATCGC CGAAGTGGGC AAATCTTCC TCGGCATCTT
 201 CATCACCATC TTCCCCGTCC TGAGCATTCT GAAAGCAGGC GAGGCAGGCG
 251 CGCTGGGCGG GGTGGTATCG CTGGTTCACG ATACGGCAGG TCATCCGATT
 301 AATACGATGT ATTTCTGGAT GAGCGGCATA TTGTCCGCAT TCTTGGATAA
 351 CGCGCCCACT TATCTCGTGT TTTTCAATAT GGCGGGCGGC GATGCCCAAG
 401 CCTTAATGAC GGGTCCCCTG TTTCATTcgc TGCTGGCGGT TTCTAtgggT
 451 tCGGTATTCA TGGGCGCACT GaccTACATc gGCAAcgcac cgaactTCAT